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Result
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2: pir2:*
3: pir3:*
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417	420.5	420.5	422.5	426	428	428.5	430.5	434	435	435.5	436.5	437.5	442	442.5	:
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ALIGNMENTS

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C;Accession: C33548
R;Kipps, T.J.; Tomhave, B.; Pratt, L.P.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr.
A;Reference number: A33548; MUID:89345575; PMID:2503826
                                                                                                                                                                                          RESULT
C33548
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                                                                                                          Ig heavy chain V-i region (783) - human
C;Species: Homo sapiens (man)
C;Jate: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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J. Exp. Med. 175, 983-991, 199
A;Tille: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH9952
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Similarity 79.2%;
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7; Mismatches
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R. Wartin, T., Duffy, S.F., Carson, D.A., Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A,Tille: Evidence for somatic selection of natural a
A,Reference number: PH0952, MUID:92202880, PMID:1552
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A;Title: Complete nucleotide sequence of the membrane form of A;Reference number: S14683; MUID:90332450; PMID:2115996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-133 <KIP>
                                                                                /Species: Homo sapiens (man)
/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
/Accession: PH0953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;34-117/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 Accession: S14683; S08047
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Matches
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                                                                                                                                          heavy chain V region (G6+ CLL-SIC)
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1-15/Domain: signal sequence #status predicted <SIG>
16-627/Product: Ig mu chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-627 <FRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor, membrane-bound (clone 201) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                             AQKFQGRVTMTADGSTSTAYMELNSLRSEDTATYYCAR-----QQNGGWYEGPLLEPRPD 115
                                                                                                                                                                                                                                                                                                                                                             OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 79
                                                                                                                                                                                                                                                                                                                                                                                     QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                               ----ALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                               AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGWY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR-----QQNGGWYEGPLLEPRPD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPY8SGWY---
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.1%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.1%; Score 509.5; DB 2
72.7%; Pred. No. 4.7e-39;
cive 10; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                      10,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 509.5; DB 2;
Pred. No. 2.5e+38;
0; Mismatches 13;
                    of natural autoantibodies
30; PMID:1552291
                                                                                                                                          human
                                                                                                                                      (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the human IgM heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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RESULT
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A;Molecule t
A;Residues:
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                                                                                                                                                                                                                                                                          Matches
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F;99-104/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;15-98/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g heavy chain V region
                                                                                                                                                                                                                                                                                                                       ;31-35/Region: immunoglobulin homology <IMM>;31-35/Region: complementarity-determining 1;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: DNA
;Residues: 1-116 <MAR>
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;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
;Accession: PH0959
                                                                                                                                                                                                                         Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                             68-98/Region: framework 3
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68-98/Region:
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Exp. Med. 175,
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 107
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-135 <MAR>
                                                                                             AQKFQGRYTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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GQGTLVTVSS 116
                                GQGTMVTVSS 130
                                                                   AQKFQGRVTITADESTSTAYMEL
                                                                                                                                       QVQLVQSGAEVKKPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duffy, S.F.; Carson, D.A.; Kipps, T.J.
175, 983-991, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR--NGYCGGDCYSRWELLRFDFS 118
                                                                                                                                                                                                                                                                                                            complementarity-determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (G6+ T-L26) - human (fragment
                                                                                                                                                                                                                      72.8%;
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                                                                                                                                   /KVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not shown
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                                                                                                                                                                                                   Score 501; DB 2;
Pred. No. 2.4e-38;
8; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        natural autoantibodies PMID:1552291
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                                                                                                                                                                                                                                      Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1933 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0958
                                                                                                                Query Match
Best Local Similarity 76.9
Conservative
                                                                                                                                                                                                                                                                                                       Superfamily: immunoglobulin V region; immunoglobulin homology keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                       Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
Exp. Med. 175, 983-991, 1992
:Title: Evidence for somatic selection of natural autoantibodies.
Reference number: PH0952; MUID:92202880; PMID:1552291
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                                                                                                                                                                                                                                                                                                                                                                                 Status: nucleic
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EXP. Med. 175, 983-991, 1992
Title: Evidence for somatic selection of natural autoantibodies
Reference number: PH0952; MUID:92202880; PMID:1552291
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Best Local Similarity
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58-98/Region:
                                                                                                                                                                                                                                                                35/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                 1-122 <MAR>
AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGGWYEGELLEEREDALDIW
                                                   QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-120 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRYTMTADGSTSTAYMELNSLRSEDTAIYYÇARQQNGGWYEGPLLEPRPDALDIW 120
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                                                                                                                                                                                                                                                       immunoglobulin homology < IMM>
                                                                                                                                                                                                                complementarity-determining 2 framework 3
                                                                                                                                                                                        complementarity-determining 3
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                                                                                                                                          72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.4%; Score 498; DB 2; 77.7%; Pred. No. 4.6e-38;
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                                                                                                                                     Score 498; DB 2;
Pred. No. 4.6e-38;
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                                                                                                                        Mismatches
                                                                                                                                                       Length 122;
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A;Molecule type: DNA
A;Residues: 1-119 <M
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
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                                                                                                                                                            99-107/Region:
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: $46390; MUID:94254092; PMID:8196048
A;Accession: $46394
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C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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1;Residues: 1-132 <FIG>
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Species: Homo sapiens (man)
Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #te
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                                                                                                                                                                                                                                                                                     -30/Region: framework
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                                                                                                                                                                                                                                                                                                  words: heterotetramer;
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                                                                                                Local Similarity
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1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARTQLPAADTG-ILEWLPSYYYYM 119
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                                                                                                                                                                                                                                                                                                                                                                                 acid sequence not shown
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                                                                                          72.3%;
76.2%;
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                                                                        9;
                                                               Score 497.5; DB 2;
Pred. No. 5e-38;
9; Mismatches 11;
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                                                                                         Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                                                                                                                             Residues:
                                                                                                                                                                                                      Accession: PH0960
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iSpecies: Homo sapiens (man)
iDate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
iAccession: PH0960
                                                                                                                                                              Molecule type: DNA
                                                                                                                                                                               Status: nucleic acid sequence
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68-98/Region:
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Species: Homo sapiens (man)
Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
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Exp. Med. 175, 983-991, 1992
itle: Evidence for somatic selection of natural autoantibodies.
Reference number: PH0952; MUID:92202880; PMID:1552291
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sywords: heterotetramer; immunoglobulin
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complementarity-determining 2
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Exp. Med. 175, 983-991, 1992
;Title: Evidence for somatic selection of natural a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A33548; PH0956
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102; Conserv
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                                                                                   PRPDALDIWGOGTMVTVSS 130
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                                                                                                                              AOKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCAR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 <KIP>
                                                                                                                                                                                                                                                                                                                                                      complementarity-determining framework 3
                                                                                                                                                                                                                                                                                                                                                                                                     complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                          framework
                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin homology
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                   complementarity-determining 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sequence not shown
                                                             FDYWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GMDVWGQGTTVTVSS
                                                                                                                                                                                                                                                                                    71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEI) - human
                                                                                                                                                                                                                                                                                Score 494.5; DB Pred. No. 1e-37;
                                                                                                                                                                                                                                                                  8; Mismatches
                                                             129
                                                                                                                                                                                                                                                                                                                                                                                                                       <MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                              DB 2,
                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                              Length
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                                                                                                                            GPRLLADVLLWF-GELSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain variable region
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                                                                                                                                                                                                                                                              19,
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GGW 104
                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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Ig heavy chain V C;Species: Homo s

region (G6+ CLL-BRA) - human (fragment) sapiens (man)

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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996 C;Accession: PH0957 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. J. Exp. Med. 175, 983-991, 1992 A;Title: Evidence for sometic selection of natural autoantibodies. A;Reference number: PH0952; MUID:92202880; PMID:1552291 A;Accession: PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-125 < M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
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                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
2. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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                                                                                                                    S
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: PH0952;
A;Accession: PH0955
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                                                                                                                                                                                                                                                                                                              F;31-35/Region: 0
F;36-50/Region: 0
F;51-67/Region: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;31-35/Region: complementarity-determining;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;51-67/Region: complementarity-determining 2;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1-30/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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;15-98/Domain: immunoglo
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: heterotetramer; immunoglobulin
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Best Local
                                                                                                                                                                                Matches
                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                        99-115/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-125 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAINWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                   QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYYCARDGCSGGSCYFWGWF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ--QNG-----GWYEGPLLEPR 113
                                          AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG------WYEGPLLEP 112
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYYY-----
                                                                                        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                           complementarity-determining
framework 3
                                                                                                                                                                                                                                                                                                                                                              complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                         framework
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                                                                                                                                                                                                                                                                      complementarity-determining 3
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                                                                                                                                                                                                               71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%; Score 490.5; DB 2; 71.5%; Pred. No. 2.3e-37; tive 10; Mismatches 10;
                                                                                                                                                                                                      71.0%;
                                                                                                                                                                              10; Mismatches
                                                                                                                                                                                                   Score 488.5; DB 2
Pred. No. 3.5e-37;
                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                Indels
                                                                                                                                                                                                                         Length 127;
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C;Accession: B33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Experimental source: the sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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Search completed: December 30, 2003, Job time: 13.4614 secs
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
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                                                                                           113
                                                                                                                                   114 PDALDIWGQGTMVTVSS 130
                                                                                                                                                                               61
                                                                                                                                                                                                        61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG------WYEGPLLEPR 113
                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-126 <KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPDALDIWGQGTMVTVSS 130
                                                                                           ---MDVWGLGTTVTVSS 126
                                                                                                                                                                            AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARVSIFGVVQHYYYYY---
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                            70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                     Score 486; DB 2;
Pred. No. 5.8e-37;
9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human
                             11:03:13
                                                                                                                                                                                                                                                                                                                                                                                                  Length 126
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R, Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A; Title: Evidence for somatic selection of natural autoantibodies.
A; Reference number: PH0952; MUID:92202880; PMID:1552291
A; Accession: PH0954
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-132 < MAR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: framework 1
F;15-98/Domain: immunoglobulin homology < IMM>
F;31-35/Region: complementarity-determining 1
F:16-50/Domain: framework 7
F;13-5/Region: complementarity-determining 1
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-176
C; Superf
F;31-35/Region:
F;36-50/Region:
F;51-67/Region:
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Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                       F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1F;36-50/Region: framework 2
                                                                                      A;Residues: 1-136 <MAR>
C;Superfamily: immunobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
                                                                                                                                                                                                R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence rosmatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                      g heavy chain V region (G6+ T-L30) - human (fragment)
;Species: Homo sapiens (man)
;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
;Accession: PH0960
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Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQXFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYYYYGMDVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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  complementarity-determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.1%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 496; DB 2;
Pred. No. 7.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Recession: A33548
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       á
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: A33548; PH0956
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PH0957
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F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-129 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
  Ig heavy chain V region (G6+ CLL-BRA) -
C;Species: Homo sapiens (man)
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F;68-98/Region: framework 3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Local Similarity 67.8%;
hes 99; Conservative 10
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                                                                                                                                                                                                                                                                61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGG--------WYEGPLLE
                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-129 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                  h 71.9%; Score 494.5;
Similarity 73.4%; Pred. No. le-
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                                                                                                                                                                                  PRPDALDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR----GPRLLADVLLWF-GELSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          framework
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                                                                                                                                          --FDYWGQGTLVTVSS
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Pred. No. 7.9e-38;
0; Mismatches 11
                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                            human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1e-37;
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0958
                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-122 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0958
                                                                                                                                                                                                                                                                                           F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
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F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
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J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
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                                                                                                                                                                                                                                                           ;51-67/Region:
;68-98/Region:
                                                                                                                                                                                                                                                                                                                                                               Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                 Query Match
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Best Local Similarity
Matches 101; Conserv
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Species: Homo saptens (man)

;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                                                                                                                                                                              Local
61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTATYYCARQQNGGWYEGPLLEBRPDALDIW 120
                                                                                                                                                           100;
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                                                             QVQLVQSGAEVKKÞGSSVKVSCKASGGTFSSYAISWVRQAÞGQGLEWNGGIÍÞIFGTANÝ
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                                                                                                                                                                                                                                                      complementarity-determining 2 framework 3
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                                                                                                                                                                      72.4%;
76.9%;
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77.7%;
                                                                                                                                            Score 498; DB 2;
Pred. No. 4.6e-38;
8; Mismatches 14
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Pred. No. 4.6e-38;
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                                                                                                                                                                                  DB 2; Length 122,
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                                                                                                                                                                                                                                                                                                    C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-119 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                             R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-132 <FIG>
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan 1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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S46394
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Best Local :
                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARTQLPAADTG-ILEWLPSYYYYM 119
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                                                                                               Similarity
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QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVWGKGTMVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AOKFOGRVIMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPD---AL 117
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                                                                                                                                                    complementarity-determining 3
                                                                         Conservative
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                                                                                        72.3%;
76.2%;
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75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;; Score 498; DB 2;
;; Pred. No. 5.1e-38;
11; Mismatches 17
                                                                    Score 497.5; DB 2;
Pred. No. 5e-38;
9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 132
                                                                    Indels
                                                                                                            Length 119;
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C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R;FriedLander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM
A;Reference number: S14683; MUID:90332450; PMID:2115996
A;Accession: S14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;16-627/Product: Ig mu chain #status predicted <NAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-133 <KIP>
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F;15-98/Domain:
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                R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Tille: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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A; Accession:
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                                                                                       g heavy chain V region (G6+ CLL-SIC) - human (fragment); Species: Homo sapiens (man); Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text; Accession: PH0953
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PH0953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISMVRQAPGQGLEWMGGIIPIFGTANY 60
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                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                                                                                                                                                                                                                       ----ALDIWGOGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.1%; Score 509.5; DB 2 72.7%; Pred. No. 2.5e-38;
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                                                                                                           17-Apr-1993 #text_change
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Ig heavy chain V region (G6+ T-L26) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH9959
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Title: Evidence for H0952; MUID:92202880; PMID:1552291
A;Accession: PH9959
A;Status: nucleic acid sequence not shown
A;Residues: 1-116 <MARP
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F:15-284/Nomain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;31-35/Region: complementarity-determining F;36-50/Region: framework 2 F;51-67/Region: complementarity-determining F;68-98/Region: framework 3
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A;Molecule type: DNA
A;Residues: 1-135 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                              F;15-98/Domain: immunoglobulin homology <IMM>F;31-35/Region: complementarity-determining 1F;36-50/Region: framework 2
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                                                                                                                                                                                                                                                                                                                                                  F;99-104/Region:
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Best Local 9
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107
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                                       121 GOGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                       AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                      QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                 OVOLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISMVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                   AQKFQGRVTITADES:
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nilarity 75.2%;
Conservative
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                                                                                                                                                                                                                                                                                  72.8%;
                                                                                                                                                                                                                                                               8
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Pred. No. 2.4e-38;
8; Mismatches 9
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Pred. No. 2e-38;
8; Mismatches
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Post-processing: Minimum Match 0%
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A; Residues: 1-128 < MAR>
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Result

Minimum Maximum

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Database

Searched:

Sequence:

OM protein -

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442.5 64.3 122 2 C49590 Ig heavy 442.5 64.3 122 2 C49590 442.6 64.2 171 2 S23623 Ig heavy 437.5 63.6 160 2 PH1671 Ig heavy 436.5 63.4 109 2 PH1671 Ig heavy 435.5 63.3 129 2 S36260 Ig heavy 436.5 63.3 129 2 S46463 Ig heavy 437.5 62.6 127 2 S34014 Ig heavy 438.6 62.3 129 2 S464639 Ig heavy 439.5 62.6 127 2 S34014 Ig heavy 420.5 62.3 129 2 S46393 Ig heavy 420.5 61.1 127 2 S36271 Ig heavy
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C:Accession: PH0952
C:Accession: PH0952
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Biddence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
Ig heavy chain V-1 region (783) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: C33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: C33548
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
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framework 3
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Pred. No. 1.4e-39;
7; Mismatches 18
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APPLICANT: COTVAIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Francine
APPLICANT: Weber, Richard
APPLICANT: Hezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASCESEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy:
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-3-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR PRILING DATE: 2001-03-21

PRIOR PRILING DATE: 2001-03-25

PRIOR FILING DATE: 2001-03-25

PRIOR FILING DATE: 2001-05-25

**THROUGH OF TO NOTE: 2001-05-25
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1190
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Query Match 73.8%; Score 524.5; DB 12; Best Local Similarity 78.9%; Pred. No. 1.4e-42; Matches 105; Conservative 6; Mismatches 15;
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ORGANISM: Homo sapiens
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78.0%;
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                                                       Length 127;
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US-10-041-860-243
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                                                                                                                                                   Sequence 325, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 243
LENGTH: 127
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APPLICANT:
APPLICANT:
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Best Local Similarity 78.9%;
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: THEREOF
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                                                                                  Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
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                                                                                                                                                                                                                                                                                                                               DVWGQGTTVTVSS 127
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Yang, Xiao-Dong
Chen, Francine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 524.5; DB 12; pred. No. 1.4e-42; 6; Mismatches 15;
                           DIRECTED TO PDGFD AND USES
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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   US-10-269-805-45

US-10-9-880-748-1190

US-10-041-860-31

US-10-041-860-325

US-10-041-860-325

US-9-880-748-1971

US-09-880-748-1777

US-09-880-748-1610

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
Sequence 31, Appl
Sequence 243, App
Sequence 325, App
Sequence 1674, Ap
Sequence 1921, Ap
Sequence 973, App
Sequence 1777, Ap
Sequence 1778, Ap
Sequence 1778, Ap
Sequence 1610, Ap
Sequence 1575, Ap
Sequence 1575, Ap
Sequence 1576, Ap
Sequence 1572, Ap
Sequence 1572, Ap
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Sequence 1190, Ap
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ALIGNMENTS

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US-10-269-805-45
US-10-269-805-45
Sequence 45, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
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US-10-269-805-45
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SEQ ID NO 45
LENGTH: 125
TYPE: PRT
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
                                                                                                                                                                                                                                                Local
                 118 AMDVWGQGTTVTVSS 132
111 GMDVWGQGTTVTVSS 125
                                                                       61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDRGIAARSAY-----YY 110
                                                                                               61 AQKPQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGG----GGAYEDVWSGEYPEYY 117
                                                                                                                                                                                                                              105;
                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                        74.6%; Score 530.5; DB 1
77.8%; Pred. No. 3.7e-43;
rative 4; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.5
Best Local Similarity 73.7
Matches 98; Conservative
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                                                                                                                                                                                                                       16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BLyS binding scFv SEQ ID 1405.
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   WPI; 2002-114799/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          common variable immunodeficiency; acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2001; 2001WO-US19110
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                                                                SM,
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                                                                                                                            HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                            Barash SC,
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73.7%; Pred. No. 2.1e-39;
tive 13; Mismatches 19
                                                                Choi GH,
                                                            Vaughan T,
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                                                                Hilbert D;
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell correct of the invention and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and condesiciency (e.g. common variable immunodeficiency (CVID) and capuired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method con the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2079-2080; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
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                                                   invention.
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á 닭 S Matches 100; Best Local Query Match 61 Similarity AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYE--DVWSGEYPEYYA 118 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY Conservative 71.4%; Score 508; DB 23; 74.6%; Pred. No. 2.3e-39; 12; Mismatches 14; Length 254; Indels 8; Gaps 60 60

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AQKLQGRVTMTTDTSMSTAYMELRSLRSDDTAVYYCAR----AFEDYDILTGYY-HHDA

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RESULT 13
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This invention describes novel antibodies that immunospecifically bind to B Lymphcyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cyrostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiADDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
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17-OCT-2000;
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114 YWGQGTTVTVSS 125
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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1; 2000US-240816P.

2; 2001US-276248P.

2; 2001US-277379P.

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No. 1.3e-39;
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                          Antibodies against B Lymphocyte Stimulating polypeptides, up the diagnosis and treatment of cancers and immune disorders
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; 2000US-240816P.
; 2001US-276248P.
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Pred. No. 1.4e-39
2; Mismatches 20
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Claim 1;

Page 2018-2019; 3148pp;

English.

novel

antibodies that immunospecifically bind

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RESULT 11
ABP45565
    Query Match
Best Local Similarity
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                                                                                                                                               B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity and can be used in vaccines to and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. The antibodies bind to BLyS in associated with aberrant expression of BLyS. They are disease administered to treat diseases associated with aberrant BLyS expression diseases, e.g. systemic lumins ervitages, and autoimmune disorders and diseases, e.g. systemic lumins ervitages.
                                                     Sequence
                                                                                    diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                           This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-27379P.
25-MAY-2001; 2001US-293499P.
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                                                                                 invention.
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                           2283-2284; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         ainst B Lymphocyte Stimulating polypeptides, useful and treatment of cancers and immune disorders -
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75.9%;
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512.5; DB
No. 9e-40;
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              23;
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RESULT 12
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XX ABP45
XX ABP45
XX ID-AU
DE Human
XX Endown
AW tumou
KW immun
KW immun
KW Syste
KW Commo
XX Homo
XX L6-JU
PR 16-JU
PR 17-OC
PR 16-JU
PR 17-OC
PR 16-JU
PR 17-OC
PR 16-MP
PR 21-MP
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PR 10-JA
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                                                                           B Lymphocyte Stimulator (BLyS) polypoptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. The antisquese disease administered to treat disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and alloys expression diseases.
                           diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel antibodies that B Lymphocyte Stimulator (BLyS) polypeptides. BL
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17-0CT-2000; 2000US-240B1EP.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
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CAMBRIDGE ANTIBODY TECHNOLOGY.
            immunodeficiency syndrome
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ABP43990-ABP47228 represent
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This invention describes novel antibodies that immunospecifically bind to CC Brymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell crown for the control of the control of the control of the invention have control of the invention and differentiation. The antibodies of the invention have control of the invention and antihads activity of BLyS. The antibodies bind to BLyS in the expression and activity of BLyS. The antibodies bind to BLyS in control of the superior of BLyS in this way to diagnose disease the bind to blys control of the second of BLyS. They may also be control of the such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and control of the such as cancer, immune, and autoimmune disorders and control of the such as cancer, immune, and autoimmune disorders and control of the such as cancer, immune, and autoimmune disorders and control of the such as cancer, immune, and autoimmune disorders and control of the such as cancer, immune, and autoimmune disorders and control of the antibodies and fragments of the antibodies described in the method control of the antibodies and fragments of the antibodies described in the method control of the antibodies and fragments of the antibodies described in the method control of the antibodies and fragments of the antibodies control of the antibodies contro
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Best Local S
Matches 104
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16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114799/15
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       117
                                               118
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                                                                                                                                                                                                                                                                al Similarity 77.0
104; Conservative
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CAMBRIDGE ANTIBODY TI
                                                                                                                                                                                            QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
DMDVWGRGTLVTVSS 131
                                          AMDVWGQGTTVTVSS
                                                                             AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDTLG---YDILTG-YPPPYYYY
                                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE---YY 117
                                                                                                                                                                           QVQLQQSGAEVKKPGASVKVSCKASGYTFTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 2324-2325; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                            257
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; 2001US-276248P.
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; 2001US-293499P.
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                                                                                                                                                                                                                                                                                     72.4%;
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                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                              Score 514.5; DB 2
Pred. No. 5.9e-40;
                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                    YGISWVROAPGOGLEWMGWISAYNGNTKY
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                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                            Indels
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밁 Ś 밁 á В Ś

S 밁 Ś

61

AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYY--A 118 QVQLVESGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY Matches Query Match

103;

Conservative

8

Local

Similarity

72.2**%**; 76.9**%**;

Score 513; Pred. No. 7. Mismatches

DB 23;

Length 249;

Indels

10;

Gaps

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This invention describes novel antibodies that immunospecifically bind to CB Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiALDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC alsociated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be cand activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent che antibodies and fragments of the antibodies described in the method of the antibodies and invention.
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
Sequence
                                                                                                                                                                                                                                                                                                                                          Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114799/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TO
                                                                                                                                                                                                                                                                                                               Page 2103-2104; 3148pp; English.
 249
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2001US-276248P.
2001US-277379P.
2001US-293499P.
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ctor; B cell
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RESULT 8
ABP45767
ID ABP4
XX ABP4
AC ABP4
XX DF 19-A
XX DE Huma
XX DE Huma
XX Eumc
KW tumm
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 100
BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
                                                                                         19-AUG-2002
                                                                                                                    ABP45767;
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17-OCT-2000; 2000US-240816P.
16-MAR 2001; 2001US-276246P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention
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(CAMB-) CAMBRIDGE ANTIBODY TO
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                                                                BLyS
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                                                                                                                                                                                                                                                                                                                                                                         100;
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                                                                                                                                                                                                        VWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                       OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWMGWISIYSGNTDY
                                                            binding
                                                                                                                                                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                   73.1%; ilarity 75.8%; Conservative 1
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                                                             BCFV
                                                                                                                                         Protein;
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                                                                                      entry)
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                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                               Score 520; DB 23;
Pred. No. 1.8e-40;
2; Mismatches 18;
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8

ABP45599;

ABP45599 standard;

Protein;

257

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RESULT 9
ABP45599
ID ABP4
XX
AC ABP4
XX
                                                                                                                                                                                                                                                                                                                                                         This invention describes novel antibodies that immunospecifically bind to CC BLymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiAlDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS cand so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC associated with aberrant expression of BLyS. They may also be CC administered to treat disease associated with aberrant BLyS expression CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CUD) and CC immunodeficiency (e.g. common variable immunodeficiency (CUD) and CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent CC of the invention
                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-)
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systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                   114
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                                                                                                                                                                                                                                                                                             Similarity 75.8
00; Conservative
                                                                                                                                    VWGQGTTVTVSS 132
                                                                                                                                                                  AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR----SYYDILTGYYP--FGMD
                                                                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
                                                                                                                                                                                                                           OVOLOOSGAEVEKPGASVKVSCKASGYTFTSYGISWVRQAPGHGLEMMGWISAYNGNTNY
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                                                                                                                 VWGKGTMVTVSS
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2001US-293499P.
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2001US-276248P.
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                                                                                                                                                                                                                                                                                                        72.4%;
75.8%;
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                                                                                                                                                                                                                                                                                                         Score 514.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                    248;
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RESULT 6
ABP44962
IID ABP44
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ARAC ABP4
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ARAC ABP4
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DT 19-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, cantirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease cascoiated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be cadministered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and ciseases, e.g. systemic lupus crythematosus, rheumatoid arthritis, common variable immunodeficiency (c.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP47920-ABP47228 represent confirmation and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP44962 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention.
16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2002
                                                                                        15-JUN-2001; 2001WO-US19110
                                                                                                                                                       10-JAN-2002
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                     common variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BLyS binding scFv SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYYAMDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 2693-2694; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARVTSLYSSSSGGYY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                  immunodeficiency; acquired
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74.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BLyS) polypeptides. BLyS is a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies that immunospecifically bind to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                  immunodeficiency syndrome
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, immunosuppressive, immunostimulant, immunomodulatory, cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency (spotomome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
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                                                                                                                                                                                       Human BLyS binding
                                                                                                                                                                                                                                                         ABP45766;
                                                                                                                                                                                                                                                                                           ABP45766 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                     BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation;
                                                                                                                                                                                                                        19-AUG-2002
                                                                                      antiAIDS; vacci
systemic lupus
                                                                  immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antials; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosous; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention.
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CAMBRIDGE ANTIBODY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             --AMDVWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARGPRGGPYYDILTG----YYLSL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVMSGEYPEYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDAFDIWGQGTMVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             describes novel antibodies that immunospecifically bind to timulator (BLyS) polypeptides. BLyS is a member of the
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                                                                                                                                                                                       SCFV SEQ ID 1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%;
74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                              133
                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 521.5; DB 2
Pred. No. 1.3e-40;
8; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
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Homo sapiens

WO200202641-A1

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RESULT 4
ABP45663
ID ABP4
XX ABP4
XX ABP4
XX ABP4
XX BL3
CX Hum
XX BL3
KW Limi
KW Limi
KW Limi
KW an
KW cc
OX HC
OX HC
VXY HC
VXY BP
PN W'
XX BP
PN BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240B15P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
           Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; bystemic lupus erythematosis; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                   HUMAN GENOME
CAMBRIDGE ANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARD--PSPYYDILTGYFLPYY-MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWGKGTLVTVSS
                                                                                                                                                                 Barash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency; acquired immunodeficiency
                                                                                                                                                                 SC,
                                                                                                                                                                                                                      ANTIBODY
                                                                                                                                                                                                                                                 SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.9%;
78.0%;
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                                                                                                                                                              Choi GH,
                                                                                                                                                                                                                   TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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Pred. No. 5.5e-41
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                                                                                                                                                        Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                           Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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RESULT 5
ABP45910
ID ABP4
XX ABP4
AC ABP4
XX 19-A
XX 19-A
XX 19-A
XX 10-A
XX 11-A
XX 1
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Best Local :
                                                                                                                                       16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomoulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                          (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200202641-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2002 (first entry)
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                              HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                       ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                  TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AA.
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Pred. No. 7.5e-41;
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61pp;

English

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RESULT 2
AAY50950
ID AAY5
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 132
This invention describes a novel polynucleotide (I) (and complement, hybridizable polynucleotides) comprising a contiguous nucleotide secoding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting presence of inhibitory antibodies directed against factor VIII. The
                                                                                                                                                                                              New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human anti-factor VIII antibody VH clone IT-2 encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-1999.
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                                                                                                                                                            Fig
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                                                                                                                                                       61pp; English
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Pred. No. 1.6e-58;
; Mismatches 0;
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLy8; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                      Antibodies against B Lymphocyte
                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                                                                                                                                                                                                                                                       (HUMA-)
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                                                                                                                                                                                                                                                                                                                               (CAMB-)
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                                                                                                                                                                        diagnosis
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                                                                                                                           1; Page 1822-1823;
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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..le-57;
                                                                                                                                                              polypeptides, useful immune disorders -
                                                                                                                                                                                                                                                                              Hilbert
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This invention describes novel antibodies that immunospecifically B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention

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Result
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Maximum DB
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Perfect score:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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Human anti-factor
Human anti-factor
Human BLyS binding
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ID AAY50953
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XX
New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; VH protein.
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RESULT 15
Q924Q1
ID Q924Q
AC Q924Q
DT 01-DE
DT 01-MA
DE V23-D
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GN V23-D
OC Mus m
OC Eukar
OC Mamma
OX NCBI
RN [1]
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Q9QXE9
ID Q9QXE
AC Q9QXE
DT 01-MA
IT
OS Mus m
OC Eukar
OC Hamma
OX NCB1
RN [1]
RP SEQUE
RA Cleme
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DR SMART
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Matches 73
                                                                                                           Q924Q1 PRELIMINARY; PRT; 142 AA.
Q924Q1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
V23-D-J-C MU protein (Fragment).
V23-D-J-C MU.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ datal EMBL; AU225174; CAB65237.1; -. HSSP; P01810; 2FBJ INTERPO; IPR0037110; Ig-like. InterPro; IPR003706; Ig MHC. InterPro; IPR003596; Ig_v. IPR003596; Ig_v. Pfam; PF00047; ig; 1. SWART; SM00406; IGy; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mdammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Q9QXE9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVÓLQÓSGPELVKPGASVKMSCKASGÝTFTDYYMKMVKQSHGKSLEWIGDINPNNGGTSÝ
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117 AA; 13000 MW; CDDE2AF84D499734 CRC64;
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Matches 75
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 11
NON_TER 142 142
SEQUENCE 142 AA; 15622 MW;
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=C57BL/6;
106
                         121 VWGQGTTVTVSS 132
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                                                                                                                                                                                Similarity
                                                                                                                       QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                  NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRG-----
                                                                                                      QVQLQQPGTELVKPGASVKLSCKASGYTPTSYMMHWVKQRPGQGLEWIGNINPSNGGTNY
                                                                                                                                                                 Conservative
                                                                                                                                                           52.8%; Score 375.5; DB 11; Length 142; 56.8%; Pred. No. 1.3e-30; tive 17; Mismatches 25; Indels 15;
                                                                                                                                                                                                                     24A265CE4EA4318B CRC64;
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Search completed: December 30, 2003, 11:01:02 Job time: 32.169 secs

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Q9Y298
ID Q9Y29
AC Q9Y29
DT 01-NO
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 481 AA; 52105 MW;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 23, Last annotation updat
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with an 1964 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
19G VH protein precursor (Fragment).
IGG VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013490; AAH13490.1; ... InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003056; Ig_v.
                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.7e-31;
.4; Mismatches 27;
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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              Query Match
Best Local Similarity
Matches 74; Conserv
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Q925S2;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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SEQUENCE
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150
                     Conservative
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the same strain.";
Int. J. Radiat. Biol. Relat. Stu
EMBL; R2240167; AAK33732.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_Mic.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 170 AA; T7978 MW; 5
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE;
Signal.
1 19
                                                                                                                                                      STRAIN-BALB/c;
Cui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repair
of the irradiated mice by treatment with
                                                                                                                                                                                                                                                   "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01772; 2FB4
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Blood 92:496-506(1998)
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                G., Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
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59.1%;
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Rodentia;
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Last annotation updat
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Pred. No. 2.7
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    5042823CC6C10F38 CRC64;
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                                                                                                                              Chem. Med. 19:71-80(2001)
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53.1%; Score 377.5; DB 56.1%; Pred. No. 1e-30; tive 14; Mismatches

DB 11;

Length

170;

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Indels

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121

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RESULT 9
Q9ULB
AC Q9U
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Best Local 9
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OBWY24;
O1-MAR-2002 (TrEMBLrel. 2
O1-MAR-2002 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9UL89;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (Tremblrel. 23, Last annotation update)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

"Identification and characterization of SNC66, a Ig-like down-regulated in colorectal cancer.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283666; AAL36987.1; -.

InterPro; IPR007710; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003306; Ig_MHC.

InterPro; IPR003306; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS00035; IG_LIKE; 4.

PROSITE; PS00259; IG_MHC; 1.

SEQUENCE 497 AA; 53665 MW;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNC66 protein.
                                                                                                                                                                                               MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
"'' R., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Clin. Immunol. Immunopathol. EMBL; AF035025; AAD56261.1; HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                    ganoy
                                                                                                                                                  "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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Last sequence update)
Last annotation updat
                                                                           87:184-192(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  rheumatic
                                                                                                                                                                                                                          Kalis N.N.,
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RESULT 10
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Q925S3;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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NON_TER
NON_TER
SEQUENCE
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                         the same strain.";
Int. J. Radiat. Biol. Relat. Stud.
EMBL; AP240166; AAA43731.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                          Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after World J. Gastroenterol. 6:709-717(2000). [2]
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                         MRP3.
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                   Pfam; PF00047; ig; 1.

SMART; SM00466; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

SEQUENCE 147 AA; 16274 MW;
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                          STRAIN=BALB/c
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              PubMed=11819679;
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80; Conserv
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OVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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IPR003006;
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116 AA;
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ilarity 62.5%;
Conservative 1
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12605 MW;
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; Ig_MHC.
; Ig_v.
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                                          55.1%; Score 391.5; DB 11; 59.1%; Pred. No. 3.2e-32; tive 15; Mismatches 26;
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Last annotation updat
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Pred. No. 1.7e-32;
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                                                                                    800594A12B97191F CRC64;
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                                                                                                                                                                                                                                                                      their precursors improving irradiation in mice.";
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Best Local :
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Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBai
EMBL; BC009851; AAH09851.1; .
InterPro; IPR000005; HTHARAC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGY; 1.
SMART; SM00406; IGY; 1.
PROSITE; PS00041; HTH ARAC_FAMILY_1; 1.
PROSITE; PS00045; IG_KE; 5.
PROSITE; PS00040; IG_MHC; 3.
Hypochetical profein—
                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                     Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                O9UL92
O9UL92:
PRELIMINARY; PRT; 124 AA.
O9UL92:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q96GA6;
Q96GA6;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                       Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 6:
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      Immunol.
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   Immunopathol.
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Pred. No. 1e-34;
13; Mismatches 2
87:184-192(1998)
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RESULT 7
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Best Local :
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Best Local S
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                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MfC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITG; PS50835; IG_LIKE; 1.
NON TEP
                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma japonicum.", Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF282622; AAG01452.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9GYZ2
Q9GYZ2;
                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
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NON_TER 1 1 1
NON_TER 124 124
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      19
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                                                                                                       QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
NOKEKDRVIMTTDKSFSTAYMDLRSLRSADSAVYYCAR
                                                                                QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMMVRQAPGHGLEWIGYINPSRGYTNY
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119 AA;
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124 AA;
                                                                                                                                                                              Conservative
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13567 MW;
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; 13580 MW;
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                                                                                                                                                                       Score 417.5; DB 5;
Pred. No. 5.5e-35;
7; Mismatches 21;
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Pred. No. 1.6e-35;
1; Mismatches 26
                                                                                                                                                                                                                                                           BA893873FD5FA6AB CRC64;
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RESULT OPERVOOR OPERV
        RESULT 3
Q9UL94
ID Q9UL
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DT 01-M
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPRO077110; Ig-like.
Interpro; IPRO03006; Ig_MHC.
Interpro; IPRO03596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS050835; IG_LIKE; 4.
PROSITE; PS05090; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW; OP
                                                                                                                                                                                                                                  Q9UL94;
Q9UL94;
01-MAY-2000
01-MAY-2000
01-MAR-2003
SEQUENCE FROM N.A. MEDLINE=98277139;
                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutharia; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                         Myosin-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BRV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; BC005951; AAH05951.1; -. HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Prostate;
Strausberg R.;
                                                                                                                                                                              (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPBYYAMD
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90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWGKGTTVTVSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCAR--RYCSYSSCQNDYY--YYYMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWGQGTMVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
tive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.9%; Score 447; DB 4; 68.2%; Pred. No. 3.1e-37; tive 10; Mismatches 28
                                                                                               Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 89
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        SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGA--
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

A Tilson M.D.;

Tilson M.D.;

Tilson M.D.;

Tilson M.D.;

Thomo sapiens putative microfibrillar protein with Ig-like dom:

A Tilson M.D.;

Thomo sapiens putative microfibrillar protein with Ig-like dom:

A Tilson M.D.;

Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

RL Submitted (TUN-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY039025; AAK82649.1; -

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003106; Ig MHC.

DR InterPro; IPR0030596; Ig_MC.

DR InterPro; IPR003596; Ig_w.

DR Ffam; PF000407; ig; 1.

DR SMART; SM00406; IGv; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; PS00335; IG LIKE; 1.

SO SEQUENCE 159 AA; T7497 MW; 5D29537E881FAF02 CRC64;

SO SEQUENCE 159 AA; T7497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96QS0 PRELIMINARY; PRT; 159 AA.
Q96QS0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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Anna5020;
Anna50256.1;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01810; 2FBJ
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Young D.C.;
"Myosin-reactive autoantibodies in
                                                  Similarity
AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARD---CGGGAYEDVWSGEYPEYY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 62.8%;
Similarity 67.4%;
89; Conservative
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                                                                                                                                          62.0%; ilarity 67.4%; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 119
119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
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                                                                                                                                          Score 441; DB 4;
Pred. No. 3.1e-37;
3; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 446.5; DB Pred. No. 6e-38;
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                                                                                                                                          23;
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VSKGFY--YY

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB
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1: sp_archea:
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sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                            sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
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sp_bacteria:*
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       258052604 residues
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    Q9UL94
Q96GA6
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Q9UL92
Q9UL92
Q9UL89
Q9UL89
Q9UL89
Q9USS3
Q91WT1
Q9Y298
Q925C3
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Q925C3
Q9Y298
                                                                                                                                                 Q9UL95
Q9BRV0
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Ogul95 homo sapien
Ogbry0 homo sapien
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Ogul94 homo sapien
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Ogul92 homo sapien
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50.1	. L		n (л : Э :	50.2	50.3	50.4	50.4	50.6	50.6	50.8	51.1	51.1	51.2	51.2	51.2	51.2	5	51.	51.6	51.	51.	51.	51.	•	•	•	•	
143	146	1 4 4		1 1	141	142	118	120	117	143	146	168	123	488	463	241	145	473	157	145	145	480	482	143	484	145	145	613	145
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ALIGNMENTS

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RESULT 1
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ID U991
AC Q9UL
AC Q9UL
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
OC Homo
OC Euka
OC Mamm
OX NCBI
RN ([1]
RP SEU
RX MEDI
RX MADI
DR PFar
DR Inte
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                                                                              Query Match
Best Local S
Matches 90
                                                                                                                                                                   O9UL95 PRELIMINARY; PRT; 125 AA.

O9UL95;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035019; AAI
HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. Immunopathol. 87:184-192(1998).
1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                              Similarity
90; Conserv
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                            AAD56255.1; -.
                                                                                                                                       125
13516 MW; 0D3CD5C232488EAC CRC64;
                                                                       63.6%; Score 452.5; DB 4; 68.2%; Pred. No. 1.6e-38; ative 11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalis N.N., Berney S.M.,
                                                                                                               Length 125;
                                                                         Indels
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Job time : 7.07717 secs

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Matches 66
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=77100368; PubMed=401950;
Adetugbo K., Miletein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 1IGC; 03-JUN-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; E90809; G1MS21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lmmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 265:299-304(1977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81234548; PubMed=6788376;
Bothwell A_L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01783;
P01783;
P01783;
P1-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region MOPC 21 precursor (Fragment)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  126
                                            122
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                                                                                                                                62
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                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                         VQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYA 61
                              WGQGTTVTVSS 132
                                                                             DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCAR--
                                                                                                         QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMDV 121
                                                                                                                                                             VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYİSSGSSTLHYA
WGQGTSVTVSS 136
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136
136
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                                                                                                                                                                                                                                                                                                                                                      15071 MW;
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; Ig_MHC.
; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; 3D-structure
                                                                                                                                                                                                                                                             23;
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
                                                                                                                                                                                                                                                                             Score 338; DB 1;
Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION MOPC 21.
D SEGMENT.
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                                                                                                                                                                                                                                                                                                                                            2276A98DBDBF7016 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGMENT
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                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA.
                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                Length 136;
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                                                                        -W-GNYP-YYAMDY 125
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                                                                                                                                                                                                                                                   12;
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RESULT 15
HV11 MOUSES
ID HV11 MOUSES
ID HV11 MOUSES
ID HV11 MOUSES
ID HV11 MOUSES
ID HV12 L1-JU
DT 21-JU
DT 21-JU
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Best Local S
Matches 71
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02038; G2MS43.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J00539; AAA38172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies: somatic m
Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
15-JUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the antibodies: somatic mutation evident in a gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bothwell A.L.M., Paskind Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81234548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
    126
                                       121 VWGQGTTVTVSS
                                                                                         80
                                                                                                                                   61
                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NPB ANTIBODIES).
                                                                                                                                                                                              1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMWGWISIYSGNTDY
                                                                                                                                                                                                                                                                                       Similarity
                                                                           NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR-----YR---LGRY-----FD
                                                                                                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
                                                                                                                                                               QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
  YWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                         137
137 AA;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              49
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68
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117
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Paskind M., Reth
                                                                                                                                                                                                                                                                                                     47.48;
                                                                                                                                                                                                                                                                                                                                                       15200 MW;
                                                                                                                                                                                                                                                                                   53.8%;
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                             Score 337; DB
Pred. No. 1.9e
l3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION S43.
FRAMEWORK.1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK.2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                  ADD5881BF44B8EC9 CRC64;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                   DB 1;
.9e-28;
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                                                                                                                                                                                                                                                                                                   Length 137;
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RESULT 12
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CC Euka
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                 PIR; A02022; GIMSAA.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                          Capra J.D., Nisonoff A.;

"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophanylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-2841979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse)
                                                                                                                                                                                                                                        SEQÜENCE
                                                                                                                                                                                                                                                           NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV00 MOI
P01741;
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SEQUENCE
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPBYYAMD 120
                                                                               OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISMVROAPGOGLEWMGWISIYSGNTDY
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                                                                                                                                                  16;
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Pred. No. 6e-2
16; Mismatches
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D SEGMENT.
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BY SIMILARITY
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Pred. No.
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RESULT 14
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HV15_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
19 heavy chain V region BCL1 precursor.
Mus musculus Mouse).
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SMART; SM00406; IGV;
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by two adjacent CH genes.",
Proc. Natl. Acad. Sci. U.S.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Blattner F.R.;
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Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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136 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 339.5; DB 1 51.5%; Pred. No. 1.1e-28; tive 16; Mismatches 33
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"A V region determinant (idiotope) expr
lymphocytes is encoded by a large set (
EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam: PF00047; ig: 1
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Best Local
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P06330;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 205.12.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
       Interrio, 1.
Interrio, 1.
Pfam: PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
PROMUNOGIODULIN V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activit
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003506; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; Irac.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
PROSITE: PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V region; PyrroLIDONE CARBOXYLIC;
                                                                                                                                                                                                                                                                                                                        SEQUENCE MEDLINE=84182519; PubMed=6201362;
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DISULFID
NON TER
SEQUENCE
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"The covalent structure of a human gamma G-immunoglobuli Intrachain disulfide bonds.",

Biochemistry 9:3188-3196(1970).

-i- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BOND
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SEGMENT.
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) expressed at high frequency i
set of antibody structural gen
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RESULT 11

HV07_MOUSE

ID HV07_MOUSE

ID HV07_MOUSE

ID H0751

DT 21-JUL

CO STRAIN

RA Bothwe

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Best Local S
Matches 71
          PDB; 1A6W; 15-UIL-98.

InterPro; IPRO07110; Ig-like.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PP00047; ig; 1.

SMART; SM00406; IGv; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Signal
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HV07 MOUSE
F01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions at as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00529; AAA38170.1; -. PIR; A90809; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Heavy chain variable region contribution to antibodies: somatic mutation evident in a gam Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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SEQUENCE
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IG HEAVY CHAIN V REGION B1-8/1 FRANEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRANEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                      CHAIN V REGION B1-8/186-2
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Best Local :
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SEQUENCE
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P01746;
                                                                                                                                                                                                                                                                                                                            Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma; Signal.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Somatic mutation in genes for the immunoglobulin heavy chain.";
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SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                                                        NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCAR----
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            STANDARD;
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T.H., Estess P.,
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Pred. No. 6.8
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InterPro; IPK...
InterPro; IPK...
Promotof; ig; 1.
R SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
IG_LIKE.

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Best Local
MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
To heavy chain V region MOPC 104E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV1A_HUMAN
P01742;
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Kehry M.R., Fuhrman J.S., Schilling
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-I region EU.
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-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
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                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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; Pred. No. 7.16
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain:
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P01757;

P01757;

21-JUL-1986 (Rel. 01, Created)

1 15-SEP-2003 (Rel. 42, Last sequence update)

I 15-SEP-2003 (Rel. 42, Last annotation update)

E 19 heavy chain V region J558.

Mus musculus (Mouse).

S Mus musculus (Mouse).
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Matches
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                              InterPro;
InterPro;
                                                                         HSSP;
                                                                                                                                                                                                    MEDLINE=80078170; PubMed=6765983; Schilling J. Clevinger B. Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies trearrangements in heavy chain V-region gene segments 283:55-40(1980).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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NON TER
SEQUENCE
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-!- SIMILARITY: COTHSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          idiotype response of the strain A mouse.",
Eur. J. Immunol. 12:1023-1032(1982)
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
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Siekevitz M., Gefter M.L., Brodeur P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEAM; PF00047; ig; 1.
WART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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NCBI_TaxID=10090;
[1]
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                                                                                              MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDON BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 WHICH OCCUR IN THE D AND J SEGMENTS. MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN. SIMILARITY: Contains 1 immunoglobulin-like
                                                                       A26242; MHMSJ5.
; P01789; 1MCP.
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72; Conserv
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IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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120 AA;
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Rodentia;
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                                                                                                                                       ES OF 10 HYBRIDOMA PROTEINS HAT SHOWN AT 1-7 POSITIONS, SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Query Match
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Matches
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Best Local
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InterPro; IPR003006; I
InterPro; IPR003596; I
Pfam; PF00047; ig; 1
SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
                                                                                                                                                                                          DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                                                    MEDIINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in lymphocytes is encoded by a large set of antibody structural gent EMBO J. 3:517-523(1994).
BIR; A02017; MEMS15.
HSSP; P01810; 2FBJ.
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SMART; SM00406; IGv.; 1.
PROSITE; PSS9085; IG LIKE; 1
Immunoglobulin V region.
DOMAIN 1 116
DISULFID 22 96
NON TER 117 117
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metaza; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN 1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain v region AC38 15.3.
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P06329;
                                                                                                                                                                                                                                                             [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                        61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                 121 VWGQGTTVTVSS 132
                                                                                        ш
                                                                                                                     l Similarity 71; Conserv
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 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCAR-
                                                                   OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                    QVQLLQPGTELVKÞGASVNLSCKASGYTFTSYWMHWIRQRÞGQGLEWIGGINÞSNGGTNY
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22 96 BY
117 117
117 AA; 13024 MW; 2
                                                                                                                   Conservative
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; Ig_MHC.
; Ig_v.
                                                                                                                               50.8%;
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53.8%; Pred. No. 2.7e-31;
tive 18; Mismatches 28
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Pred. No. 5.1e-31;
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D SEGMENT.
J SEGMENT.
SY SIMILARITY.
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BY SIMILARITY.
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; Murinae; Mus.
WDYEGDRYF--D
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                                                                                           Query Match
Best Local S
Matches 75
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                       EMBL; J00240; AAA52988.1; -. PIR; A02024; HVHUHG. HSSP; P01772; 2FB4.
                                                                                                                                                                                        Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01743;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
7~ heavy chain V-I region HG3 precursor.
                                                                                                                                         SEQÜENCE
                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=83144028; PubMed=6298778;
Rechard G., Ram D., Glazer L., Zakut R., Givol
"Evolutionary aspects of immunoglobulin heavy
(VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80.855-859(1883)
                                                                                                                                                     NON_TER
                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV18_HUMAN
P01743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like domain.
80
                    19
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                                                                                                     Similarity
                                                 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIXSGNTDY 60
               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                     QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVMSGEYP-EY-YA 118
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                                                                                                                                        117 AA;
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117
                                                                                         Conservative
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117
                                                                                                                                       12946 MW;
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                                                                                                  54.3%;
76.5%;
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                                                                                       6;
                                                                                                  Score 386;
Pred. No. 1
                                                                                                                                                              IG HEAVY CHAIN V-I REGION HG3 IG-LIKE.
                                                                                                                                    2D3F92FC60CD1FE7
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                                                                                     Mismatches
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RESULT
HV03_MO
ID HV
AC P0
DT 21
DT 15
DE IG
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HV1G_HUM
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Best Local
        3_MOUSE STANDA
HY03_MOUSE STANDA
P01747;
21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
15 heavy chain v regi
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1
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NON TER
SEQUENCE
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G0; G0:0005576; C:extracellular; NAS.

G0; G0:0003823; F:antigen binding activity; NAS.

G0; G0:0006955; P:immune response; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X07448; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T.,
Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV1G_HUMAN
P23083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
15 heavy chain V-I region V35 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                              61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                                                                                                                             . Similarity
75; Conserv
                                                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEMMGRINPNSGGTNY
                                                                                                                                                                                                                                      QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                               AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
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20 117 IG
20 >117 IG
117 117 IG
117 AA; 13009 MW;
                      (Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 42, Last annotation
ain V region 36-65.
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                                                                                             STANDARD;
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76.5%;
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Pred. No. 3.1e-33;
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                                                                                             PRT;
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                                    update)
on update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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Result
No.
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Maximum Match
Listing first
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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323.5
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367.5
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length: 2000000000
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     SwissProt_41:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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HV02_MOUSE
HV12_HUMAN
HV51_MOUSE
HV07_MOUSE
HV07_MOUSE
HV06_MOUSE
HV15_MOUSE
HV15_MOUSE
HV11_HUMAN
HV01_HUMAN
HV01_MOUSE
HV14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV1G_HUMAN
HV03_MOUSE
HV13_MOUSE
HV50_MOUSE
HV50_MOUSE
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Compugen Ltd.
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P01743 homo sapien
P23083 homo sapien
P23083 homo sapien
P01747 mus musculu
P01757 mus musculu
P01746 mus musculu
P01746 homo sapien
P06330 mus musculu
P01751 mus musculu
P01751 mus musculu
P01751 mus musculu
P01753 mus musculu
P01755 mus musculu
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P01755 mus musculu
P017627 mus musculu
P01771 homo sapien
P01773 mus musculu
P01778 mus musculu
P01778 mus musculu
P01778 mus musculu
P01779 homo sapien
P01781 homo sapien
P01781 homo sapien
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sapien
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ALIGNMENTS

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RESULT 1

HV1C HMAN

ID HV1C H
AC P01744

AC
Query Match
Best Local S
Matches 84
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P01744;
21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16 heavy chain V-1 region ND precursor (Fragments).
Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SW00406; IGv; 1.
SMART; SW00406; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                               DOMAIN
MOD RES
DISULFID
CONFLICT
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
NON TER
SEQUENCE
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HSSP, P01789; LMCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; F:antigen binding activity; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR001110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennich H.H., Johansson S.G.O., von Banr-Lingstrom A.,

(In) Bach M.K. (eds.);

Immediate hypersensitivity: modern concepts and developments, pp.1-36,

Marcel Dekker, New York (1978).

-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=83065234; PubMed=6815656;

MEDLINE=83065234; PubMed=6815656;

Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney v.

Bell L.O., Gould H.J.;

"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";

proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-147.
                              Similarity
                                                                                                            125
147
147
   60.1%; Score 427; Dilarity 62.7%; Pred. No. 7.7%; Conservative 16; Mismatches
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41
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53
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115
21
54
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VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V-I REGION ND IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                     948F9F72A5366C20 CRC64;
                              DB 1; Length 147; .7e-38;
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Indels

8

Gaps

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RESULT 15
S36265
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C.Accession: S36265
R.Gariffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
A.Fille: Human anti-self antibodies with high specificity from phage display libraries.
A.Reference number: S36256; MUID:93178448; PMID:7679990
A.Accession: S36265
A.Status: preliminary; nucleic acid sequence not shown
A.Residus: preliminary; nucleic acid sequence not shown
A.Residus: 1-118 <GRI>A.Fesidus: 1-118 <GRI>A.Cross references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C.Superfamily: immunoglobulin v region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:14 Job time: 13.6531 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000 C;Accession: S68170 R;Boeldicke, T.; Haase, B.; Boecher, M.; Lindenmaier, W. Eur. J. Biochem. 234, 397-405, 1995 A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and recombinan A;Reference number: S68170; MUID:96128166; PMID:8536681
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                                                                                                                       121 VWGQGTTVTVSS 132
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                                                                                                                                                      61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSG----
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                                                                                                                                                                                                                                                          1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 63.4%; Score 451; DB 2; Length 118; Similarity 68.2%; Pred. No. 1.3e-34; 90; Conservative 8; Mismatches 20; Indels
                                                                                                                                                                             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                  YWGQGTLVTVSS 118
                                                                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGBYPEYYAMD 120
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Ig mu chain precursor, membrane-bound (clone 201) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: $14683; $80807
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A;Reference number: $14683; MUJD:90332450; PMID:2115996
A;Accession: $14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; CulBinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, Bubmitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity A; Reference number: S31585
A; Accession: S31600
RESULT 12
PH1667
                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-136 < CUI>
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                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                                                                                            QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                      VWGQGTTVTVSS 132
                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                              IWGQGTMVTVSS 135
                                                                                                                                                         AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR----
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Pred. No. 7e-35;
8; Mismatches 27;
                                                                                                                                                                                                                                                                                                                  Score 460; DB 2;
Pred. No. 2.2e-35;
8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin diversity operate
                                                                                                                                                                                                                                                                                                                                                        Length 136;
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  Ig heavy chain V region - human (fragment) N;Alternate names: anti-cytomegalovirus gl C;Species: Homo sapiens (man)
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Ig heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1666
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1666
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(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
(;Accession: PH1667
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
30. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1667
A;Accession: PH1667
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A;Residues: 1-114 <HID-
A;Residues: 1-20 ccll
A;Experimental source: B ccll
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                         A;Experimental Bource: B cell C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-118 <HIL>
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113
                                            127
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                                                                                           62 ITRDTSASTAYMELSSLRSEDTAVYYCARVTLDGGIKFY-----YYYGMDVWGQGT
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                                                                                                                    MTTDTSRRTAYMELRSLRSDDTAVYYCAR----DGGGGAYEDVWSGEYPEYYAMDVWGQGT 126
                                                                                                                                                                                                                EVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMMGWISIYSGNTDYAQKFQGRVT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYAQKFQGRVT
TVTVSS 118
                                                                                                                                                                                    EVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKYAQKFQGRVT 61
                                            TVTVSS 132
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Pred. No. 6.4e-35;
                                                                                                                                                                                                                                                                                                         Score 453; DB 2; Pred. No. 8.2e-35;
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                   F;51-67/Region: complementarity-determining F;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                    F;31-35/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                    F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-132 <MAR>
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A;Molecule type: mRNA
A;Residues: 1-131 <MOR>
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Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26792
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                                                                                                         Similarity
                                                                                       MDVWGQGTTVTVSS 132
                                                                                                                       AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARP--HASIDDFWSGYYPNYYYYG
                                                                                                                                             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAXEDVWSGEYPE--YYA 118
                                                                 MDVWGQGTTVTVSS
                                                                                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARDSRGYSYYDFWSG-YFYYYYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                                                                                                                 66.5%;
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                                                                 132
                                                                                                                                                                                                                                                               Score 473; DB 2;
Pred. No. 1.4e-36;
9; Mismatches 26
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                                                                                                                                                                                                                                                                                                Length 132
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S34014

Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0.2-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four huma
A·Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                               F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                         A/Experimental source: the sequence was determined from the differentiated C/Superfamily: immunoglobulin V region; immunoglobulin homology C/Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-133 < KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region
A;Reference number: A33548; MUID:89345575; PMID:2503826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
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A;Accession: S3401
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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YGMDVWGQGTTVTVSS
                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGBYPE----Y 116
                                                                                                                                                                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                    YAMDVWGQGTTVTVSS 132
                                                                AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGW---
                                                                                                                                        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQMVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPSSGNTGY
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                                                                                                                                                                                                                                         65.0%;
69.1%;
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71.2%;
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Pred. No. 1.3e-35;
8; Mismatches 27;
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Pred. No. 9.7e-36;
2; Mismatches 21;
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anti-PR2 erythrocyte autoantibody heavy chain precursor - C:Species: Homo sapiens (man) C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_C:Accession: PL0105
                                                                               R;Silberstein,
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A; Molecule type: mRNA
A; Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118, 'T', 120-124 <JON>
A; Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118, 'T', 120-124 <JON>
A; Cross-references: EMBL: X61647; NID: 937667; PIDN: CAA43828.1; PID: 91335368
A; Note: the difference for residues 41-60 results from misplacement of 10 }
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                               A; Reference number:
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S19665
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submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: By-passing immunization. Human antibodies from A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19665
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C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter J. Mol. Biol. 222, 581-597, 1991
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A;Residues: 1-124 <MAR>
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                    Silberstein, L.E.; Litwin, S.; Carmack, C.E.
Exp. Med. 169, 1631-1643, 1989
Title: Relationship of variable region genes expressed
Reference number: PL0106; MUID:89235583; PMID:2541221
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     97;
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                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY
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99; Conservative
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76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.4%;
70.8%;
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Pred. No. 8e-38;
7; Mismatches
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Pred. No. 8.3e-40;
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                                                                RESULT 6
S26792
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains alignment of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:231680; NID:g509786; PIDN:CAA83485.1; PID:g1335146 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #sext_change 20-Jun-2000
C;Accession: S46393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu C;Comment: The antibody is one of the cold agglutinins that preferentially bi C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: autoantibody; hemagglutinin F;1-19/Domain: signal sequence #status predicted <SIG>F;34-11/Domain: immunoglobulin homology <IMM>F;49-19/Region: complementarity-determining 1
F;69-84/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;118-131/Domain: D region <DRG>
F;132-144/Domain: J4 segment <JSG>
F;145-160/Domain: C region <CRG>
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A;Molecule type: mRNA
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                                                                         121 VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 73.9
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGBYPEYYAMD 120
                                                                                                                                                                                                                                                                                                       ÓVOLVOSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                               AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARD---SAYYYDSSGYYSANYYMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- DYWGQGTLVTVSS 144
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73.5%;
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70.6%;
129
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Pred. No. 4.1e-37;
6; Mismatches 26
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Pred. No. 2.8
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Maximum DB
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ig heavy chain V r
anti-pR2 erythrocy
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4 4 5 4	43	42	41	40	39	38	37	36	35	34	υ u	32	31	30
411.5	412	413	414	416	417.5	418.5	419	419	419.5	425.5	426	426	427	427
57.9 57.3	57.9	58.1	58.2	58.5	58.7	58.9	58.9	58.9	59.0	59.8	59.9	59.9	60.1	60.1
109	116	98	111	120	126	148	120	110	142	135	132	122	143	132
NN	ผ	N	N	N	N	N	N	2	N	N	N	N	_	N
PH1668 B49590	PH0959	S26918	\$21925	S31999	144151	S29257	PH0962	PH1669	A32483	PH0953	S46394	PH0958	E1HUND	S31596
Ig Ig	Ig.	Ig	Ig	Ig	Ig	ξI	PI	Ig.	Įg	1g	Į.	Ig.	Ig	1g
Ig heavy Ig heavy	_	_	_	_	_	_	_	Ig heavy		_	_	_	_	
	heavy	heavy	heavy	heavy	heavy	heavy	heavy	_	heavy	heavy	heavy	heavy	heavy	heavy

ALIGNMENTS

RESULT S36260

Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries
A;Reference number: S36256; MUID:93178448; PMID:7679990

from phage display libraries

A; Accession: S36260

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Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S38271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-129 <GRI>
A;Cross-references: EMBL:218851; NID:g33124; PIDN:CAA79303.1; PID:g939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                           A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-122 <GRI>
                                                                                                                                                                                                                                                                                                                               RESULT
S36271
A;Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.2%;
79.5%;
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Pred. No. 5.6e-41;
4; Mismatches 20
                                                                                            sequence not
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Sequence 4, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-217-918-4
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                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, willaim M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
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; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.5%; Score 471; DB 3; Length 128; Best Local Similarity 72.6%; Pred. No. 2e-41; Matches 98; Conservative 6; Mismatches 19; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1413
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                       STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 YFDYWGQGTLVTVSS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPI-FGSTK 59
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Search completed: December 30, 2003, 11:05:31 Job time: 14.284 secs
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; MOLECULE TYPE: protein
US-08-217-918-4
                                                                                                                                                                                                                                                                                                    Query Match 68.5
Best Local Similarity 70.7
Matches 94; Conservative
                                                                        135 DVWGQGTTVTVSS 147
                                                                                                                                                     80
                                                                                                                                                               61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRP---DAL 117
                                                                                                                                                                                                                  20 QVQLVQSGAEVKKVGCSVKVSCKASGGTFSNFAISWVRQAPGQGLEMMGRIMPLFVTSTY 79
                                                                                                                                                                                                                                            1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWWGGIIPIFGSTKY 60
                                                                                                    DIWGOGTMVTVSS 130
                                                                                                                                           AQXFQGRVTISADASTSTAYMELSSLRSDDTAMYYCARD-----ITAPGAAPTPLNFYGM 134
                                                                                                                                                                                                                                                                                            68.5%; Score 471; DB 1; Length 147; 70.7%; Pred. No. 2.4e-41; tive 13; Mismatches 18; Indels
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US-08-202-047-22
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ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-652-816A-9
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                                                                                                                                                                                                                                                                                   APPLICANT: CHESNUT, Robert W. APPLICANT: POLLEY, Margaret J. APPLICANT: PAULSON, James C. APPLICANT: JONES, S. Tarran APPLICANT: SALDANHA, Jose W. APPLICANT: BENDIG, Mary M.
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                           tent No. Sauver-
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                               APPLICANT: BENDIG, Mary M.

TITUE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB92/02240 FILLING DATE: 02-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: GB 9525004.9
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-SEP-
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/244,597 FILING DATE: 01-JUN-1994
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93; Conservative
                                                                                                                                                       San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGTMVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKFQGRVTMTADGSTSTAYMELNSLRSEDTATYYCARQQNGGWYEGPLLEPRPDALDIW 120
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                                                                                                                                       USA
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24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.5%; Score 471.5; DB 2; 71.5%; Pred. No. 1.7e-41; ative 13; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB 9206372.6
                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICANT: PAULSUN,
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
ALDRESTOR, ANDRESS: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: One Market plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-964-690-22
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                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/364,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CHESNU
APPLICANT: POLLEY
FILING DATE:
CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1.128
OTHER INFORMATION: /label= HUMAN_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ALDIWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 72.6%;
98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 128 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08964690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHESNUT, Robert W. POLLEY, Margaret J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 471; DB 1
Pred. No. 2e-41;
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                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 128;
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RESULT 11
US-08-652-816A-1
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                                                                                  APPLICATION NUMBER: US/08/652,816A FILING DATE: 23-MAY-1996 PRIOR APPLICATION DATA: APPLICATION UNMBER: GB 9125579.4 FILING DATE: 02-DEC-1991 PRIOR APPLICATION NUMBER: GB 9125579.8 APPLICATION UNMBER: GB 9125579.8 FILING DATE: 02-DEC-1991
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ywence 1, Application US/08652816A
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
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APPLICANT: Allen, DJ
APPLICANT: MCCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Specific TITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/OFFILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA;
                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: Jim
                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 (
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 69.7%;
Local Similarity 70.1%;
es 94; Conservative 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSITPSFGTANY
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                                                                                                                                                                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                            United States of America
                                    24-MAR-1992
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                                                   GB 9206318.9
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South Wacker Drive
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RESULT 12
US-08-652-816A-9
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APPLICANT: Osbourn
APPLICANT: Allen,
APPLICANT: McCaffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local
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                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATB: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
                           APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                    COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Spi
TITLE OF INVENTION: mei
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: GB 9:
FILING DATE: 07-DEC-1995
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TELECOMMUNICATION INFORMATION:
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NAME: David W. Clough
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                                                                                                                                                                                                                                                                       CITY: Chicago
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5. 5872215
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                                                                                                                                                                                                                                                          Illinois
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                                                                                                                                                                                                                                                                                        E: Marshall, O'To
                                                                                                                                                                                                                                                                                                                                                                                             McCafferty, JG
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01-JUN-1994
02-DEC-1991
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72.5%;
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                GB 9125579.8
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                                                                                                                                                                                                                                                                                        O'Toole, Gerstein, Murray & Borun
ower, 233 South Wacker Drive
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FILING DATE:

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Query Match
Best Local Similarity
Tarches 95; Conserve
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; LOCATION: 1..120
US-08-428-197-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Applicat GENERAL INFORMATION:
                             CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: FD-2
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                       STREET: 1000
CITY: LOS Angeles
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application PC/TUS9310555
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1880 Century Park East - Suite 500
                     (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SILVERMAN, GREGG J.
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                                                                     FD-2630
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RESULT 10
US-08-652-816A-8
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                                                                                                                                    APPLICATION NUMBER: GB 9125579.4

FILING DATE: OZ-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION UNMBER: GB 9125579.8

FILING DATE: OZ-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

OR OZOGOZO

PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8,
                                            PAPELICATION NUMBER: GB 920
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                   FILING DATE: 07-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/652/01/
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 9125579.4
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods, MUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linea MOLECULE TYPE: pe IMMEDIATE SOURCE: CLONE: KAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 QGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDY------GRP--FDFWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VHĽVOSGAEVKKÞGSSVKVSCKASGGTFSSYAISWVRQAÞGOGLEWNGGIIÐIFGQANYA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQLVQSGAEAKKPGSSVKVSCKASGDTFNSFDISWVRQAPGQGLEWMGGIIPIFGSTKVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
MBER: GB 9610824.6
23-MAY-1996
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73.6%;
                                                                                                                            GB 9206372.6
                                                                      GB 9525004.9
                                                                                                                                                                                                                                                                                                                                             US/08/652,816A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 480.5; DB ; Pred. No. 2e-42; 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
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US-08-983-607-50
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TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 73.1 Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.
COMPUTER: IBM PC
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IBS
FILING DATE: June 28, 1996
CLASSIFICATION: 435
                                                                                                                                  SOFTWARE: Word Processing CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
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REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              STREET: 266 Whit
CITY: New Haven
STATE: Connection
                                                                                  FILING DATE: AF
                                                                                            APPLICATION NUMBER: US/08/98
FILING DATE: April 27, 1998
                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
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COMPUTER: II
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3 6140470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                            Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08983607
                                                                                                                                                                                                                                                          United States of America
INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
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73.1%; Pred. No. 1.2e-42;
ative 11; Mismatches 15
                                                                                                                                                                                                        1.44 Mb diskette
                                               PCT/IB96/01032
                                                                                                                   US/08/983,607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 121;
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RESULT 8
US-08-428-197-13
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                                                                                                                                                                                                                                                                                                                                                                                                                          patent No. 5891438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFOR APPLICANT:
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METITILE OF INVENTION: VAC.
TITLE OF INVENTION: VAC.
TITLE OF INVENTION: THEINUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
CLONE: 2-71
FEATURE:
NAME/KEY: heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                    CLASSIFICATION:
                                                                                                                                                                                                                         STREET: 1880 Centricity: Los Angeles STATE: California
                                                      FILING DATE:
                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mary M. Krinsky REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 VSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 VTITADKSTSTAYMELSSLRSEDTAVYYCAR--GGGRY-----DAFDIWGQGTLVT 116
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                                                                                                                                                                                             90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKYAQKFQGR 67
                                                                                                                                                                                                                                                        E: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08428197
                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                               SILVERMAN, GREGG J.
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                                                                                                                                                                                                                                                                                                                                        METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED VACCINATION WITH A B-CELL SUPERANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.0%;
77.2%;
                                                                                                                                                                                                                                                                                                                               THEREOF
PCT/US93/10555
                                                                     US/08/428,197
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Pred. No. 1.5e-42;
7; Mismatches 10
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AND CONJUGATES
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PCT-US93-10555-12
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                                                                                                                                                                                     RESULT 5
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; NAME/KEY: Peptide
; LOCATION: 1..120
US-08-428-197-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION.

PRIOR APPLICATION NUMBER: PCT/US93/10555

FILING DATE: 29-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: FD-2630

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEPHONE: (619) 455-5110

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TUTEL APPLICATION ACIDS
           Sequence 12, Application PC/TUS9310555

GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROTTILE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: B
TOPOLOGY: linea
MOLECULE TYPE: pe
IMMEDIATE SOURCE:
CLONE: BOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SILVERMAN,
TITLE OF INVENTION: N
TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/428,197 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1880 Centu
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                 112
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ဝ္ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                            2 VQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o 70.4%;
Similarity 75.2%;
                                                                                                                                                                                                                                                                                                                 QKFQGRVTITTDESTSTÄYMEVSSLÄSEDTÄLYYCÄR-----EGRRMAINP--FDYWG 111
                                                                                                                                                                                                                                                                                                                                       QKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIWG 121
                                                                                                                                                                                                                                             QGTLVTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 484.5; DB 2; Length 120; Pred. No. 7.7e-43;
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US-08-232-081B-41
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                                                                                                                                                                                                                                                   Sequence 41,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/ACEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                             APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                STREET: PO DO...
CITY: FALLS CHURCH
STATE: VA
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1:
MOLECULE TYPE:
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CLONE: BOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STREET: 1880 Centur
CITY: Los Angeles
STATE: California
                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1..120
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                                                                                                                                                                                                                                                                                                                                                                                      122 QGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Conservative
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5886152
                                                                                E: BIRCH,
PO BOX 747
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1880 Century Park East - Suite 500
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                                                                                               STEWART, KOLASCH AND BIRCH
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75.2%;
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Pred. No. 7.7e-43;
9; Mismatches 14;
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                                                                                                                                                                                                                                       ; LENGTH: 120 amino acids
; TYPE: maino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-57
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/99/025,769B

FILING DATE: 18-PEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-MG-1995

AFTORNEEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-025-769B-57
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Best Local Similarity 76.9%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moroney, Šimon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James
STREET: 1251 Aver
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
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                  121 GQGTMVTVSS 130
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                                                          AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                     OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIIPIFGTANY 60
                                                                                                                        OVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                           AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGDGFY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                  (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ge, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knappik, Achim
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Pred. No. 1.1e-45;
9; Mismatches 11;
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RESULT 4
US-08-128-197-12
; Sequence 12, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-21
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US-09-025-769B-21
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knappik, Ach
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
110 GQGTLVTVSS 119
                               121 GOGTMVTVSS 130
                                                                       61
                                                                                       61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
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111 GQGTLVTVSS 120
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                                                                                                                                                                   QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMQGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10021
                                                                   AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARAP--GYCSG-----
                                                                                                                                           QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFFTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                             119 amino acids
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                                                                                                                                                                                                                      72.2%;
ilarity 76.2%;
Conservative
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(212)596-9090
77 TO NO: 21:
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Liming
TV, Simon
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                                                                                                                                                                                                                    Score 496.5; DB 4;
Pred. No. 4.4e-44;
B; Mismatches 12;
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                                                                                                                                                                                                                                                        Length 119;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                               328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 30, 2003, 10:47:45; Search time 13.2007 Seconds (without alignments)
416.677 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 ,
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688
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US-08-225-081B-41

US-08-232-081B-41

US-08-232-081B-41

US-08-232-081B-41

US-08-232-10555-13

PCT-US93-10555-13

PCT-US93-10555-13

US-08-652-816A-8

US-08-652-816A-9

US-08-652-816A-9

US-08-202-047-22

US-08-202-047-22

US-08-217-918-4

US-08-652-816A-6

US-08-217-918-4

US-08-521-521-45

US-08-525-539A-77

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             Sequence 57,
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Sequence 12,
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          35, Appl
57, Appl
21, Appl
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29, Appl
20,                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1...

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION UNMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFRENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDBURSS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-35
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US-09-025-769B-35
Query Match 74.4%;
Best Local Similarity 76.9%;
Matches 100; Conservative
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Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York
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US-08-714-017-53
US-08-475-680-53
US-08-652-816A-7
US-09-199-149-3
US-09-199-149-3
US-09-355-925-7
US-09-355-925-8
US-08-579-378A-8
US-08-579-378A-12
PCT-US93-11612-12
US-08-253-877C-19
US-08-68-253-877C-19
US-08-603-024-18
US-08-603-024-18
US-08-450-809-14
PCT-US95-00067-2
US-08-836-561-63
US-08-836-561-63
       9,
Score 512; DB 4; Length 120;
Pred. No. 1.1e-45;
9; Mismatches 11; Indels
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Sequence 7, Appli
Sequence 7, Appli
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Sequence 7, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 63, Appl
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Result No.

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496.5 484.5 482.5 480.5 480.5 471.5 471.5 471.5 471.5 471.5 471.5 471.5 471.6

Database

Minimum DB Maximum DB

Sequence:

protein on:

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Sequence 1866, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
ITITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
FRIOR APPLICATION NUMBER: 60/240,816
FRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/270,3499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN PARENTIN PARENT PARENTIN                                                                 Ś
                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Homo sapiens US-10-269-805-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-269-805-35; Sequence 35, Application US/10269805; Publication No. US20030124129A1; GENERAL INFORMATION:
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LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1866
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 125
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Best Local :
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
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                                                                                                                                Local Similarity 78.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 73.8%; Score 508; DB 11; Length 254; Local Similarity 71.4%; Pred. No. 5.1e-39; es 100; Conservative 10; Mismatches 8; Indels 2
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1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                                                                                                 Gaps
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Search completed: December 30, 2003, 11:45:22 Job time : 28.8798 secs
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US-10-269-805-9
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SEQ ID NO 9
LENGTH: 121
TYPE: PRT
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Publication No. US20030124129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
                                                                      112 GOGTMVTVSS
                                                                                                  121 GOGTMVTVSS 130
                                                                                                                              61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAA-----FSPFTE--TDAFDIW
                                                                                                                                              61 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
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FILE GREERENCE: PF523
CURRENT APPLICATION NUMBER: U5/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 1509
LENGTH: 233
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-880-748-1509
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Best Local Similarity 76.5
Matches 100; Conservative
                                                                                                                          Sequence 47, Application US/10047542 Publication No. US20020168367A1 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOPF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y Match 74.3%;
Local Similarity 72.1%;
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                                                                                                                                                                                                                                                                         74.4%; Score 512; DB 15; 76.9%; Pred. No. 9.8e-40; tive 9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 511; DB 11; Length 253; Pred. No. 2.7e-39;
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APPLICANT: Ruben et al.

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/279,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 47
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US-09-880-748-1880
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Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1880
LENGTH: 253
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                                                                                                                                                                                                                                                                    Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
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TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                             / Match 73.9%; Score 508.5; DB 11; Length 253;
Local Similarity 74.6%; Pred. No. 4.6e-39;
1es 100; Conservative 11; Mismatches 12; Indels 11;
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114
                                       117 LDIWGOGTMVTVSS 130
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                                                                                                                                                                                                       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPCQGLEWMGGIIPIFGSTKY 60
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FDIWGRGTMVTVSS 127
                                                                                                                                                                           , Application US/09880748 o. US20030059937A1
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72.7%; Pred. No. 9.9e-39;
tive 10; Mismatches 13
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Sequence 25, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
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US-09-880-748-1881
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                                        ; ORGANISM: Homo sapiens
US-10-269-805-25
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LENGTH: 244
TYPE: PRT
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GENERAL INFORMATION
Query Match
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Best Local :
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                              LENGTH: 124
TYPE: PRT
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Local Similarity 76.9%;
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74.6%;
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Pred. No. 1.2e-39;
Score 513;
DB 15;
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Length 124;
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US-10-125-687-1
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TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
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Publication No. US20020142255A1
GENERAL INFORMATION:
                                                SOPTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10125687
Publication No. US20030054407A1
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Best Local Similarity 76.9%;
Matches 100; Conservative
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                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
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                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                         GOGTLVTVSS 120
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                  Human consensus antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 14;
Pred. No. 9.8e-40;
9; Mismatches 11
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 118
TYPE: PRT
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US-10-300-675-6
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Best Local S
Matches 99
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SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10300675
Publication No. US20030198638A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watkins, Jeffry D.

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519

CURRENT APPLICATION NUMBER: US/10/300,675

CURRENT FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: US 09/989,901

PRIOR FILING DATE: 2001-11-19
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                         LENGTH: 118
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   109
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                                                                                                                                                1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
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                                                                                                                                                                                                                    Similarity
                              GOGTMVTVSS 130
                                                         AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDSSGWYH-----
                                                                         AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                        QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
GQGTLVTVSS 118
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                  75.1%;
76.2%;
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76.9%;
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                                                                                                                                                                                             Score 517; DB 12;
Pred. No. 3.3e-40;
9; Mismatches 10;
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Pred. No. 1.2e-40;
B; Mismatches 10;
                                                                                                                                                                                                                             Length 118;
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                                                                                                                                                                                             Indels 12;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                          Matches
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/10300675 Publication No. US20030198638A1 GENERAL INFORMATION:
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Best Local Similarity 76.2%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
                                                                                                                                                                                                                                                               LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
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                                                                                                                                                                                                                                                       FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 118
                                                                                                                                                          Local
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                                                                                                                                                          Similarity
AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                             QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                        Conservative
                                                                                                                                                  75.0%;
76.2%;
                                                                                                                                Score 516; DB 12;
Pred. No. 4.1e-40;
8; Mismatches 11
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Pred. No. 4.1e-40;
8; Mismatches 11;
                                                                                                                                                                                                                             variant
                                                                                                                                    11;
                                                                                                                                                                      Length 118;
                                                                                                                                Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                   d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO9C_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
        US-10-269-805-19
US-10-300-675-14
US-10-300-675-10
US-10-300-675-10
US-10-300-675-12
US-09-880-748-1881
US-10-25-687-1
US-10-25-687-1
US-10-25-687-1
US-10-25-687-1
US-10-125-687-1
US-10-269-805-3
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Sequence 19, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appl
Sequence 1881, Appl
Sequence 1881, Appli
Sequence 25, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1509, Appli
Sequence 1880, Appli
Sequence 1866, Appli
Sequence 1866, Appli
Sequence 35, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                   RESULT 1

US-10-269-805-19

Sequence 19, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

ITITLE OF INVENTION: ANGIOPOLISTIN-2 SPECIFIC BIN

FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR PILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOPTWARE: Patentin version 3.1

SEQ ID NO 19

LENGTH: 121

TYPE: PRT

ORGANISM: Homo Bapiens
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                                                                                                                                                                                         1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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                                               GOGTMVTVSS
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                                               121
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US-09-880-748-1733
US-99-880-748-1718
US-10-151-882-15
US-99-880-748-155
US-99-880-748-1719
US-99-880-748-1737
US-99-880-748-1737
US-99-880-748-1737
US-99-880-748-1737
US-10-308-817-191
US-99-880-748-1749
US-99-880-748-1759
US-09-880-748-1728
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US-09-880-748-1728
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US-10-269-800-748-1813
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US-09-880-748-1866
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US-09-880-748-1866
US-09-880-748-1866
US-09-880-748-1813
US-10-269-805-37
US-10-269-805-37
US-10-269-805-37
US-10-269-805-37
                                                                                                                                                                                                                                       Score 524.5; DB 15; Length 121;
Pred. No. 7e-41;
9; Mismatches 10; Indels 9;
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Sequence 1733, Ap
Sequence 1734, Ap
Sequence 1718, Ap
Sequence 1879, Ap
Sequence 1879, Ap
Sequence 1879, Ap
Sequence 1873, Ap
Sequence 1737, Ap
Sequence 1737, Ap
Sequence 1741, Ap
Sequence 1741, Ap
Sequence 1745, Ap
Sequence 1727, Ap
Sequence 1728, Ap
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Sequence 1728, Ap
Sequence 1736, Ap
Sequence 1746, Ap
Sequence 1746, Ap
Sequence 1747, Ap
Sequence 1747, Ap
Sequence 1748, Appli
Sequence 1748, Ap
Sequence 1748, Ap
Sequence 1748, Ap
Sequence 1813, Ap
Sequence 1813, Ap
Sequence 1748, Ap
Sequence 1748, Ap
Sequence 174, Appli
Sequence 1748, Ap
Sequence 174, Appli
Sequence 1748, Appli
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Sequence 1748, Appli
Sequence 1748, Appli
Sequence 1915, Ap
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                                                                                                                                                                                                                                     Gaps
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Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Perfect score:

US-09-674-752-23 688

OM protein -

9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext

Result No.

Query Match

Length

BB

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ecore Pred. No.

113 113 154 154 154

524.5 527 516 516 514.5 513 513 512 519.5 509.5 509.5 509.5 509.5 509.5

76.2 75.9 75.1 75.0 74.6 74.6 74.4 74.3 73.8

118 118 118 118 118 244 124 120 120 120 120 125 325 325 325 3

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                                                                                                                                                                                                                                                                                                                       This invention describes novel antibodies that immunospecifically bind to CC Blymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiALDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS can so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC associated with aberrant spression of BLyS. They may also be cadministered to treat diseases associated with aberrant BLyS expression CC and activity such as cancer, immune, and autoimmune disorders and ciseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (cup) and cc immunodeficiency (e.g. common variable immunodeficiency (cup) and cc acquired immunodeficiency (syndrome (AIDS)). ABP43990-ABP47228 represent confiction of the antibodies described in the method
                                                                                                                                                                                    Query Match 73.0
Best Local Similarity 75.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                    the antibodies and of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2470-2471; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60
                                                                                                                                                                                                                                                                             248 AA;
                                                                                                                                                                         73.0%; Score 502.5; DB 23; Length 248; 75.2%; Pred. No. 2.8e-40; ative 9; Mismatches 13; Indels 11; Gaps
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Search completed: December 30, 2003, 10:54:29 Job time: 41.903 Becs 밁 113 DYWGOGTLVTVSS 125 118 DIWGQGTMVTVSS 130

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cancer

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RESULT 14
ABR01518
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Best Local S
Matches 100
Claim
                             New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign pros
                                                                                                                                                                                                                                                                                                    Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
                       hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a human 1gM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-scFvs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-scFv is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
                                                                                       N-PSDB;
                                                                                                                         Pan C,
                                                                                                                                                  (FARB )
(MORP-)
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                                                                                                                                                                                                                                                             WO200286085-A2
                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                              BAYER CORP.
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                                                                                       ABZ74789
                                                                                                                       Knorr AM,
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                     or lung cancer
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ilarity 74.6%;
Conservative 1
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                                                                                                                       Schauer
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Pred. No. 2.2e-40;
                                                                                                                     Hirth-dietrich
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20; Page 158-159;

228pp;

English

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RESULT 15
ABP45722
ID ABP45722
ID ABP45722
ID ABP45727
XX ABP457
XX 19-AUI
DT 19-AUI
DE Human
XX Lumou
KW Lumou
KW immun
KW system
KW commo:
XX System
KW 10-J00
XX 10-J0
XX 11-J0
XX 11-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor; B cell proliferation; B cell differentiation; humannesuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; ribeumatoid arthritis; CVID; AIDS; common variable immunodeficiency; accuired immunodeficiency;
                                                                                                                                                               16-JUN-2000; 2000US-212210P
17-OCT-2000; 2000US-240816P;
16-MAR-2001; 2001US-276248P;
21-MAR-2001; 2001US-277379P;
25-MAY-2001; 2001US-293499P
                                                                                    (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200202641-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                 CAMBRIDGE ANTIBODY
                                                                                                            HUMAN
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                           Barash
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                        Choi GH,
                                                                                 TECHNOLOGY.
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Pred. No. 2.6e
10; Mismatches
                     Vaughan
                     H
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ARBSULT 12
AAB3683
ID AAB36
XX AAB36
XX 16-FE
XX 16-FE
XX Human
XX Human
XX CTN-C
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Best Local Sim
Matches 101;
                                                                                                                                                                                                                                                                                         Human; antibody cTN-C.
  20-APR-1999;
                                                        19-APR-2000;
                                                                                                                 26-OCT-2000
                                                                                                                                                                       WO200063699-A1
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          Recombinant human antibody scrv TN11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36083 standard; Protein;
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113 DIWGRGTLVTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS03455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPD---AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLVQSGAEVXXPGSSVXVSCKASGGTESSYAISWVRQAPGQGLEMMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREAS-----LNLWPDPTWAF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                        2000WO-EP03550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
99IT-FI00094
                                                                                                                                                                                                                                                                                                                    scFv; TN11; Tenascin-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                members of antibody molecules which bind in the treatment of obesity and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 504.5; DB 2:
Pred. No. 8.4e-41;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                 TN-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                 domain C-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125;
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RESULT 13
AAU97198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a recombinant human antibody scFv. Antibody TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (cTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligands used for diagnosis and treatment of human neoplasias, capable of identifying the tenascin-C isoform containing doma: tenascin-C -
                                    WPI; 2002-463261/49
                                                                                                                                                                                                                                            Human; anti-epidermal growth
                                                                                                                                                                                                                                                                   Human anti-EGFR single-chain
                                                                                                                                                                                                                                                                                            27-AUG-2002
                                                                                                                                                                                                                                                                                                                                          AAU97198 standard; protein; 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                          13-OCT-2000; 2000US-240353P
                                                                                                                                 12-OCT-2001; 2001WO-US31857
                                                                                                                                                                                 WO200230984-A1
                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                anti-EGFR-scFv;
                                                                                                                                                                                                                                                                                                                    AAU97198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5-6; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                          18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human neoplasias.
                                                                                   (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHIL-) PHILOGEN SRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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DB; AAC67868.
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                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                           χ̈́P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        GRGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                              GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSRRITIFGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG1IPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 AA;
                                                           Curiel DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                IgM; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%;
76.9%;
                                                          Bonner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                             factor receptor single-chain antibody;
tumour growth; clone pSEX81-63; cytostatic
                                                                                                                                                                                                                                                                    antibody isolated from clone pSEX81-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 504.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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domain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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Novel human anti-epidermal growth factor receptor single-chain antibody useful for diagnostic location and assessment of tumour growth, and in

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RESULT 10
ABP45855
ID ABP45855
XX ABP45
XX ABP45
XX IP-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B16P.
16-MAR-2001; 2001US-276246P.
21-MAR-2001; 2001US-277379P.
                                                                                                                                                                                                                                                                                                                                                   BLy8; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomoublatory; antitheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                           15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                        10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic, immunosuppressive, immunostrimulant, immunomodulatory, inhibit the expression and activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in abiological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression of activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (e.g. common variable immunodeficiency (c.g. common variable immunodeficiency (e.g. common variable immunodeficiency (e.g. common variable immunodeficiency (evil) and the antibodies and fragments of the antibodies described in the method of the invention.
                                                                                                                                                                                                                                                                 WO200202641-A1
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human BLyS binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45855 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a metumour necrosis factor (TNF) super family and induces B c proliferation and differentiation. The antibodies of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2645-2646; 3148pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDIWGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTADGSTSTAYMELNSLRSEDTATYYCARQQN----GGWYEGPLLEPRPDA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDIWGRGTMVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARESHYDILTGYYSNP-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLQQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 describes novel timulator (BLys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scrv SEQ ID 1866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 508.5;
Pred. No. 7.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies that immunospecifically bind polypeptides. BLyS is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
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RESULT 11
AAU02555
ID AAU02525
AC AAU02
XX AAU02
XX 29-AU
XX Anti-
XX Anti-
XX Anti-
XX Heart
XX Heart
XX Homo
XX Homo
XX Homo
XX Homo
XX 19-AF
PN 11-OC
XX 11-OC
XX 12-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel antibodies that immunospecifically bind to CC Blymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiAlDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS of and so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC and so may be used to this way to diagnose disease CC associated with aberrant ENyS expression of BLyS. They may also be composed to treat diseases associated with aberrant BLyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (cVID) and CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 100
                            11-OCT-2000; 2000WO-GB03900
                                                                                                WO200127279-A1
                                                                                                                                  Homo sapiens.
                                                                                                                                                            Antibody; adipocyte; heavy chain; light chain; obesity; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                            Anti-adipocyte monoclonal antibody heavy chain, FAT 41
                                                                                                                                                                                                                                                    29-AUG-2001
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                                                                                                                                                                                                                                                                                                              standard; Protein; 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQ-----NGGWYEGPLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                      EPRPDALDIWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA;
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71.4%;
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Pred. No. 8.5e
10; Mismatches
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12-OCT-1999;

9905-0158812

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RESULT 8
ARB45498
AID 45498
AID ABP4
AX ABP44
AX ABP4
AX BLY8
AX ELUNO
AX ELUNO
AX EVANT
AT EVANT
AX E
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                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                               Claim 1; Page 2203-2204; 3148pp; English
                                                                                         Antibodies against B Lymphocyte Stimulating polypothe diagnosis and treatment of cancers and immune
                                                                                                                                                                                         WPI; 2002-114799/15
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CAMBRIDGE ANTIBODY TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQGTLVTVSS 116
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76.9%;
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Pred. No. 3e-41;
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                                                                                            polypeptides, useful
immune disorders -
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RESULT 9
ABP45869
ID ABP4
XX ABP4
XX ABP4
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XX Enmm
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XX BY8
XX BOD
10-1
XX HOM
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                                                                                                                                                                               16-JUN-2000; 2000US-212210P: 17-OCT-2000; 2000US-240816P: 16-MAR-2001; 2001US-276248P: 21-MAR-2001; 2001US-277379P: 25-MAY-2001; 2001US-293499P
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                                                                                         (HUMA-) HUMAN GENOME SCI INC
(CAMB-) CAMBRIDGE ANTIBODY T
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                                                                                               TECHNOLOGY.
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Best Local Similarity
Matches 100; Conserv
The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of conformations in the method is useful for constructing a library of structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, peptides and nucleci acids. The libraries constructed are useful as a peptides and nucleic acids. The libraries constructed are useful as a
                                                                                                                                                                                                               Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures into structural ensembles
                                                                                                                                                                                       Disclosure; Fig 13B; 119pp; English.
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Best Local S
Matches 100
                                                                                                                                                                                                           New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a in which TIMP-1 is elevated, e.g. liver fibrosis, benign proshypertrophy or lung cancer -
                                                                                                                                                                  Claim 20; Page 173; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB )
(MORP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer
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The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (1 and neutralises a matrix metalloprotease (MMP)-inhibiting activity TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region a variable light chain (VLC)DR3 region. An antibody preparation of invention has hepatotropic, cytostatic, nephrotropic and cardiant

region and

(TIMP-1)

Claim 1; Page 2646-2647; 3148pp; English

This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell crown of the conversation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, compared to and antiALDS activity and can be used in vaccines to can thibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in cC and so may be used to detect and quantitate the presence of BLyS in cC associated with aberrant expression of BLyS. They may also be cambinistered to treat diseases associated with aberrant BLyS expression cC and activity such as cancer, immune, and autoimmune disorders and cc immunodeficiency (e.g. common variable immunodeficiency (cvID) and cc acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent confirmed the invention.

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RESULT 4
AAW27550
ADW27550
ADW27550
AW2752
AC AAW2
AC AAW2
AC Huma
XX Huma
XX Huma
XX Homc
XX Hom
             Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
                                                                                                                                                                                                                                                                                                                               Ge L,
                                                                                                                                                                                                                                            WPI; 1997-179277/16.
                                                                                                                                                                                                                                                                                                                                                                                            (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09708320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                           Ilag V,
                                                                                                                                                                                                         AAT87948
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                                                                                                                                                                                                                                                                                                                      Knappik A,
                                                                                                                                                                                                                                                                                                                  Moroney S,
                                                                                                                                                                                                                                                                                                             Pack P,
                                                                                                                                                                                                                                                                                                         Plueckthun A;
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The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two conformations. The method is useful for constructing a library of artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies

Disclosure; Page 98-99; 119pp; English.

into structural ensembles

밁 5 멍 S 밁 ঠ

112 121

GKGTMVTVSS

121

GOGTMVTVSS 130

61 13 بر

AQKFQGRVTITADKSTSTAYNELSSLRSDDTAVYYCARDSGSYYY-----DAFDIW AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY 60 Query Match Best Local Sim Matches 100;

Similarity

74.8%; 76.9%;

Score 514.5; Pred. No. 1.9e 9; Mismatches

.9e-41; DB 23; 12;

Indels Length

Gaps

244; 9.

Conservative

Sequence

244 AA;

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RESULT 5
ABJ18672
ID ABJ1
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                               Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-093043/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luo P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2001; 2001US-284407P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2002; 2002WO-US12202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody library related heavy variable chain protein region SEQ ID No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogenecity; antibody therapeutic
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76.9%;
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Pred. No. 1.5e
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human LH13 monoclonal antibody heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY99558 standard;
The present sequence is the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively antigens which are not present on normal cells. Thus monoclonal antibodies can be produced that are specifically directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cytotoxic; heavy chain variable region.
                                                                                                                                            Claim
                                                                                                                                                                                            determining region
                                                                                                                                                                                                                     New tumor-specific human and diagnosis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                     Watkins JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1999;
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DB; AAA48411.
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                                                                                                                                      Page 82-83; 84pp; English
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                                                                                                                                                                                                                     comprises
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Pred. No. 2.2e-58;
Mismatches 0;
                                                                                                                                                                                                                  l antibody, useful for the treatment at least one complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 130;
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RESULT 3
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Matches 99
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                                                                                                                                                            16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B16P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficie systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding scFv SEQ ID 1881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP45870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP45870 standard;
                                                                                                                                                                                                                                                                                                                  WO200202641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-2002
                                                        WPI; 2002-114799/15
                                                                                                                  (HUMA-)
                                                                                                                                                                                                                                                                                    10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                      15-JUN-2001; 2001WO-US19110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
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                                                                                      MS,
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                                                                                                                HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVIMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDSSGWYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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                                                                                      Barash
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76.2%;
                                                                                      Choi
                                                                                                                    TECHNOLOGY
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Pred. No. 5e-42;
9; Mismatches
                                                                                      Vaughan
                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                      Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118;
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Antibodies the diagnos

ibodies against diagnosis and t

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Stimulating polypeptides, u cancers and immune disorders

useful for

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Title:
Perfect score:
Sequence:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                   4004
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seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                              is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-674-752-23
688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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1: /SIDS1/gcgdata/g
                                                                                                                                                                                                                                                                                                                                                                                                        | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:
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    AAY50948
AAY99558
ABP45870
AAB9457570
ABJ18677
ABJ18718
ABP01538
ABP45498
                                                                                                                                                                                                                                                                                       SUMMARIES
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Human anti-factor
Human LH13 monoclo
Human BLyS binding
Human Ab heavy cha
Antibody library r
Antibody library r
Human anti-TIMP-1
Human BLyS binding
                                                                                                                                                                                                                      Description
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ALIGNMENTS

RESULT 1 AAY50948

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New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; VH gene.
                                             WPI; 2000-053102/04.
                                                                                                                  08-MAY-1998;
                                                                                                                                        07-MAY-1999;
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                    Human anti-factor VIII antibody VH clone EL-14 encoded protein.
                                                                                                                                                                                                                                                                                           23-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                 AAY50948;
                                                                                                                                                                                                                                                                                                                                        AAY50948 standard; Protein; 130
                                                                    Voorberg JJ, Van Den Brink EN,
                                                                                                                                                              18-NOV-1999.
                                                                                                                                                                                    WO9958680-A2
                                                                                           (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                  98EP-0201543.
                                                                                                                                         99WO-NL00285
                                                                                                                                                                                                                                                                                                                                        ₹
                                                                    Turenhout EAM
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80

NEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFCTR--GGGW-----AFDYW 126

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RESULT 14

Q924Q1

ID Q924Q

AC Q924Q

DT 01-DE

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COC Mamman

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RESULT 15
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OC Mamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
PEam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 112 112
SEQUENCE 142 AA; 15622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOZONO Y., KOZONO H., AZUMA T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1; --
                                                                                                                                                                                                                                           O95978;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
VH1 protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q924Q1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  TISSUE=Peripheral blood;
Jox A., Zander T., Kuepp
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             095978
                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGABAKKPGSSVKVSCKASGDTFNSFPISMVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQGTSVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
Kueppers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15622 MW; 24A265CE4EA4318B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.7%; Score 383.5; DB 11; Length 142; 57.7%; Pred. No. 3.5e-32; tive 18; Mismatches 24; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
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     Irach
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  Kanzler H.,
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     Kornacker
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Best Local S
Matches 81
                                                                                                                                                                                                                                               InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                Bohlen H., Diehl V., Wolf J.;

"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated w somatic mutations within the untranslated regions of rearranged class switch recombinated Ig genes.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ005570; CAA06599.1; -.

HSSP; P01772; ZFP4.

HSSP; P01772; ZFP4.
                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                               NON TER
 130
                        117
                                                                                                                                                  81;
                                                 80
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                                                                                                                         -
                                                                                                                                                               Similarity
                                                                                                ---WGQGTPVTVSS
                                                                  AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGW----YEGPLLEPRPDA 116
                       LDIWGQGTMVTVSS 130
                                                 AEKFOGRLTMTRNTSTTTVYMELSRLRFEDTAVYFCGR--GGRWRSGNYNGH-----
                                                                                                                                                                                            1 21 POTENTIAL.
157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
                                                                                                                                                   Conservative
                                                                                                                                                  55.6%; Score 382.5; DB 60.4%; Pred. No. 5e-32; tive 10; Mismatches
                                                                                                                                                                           DB 4;
                                                                                                                                                   26;
                                                                                                                                                      Indels
                                                                                                                                                                             Length
                                                                                                                                                                               157;
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Search completed: December 30, 2003, 11:01:02 Job time : 32.6816 secs

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RESULT 12
Q921C4
ID Q921C
AC Q921C
AC Q921C
O1-MA
DT 01-MA
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DT 01-MA
COS Mus m
OC Eukar
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                                O9Z1C4

PRELIMINARY; PRT; 118 AA.

O9Z1C4;

O9Z1C4;

O9Z1C4;

O1-MAY-1999 (TrEMBLrel. 10, Created)

O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Anti-porcine VCAM mAb 3F4 heavy chain variable regic

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                     Matches
 SEQUENCE FROM N.A. STRAIN=Balb/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Song X.T., Feng Z.Q., Guan X.H.;

"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GYZ2

PRELIMINARY; PRT; 119 AA.
Q9GYZ2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Monoclonal anti-idiotypic antibody NP30 heavy cha
                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; D
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282622; AAG01452.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE
                                                                                                                                                                                              110
                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                    NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCARYYDDHY-----
                                                                                                                                                                                                                                              AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                                                                                                              QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                GOGTMVTVSS 130
                                                                                                                                                                                            COCTIVIVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRL-GRWY------
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                                                                                                                                                                                                                                                                                                                                                                              119 J
119 AA;
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                              13567 MW;
                                                                                                                                                                                                                                                                                                                                           57.0%;
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                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                            Score 392.5; DB 5; Length 119;
Pred. No. 3.2e-33;
14; Mismatches 26; Indels 11
                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                            BA893873FD5FA6AB
                                                                        cation update)
variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Digenea;
                                                                        (Fragment).
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RESULT OPEN COLUMN COLU
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Best Local S
Matches 77
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dan Submitted (SEP-2001) to the EMBL/GenBank/DDBJ dan Submitted (SEP-2001); Ig-like.

InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MGC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NON TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 52.1 kDa protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91WT1;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALL 60
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NON_TER
SEQUENCE
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"Humanized porcine VCAM-specific monor area po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cells.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U78801; AAD00293.1;
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
61 AOKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGGWYEGPLLEPRPDALDIW
                                                                                                                                   20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
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                                                                                                                                                                                                                                                                                          . Similarity
77; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 75; Conserv
                                                                                                                                                               QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                       OVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOGTTLTVSS 118
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                  56.5%;
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57.7%;
                                                                                                                                                                                                                                                                          ; Score 388.5; DB 11; ; Pred. No. 4.8e-32; 17; Mismatches 23;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                              97DF68D159463F65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90EEC559D31EC4FC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВG
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with chimeric
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SOUTH THE TRANSPORT OF 
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RESULT
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ID Q9
AC Q9
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OC EU
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RA Habibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Kusanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Sugiyama T., Isogai T., Sugano S.;
RI Sugiyama CDNA sequencing project.";
RA Sugiyama A.,
RA 
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Best Local S
Matches 83
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein FLJ25298.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96DK0
                                                                                                                               Q9BRV0
Q9BRV0;
Q1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Mecazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                          Created)
                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 3.6e-34;
1; Mismatches 26,
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 14;
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RESULT 10
Q8VCX7
ID Q8VCX
AC Q8VCY
AC Q8VCY
DT 01-M
DT 01-M
DT 01-M
DT 01-M
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Best Local S
Matches 81
                                                                                        Matches
                                                                                                          Query Match
Best Local (
                                                                                                                                                                         Strausberg R.;
Submitted (DEC-2001) to the EME
Submitted (DEC-2001) to the EME
EMBL; BC018315; AAH18315.1; -.
MGD; MG1:96448; Igh-6.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
SMOSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBVCX7 PRELIMINARY; PR
OBVCX7; PRELIMINARY; PR
OBVCX7; Crea
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 67.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGH-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 -- YMDVWGKGTTVTVSS
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                                       1 QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCONDYYYY-----
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                                                                                     Conservative
                                                                                                                                                                                67855 MW;
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59.2%;
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                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                        Score 397; DB
Pred. No. 8.5e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 407; DB 4
Pred. No. 6e-34;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OA9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613
                                                                                          DB 11;
3.5e-33;
hes 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 500;
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RESULT Q96QSO DT DT COC Q0 COC QC COC
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Q9Y298;
01-NOV-1999
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY039025; AAK82649.1; -.
SEQUENCE FROM N.A.
MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L
                                                                                                                                                   Homo gapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                          IGG VH.
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 85
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Best Local S
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
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HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL94;
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                   HSSP;
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                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                  fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis
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150 AA;
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Primates;
                                                                                                                                                       13205 MW; 13E64F5345F4A16E CRC64;
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64.6%;
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                                                                 12;
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                                                               Score 420.5; DB 4;
Pred. No. 3.9e-36;
2; Mismatches 21;
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RESULT POPULS SOLUTION OF SOLU
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EMBL; AF035019; AAD56255.1; -.
HSSP; P01810; 2FBJ.
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MEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                      Q9UL92
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Mammalia; Eutheria; Primates;
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Pred. No. 1.9e-39;
Wismatches 25; Indels
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                 chain variable
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DR Pfam; PP00047; Ig_v.
DR SMART; SM00406; IG; 1.
NR PROSITE; PS50835; IG_LIKE; 1.
T NON_TER 124
SEQUENCE 124 A 2
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Best Local S
Matches 89
                                                                                                                                                                                                           InterPro; IPRO00005; HTHARAC.
InterPro; IPR00710; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
PROSITE; PS00040; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; 55EF536E
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O96GA6;
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
O1-MAR-2003 (TrEMBLrel. 23,
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EMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2FB4.
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MEDLINE=99277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC009851; AAH09851.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
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                                                                             89;
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       QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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Primates;
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Last sequence update)
Last annotation updat
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                                                                      Score 438.5; DB
Pred. No. 4e-37;
8; Mismatches
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Perfect score:
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688
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sp_unclassified:*
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(c) 1993 - 2003 Compugen Ltd.
 09UL89
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Ogul89 homo sapien
Qgul95 homo sapien
Qgul95 homo sapien
Qgul96 homo sapien
Q96ga6 homo sapien
Q96g80 homo sapien
Q90298 homo sapien
Q90194 homo sapien
Q901v0 homo sapien
Q90rv0 homo sapien
Q90rv7 mus musculu
Q90r22 schistosoma
Q921c4 mus musculu
Q921d4 mus musculu
Q924d1 mus musculu
Q924d1 mus musculu
Q924d1 mus musculu
Q9298 homo sapien
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360	361	361	361	363	363	363.5	364	364.5	364.5	365	367.5	368.5	369.5	370	370	370.5	371	371	371.5	373	375	375	376	376	377.5	380	380.5	382
52.3	52.5	•	•	52.8	•	•	•	53.0	•	53.1	53.4	53.6	53.7	53.8	•	53.9	•	53.9		٠	•		•	54.7		•		•
141	145	143	137	473	143	142	143	146	140	463	117	480	146	145	143	147	143	143	144	145	482	143	145	145	473	145	497	145
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Best Local S
Matches 92
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InterPro; IPR003006; Ig_MGC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG LIKE; 1.
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5 VQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKYAQKF 64
                                                                                                              l Similarity
92; Conserv
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116 AA;
                                                                                                                  Conservative
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12605 MW; C8F9131DE13EA898 CRC64;
                                                                                                                                            67.2%;
72.4%;
                                                                                                              8;
                                                                                                           Score 462; DB 4; Length 116;
Pred. No. 1.8e-40;
8; Mismatches 15; Indels
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RESULT 15
HV48 MOUS
ID HV48
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HV48_MOUSE STANDARD; PRT; 138 AA.
P03980;
P03980;
23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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NON TER
SEQUENCE
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Cell 24:625-637(1981)
                                                                                                                             MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A02038; G2MS43.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NPB ANTIBODIES).
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                                                                                                                                                                                                                                      GOGTMVTVSS 130
                                                                                                                                                                                                                                                                                                  QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                          NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARYRLGRYF--
                                                                                                                                                                                                                                                                           QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50835; IG LIKE;
                                                                                                                                                                            GOGTTLTVSS 137
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50
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69
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118
113
123
123
137 AA;
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54
68
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117
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137
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                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 354; DB 1;
Pred. No. 1.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                            ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   2 SEGMENT.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                Length 137;
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DOMAIN
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SEQUENCE FROM N.A.
MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                           "Illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                 PROSITE
                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                             InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                   PIR; A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                                                                           Tucker P.W.;
                                                                                                                                                                                                                                                                        mmunoglobulin
129
                 121
                                     80
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                                                                                             Н
                                                                                                                l Similarity
69; Conserv
                  GQGTMVTVSS 130
                                    NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCAR--SDGYY----
                                                     AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                        QVQLVQSGABAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
GOGTLVTFSA 138
                                                                           QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY
                                                                                                                                                                                                                                                                                   PS50835;
                                                                                                                                                       138 AA;
                                                                                                                Conservative
                                                                                                                                                                                   21
50
55
69
118
128
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335; IG_LIKE;
1 V region; Si
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49
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68
85
117
127
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115
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; Ig_MHC.
; Ig_v.
                                                                                                                                                       15576
                                                                                                                       50.1%;
                                                                                                                                                                                                                                                                        Signal.
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                                                                                                                21;
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                                                                                                                        Score 344.5;
Pred. No. 1.
                                                                                                                                                                                                             IG HEAVY CHAIN V REGION TEPC 1017.

REMEMORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                         FRAMEWORK-4.
BY SIMILARITY
                                                                                                                                                                                            FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                       748157E4C6907B8E CRC64;
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   J.E., Blattner F.R., Mushinski
                                                                                                                No. 1.6e-28; smatches 29;
                                                                                                                                   DB 1;
                                                                                                                 Indels
                                                                                                                                  Length 138;
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                                      DWEVYW
                                                                                                                Gaps
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Search completed: December 30, 2003, 10:55:49 Job time: 7.96994 secs

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InterPro; IPMC.
InterPro; IPMC.
InterPro; IPMC.
InterPro; IPMC03596,
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                                                                                        Query Match
Best Local S
Matches 71
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Best Local S
Matches 74
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin v region.
DOMAIN
NON TER 114 114
NON TER 114 114
                                                                                                                                                                                                                                                                                                                                                            HSSP, P01810; 2FBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphocytes is encode
EMBO J. 3:517-523(19)
PIR; A02037; MHMS15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e
lymphocytes is encoded by a large se
EMBO J. 3.517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
19 heavy chain V region AC38 15.3.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P06329;
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                                                                                    Similarity 54.2
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QVQLLQPGTELVKPGASVNLSCKASGYTFTSYMMHWIRQRPGQGLEWIGGINPSNGGTNY
                     QVQLVQSGAEAKKPGSSVKVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
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milarity 58.7%;
Conservative 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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12555 MW; 99DD8F0B6A69F4BE
                                                                                                     52.0%;
54.2%;
                                                                                    18;
                                                                         Score 358; DB
Pred. No. 5.7e-
18; Mismatches
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Pred. No. 3.4e
17; Mismatches
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                                                                                                                                                                                                      V SEGMENT.
D SEGMENT.
J SEGMENT.
3Y SIMILARITY.
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                                                                                                                                                              914453F426F09834 CRC64;
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) expressed at high frequency in B
set of antibody structural genes.";
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                                                                                DB 1; I
5.7e-30;
les 30;
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§.4e-30;

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; Murinae; Mus
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Dildrop R., Bovens J., Siekevitz M., Be
"A V region determinant (idiotope) expi
lymphocytes is encoded by a large set of the set of
                                                                                                                                                  HV11 MOUSE
P01755;
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01-JAN-1988 (Rel. 06,
15-JUL-1999 (Rel. 38,
1g heavy chain V reginum user musculus (Mouse).
    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertei
Mammalia; Eutheria; Rodentia; Sciurognathi; M
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SEQUENCE
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DOMAIN 1
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HV51_MOUSE
P06330;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                  GQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMMWVKQSHGKSLEWIGDINPNNGGTSY
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                                                                                                                                                                                                                                                                             GIGITVIVSS
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118
118
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ilarity 54.6%;
Conservative 1
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(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
in V region AC38 205.12.
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 354; DB 1; i
Pred. No. 1.4e-29;
7; Mismatches 30;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94F7BEE4C762A018 CRC64;
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expressed at high frequency in B
set of antibody structural genes.";
                                                                                                                                                                      137
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Best Local :
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P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
15-SEP-2003 (Rel. 42, Last annotation updat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Amino acid sequence of the variable region of heavy chain in inmunoglobulin (Mot) having unusual papain cleavage sites."; Mol. Immunol. 23:169-174(1986).
PIR, A02025; HYHUMO.
HSSP; P01772. PER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
SEQUENCE
                                                                                                                                                           Ig heavy chain V region B1-8/1
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                          MOUSE
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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66; 66
66; 66;
                                                             "Heavy chain variable region contribution antibodies: somatic mutation evident in a
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
  Thie
                                                                                                      MEDLINE=81234548; PubMed=6788376;
                                                                                                                   STRAIN=C57BL/6;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=10090;
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Mammalia; Eutheria; Primates;
                                                                                   Baltimore D.;
                                                                                            Bothwell A.L.M., Paskind
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activ
GO:0006955; P:immune response; NAS.
                              1 24:625-637(1981).
MISCELLANEOUS: THE B1-8 NAKING ANTIBODIES TO THE
SWISS-PROT entry is
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                     ANTIBODIES).
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Pred. No. 2.6e
12; Mismatches
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Sciurognathi;
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity; NAS
                                                                                                                                                                                          precursor.
  H
                              WRNA WAS CLONED FROM A HYBRIDOMA (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                            Imanishi-Kari T.,
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 18
                                                                                                                                                           Vertebrata;
thi; Muridae;
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produced
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through
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; Murinae; Mus
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collaboration
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Best Local S
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21-JUL-1986
21-JUL-1986
15-SEP-2003
                             STRAIN=A/J;

MEDLINE=79195438; PubMed=109536;

Capra J.D., Nisonoff A.;

Capra J.D., Nisonoff A.;

"Structural studies on induced antibodies with defined i specificities. VII. The complete amino acid sequence of chain variable region of anti-p-azophenylarseenate antibo mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
NON TER
SEQUENCE
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region (Anti-arsonate anti
Mus musculus (Mouse)
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                  SEQUENCE
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or send an email to license@isb-sib.ch).
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SMART; SM00406; IGV;
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PDB; 1A6W; 15-JUL-98.
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                                                                                                                                       NCBI_TaxID=10090;
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Immunoglobulin V region; Signal;
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InterPro; IPR003006;
InterPro; IPR003596;
MISCELLANEOUS: ANTIBODY THE IGG1 SUBCLASS. THERE REGION SEQUENCE.
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Rodentia;
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Ig_MHC.
Ig_v.
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Pred. No. 3.3e
17; Mismatches
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JH2 SEGMENT.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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           HETEROGENEITY 1
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e antibody).
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3.3e-30;
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Schilling J. Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).

-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS,
WHICH OCCUR IN THE D AND J SECMENTS.

-i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-i- SIMILDARITY: Contains 1 immunoglobulin-like domain.
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region J558.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A26242; MHMSJ5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01789; 1MCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      госат
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                                                                                                             AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGWYEGPLLEPRPDALDIW 120
                                                                                                                                                                                    OVQLVQSGAEAKKPGSSVXVSCKASGDTENSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                      GQGTMVTVSS 130
                                                                            NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-
                                                                                                                                                                 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTTVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQLQOSGPELVKPGASVKMSCKASGYTFTDYYMKMVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                                                                                                   22
117
117 AA;
                                                                                                                                                                                                                                                            53.3%;
ilarity 55.4%;
Conservative 18
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                                                                                                                                                                                                                                                                                                                                               13024 MW; 292E2AF4BE447E41 CRC64;
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                                                                                                                                                                                                                                                              18;
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Pred. No. 5.9e
18; Mismatches
                                                                                                                                                                                                                                                         Score 366.5; DB 1
Pred. No. 7.4e-31;
8; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3CF8ACE4BE447E41 CRC64;
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OF
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RESULT 9
HV1F HUMAN
ID HV1F HUMAN STANDARD; PRT; 125 AA
AC P06326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 heavy chain V-I region Mot.
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ID HVO3_MO
ID 
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Best Local S
Matches 74
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NON TER
SEQUENCE
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P01746;
P01746;
P01746;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Somatic mutation in genes for the variable immunoglobulin heavy chain."; Science 216:309-311(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra J.D.;
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                                                                                                                                                                                                                                                                                                                                             WGQGTMVTVSS 130
                                                                                                                                                                                                                                                                                                                                                                                                  NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY
                                                                                                                                                                                                                                                                                             WGQGTPLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.8%; nilarity 56.5%; Conservative 18
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T.H., Estess P.,
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                                                                                                                                                                                                                                                                                             140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 363.5; DB 1;
Pred. No. 1.9e-30;
8; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V REGION IG-LIKE.
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RESULT
HV03_M
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Best Local S
Matches 74
                                                                                                                                   HV03 MOUSE STANDARD; PR
P01747;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 02, Last seque
15-SEP-2003 (Rel. 42, Last annot
19 heavy chain V region 36-65.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
NCEI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
                               SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeu
Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
NON TER
                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
GO; QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDIJNE=88296408; PubMed=2841108;
Matsuda F. Lee K.H., Nakai S., Sato
Ohno H., Fukuhara S., Honjo T.;
Dispersed localization of D segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07448; -; NOT_ANNOTATED_CDS.
PIR; S00476; HVHU35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO´J. 7:1047-1051(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human). Eukaryota; Mammalia; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy-chain locus
                genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain V-I region V35 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
20
20 >
117
117 AA;
              basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
>117
117
of antibody production: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.2%;
75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                       sequence up
                                                  Brodeur P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 380; DB
Pred. No. 3e-3
6; Mismatches
                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V-I REGION IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE61CE63F8CE97BD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity; ; NAS.
                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                         update)
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                                                    Riblet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kodaira M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                  70
    dominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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HV12
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Best Local S
Matches 75
DISULFID CARBOHYD NON_TER
                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                     Immunoglobulin
DOMAIN
                                                                                                                                                                          "Complete amino acid sequence of a m heavy chain constant region domains. Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF T PROTEIN HAS ALSO BEEN DETERMINED
                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
HV12
                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region MOPC 104E.
                                                                                                                               PIR; A02039; MHMS4E.
HSSP; P01789; 1MCP.
                                                                                                                                                 PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                            SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE MEDLINE-83075344; PubMed=6816276; Mehry M.R., Fuhrman J.S., Schilling J.W....
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                Ig heavy chain V reg
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGMENT, JH2.
-!- SIMILARITY: Con
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
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 PS50835; IG_LIKE; 1.

obulin V region; Glycoprotein.

1 16 IG-LIKE.
2 96 BY SIMILARITY
55 55 N-LINKED (GLC)
117 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ--QNGGWYEGPLLEPRPDALDI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGQGTTLTVSS
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120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.9%;
                                                                                                                                                                                    SEQUENCE OF THE LIGHT
                                                                                                                                                                                                                                            Schilling J.W., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 370.5; DB Pred. No. 3e-31;
                                                                                                                                                                                                                       of a mouse mu
                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                   117
            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                     ASN-55.
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                                                                                                                                                                                                                       chain:
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
                                                                                                                                                                                     QF
                                                                                                                                                                                                                    homology
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                                                                                                                                                                                                                                          Sibley C.H.,
                                                                                                                                                                                    THIS IGM MYELOMA
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AUTHORS
TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAME
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RESULT 3
HV1C_HUMAN
ID HV1C_HUMAN
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Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NON_TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 - SEP-2003 (Rel. 42, Last annotation update)
17 - Sep-2003 (Rel. 42, Last annotation update)
18 - Sep-2003 (Rel. 42, Last annotation update)
19 - 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003956; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00240; AAA52988.1; -. PIR; A02024; HVHUHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene subgroups.";
:. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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                                                                                                                              90
                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQQNGGW--YEGPLLEPRPDALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GGLVTVSS 117
                                                                                                                                                                                                                         QVQLVQSGAEVKKPGASVKVSCKASGYTENSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                                                                                  QVQLVQSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGGIIPIFGSTKY
                                                                                                                                                        AQKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR 98
                                                                                                                              AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                     20
20 >
117
117 AA;
                                                                                                                                                                                                                                                                                                                       59.9%;
ilarity 82.7%;
Conservative
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       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
>117
117
                                                                                                                                                                                                                                                                                                                                                                                                                          12946 MW;
                                                                                                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                                                                                                     Score 412; DB 1; 1
Pred. No. 1.6e-35;
5; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-I IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          2D3F92FC60CD1FE7
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          147
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                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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                                                                                                                                                                                                                                                                                                                            Indels
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(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 42, Last annotation updat

STANDARD;

PRT;

117

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RESULT 4
HV1G HUMF
ID HV1C
AC P23C
DT 01-N
DT 01-N
DT 15-S
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Best Local S
Matches 79
HUMAN
HV1G HUMAN
P23083;
01-NOV-1991
01-NOV-1991
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
MOD RES
DISULFID
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-I region ND precursor (Fragmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01789; IMCP.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
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O1-MAR-2001 (TrEMBLrel. 16, Created)

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D-alanine:D-alanine ligase.

Enterococcus faecium (Streptococcus faeci

Bacteria; Firmicutes; Lactobacillales; En

NCBI_TaxID=1352;
STRAIN=A902;
Gold H.S., Eliopoulos G.M., Mc
"D-alanine:D-alanine ligase of
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EMBL; AF215736; AAG49141.1; -
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Pfam; PF01820; Dala Dala IIgas; 1.
TIGRFAMs; TIGR01205; Dala Dala DalaTIGR;
PROSITE; PS00843; DALA DALA LIGASE 1;
PROSITE; PS00844; DALA DALA LIGASE 2;
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Tulkens P.M., Courvalin P.,
"Sequencing of the ddl gene
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SEQUENCE FROM N.A.
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01-VUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
D-alanine:D-alanine ligase
Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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                                  Q9H685 PRELIMINARY; PRT; 322 AA.
Q9H685;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ22501.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP000061; BAA80534.1; -
InterPro; IPR001005; Myb_DNA_binding.
PROSITE; PS00334, MYB_Z; 1. -
LYase; Pyruvate; Complete proteome.
SEQUENCE 403 AA; 47103 MM; 6B68528AD393DDD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., P. Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.", DNA Res. 6.83-101(1999)
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STRAIN=K1;
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01-NOV-1999 (TremBLrel.
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403AA long hypothetical
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Desulfurococcaceae; Aeropyrum.
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01-NOV-1999
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InterPro; IPR005905; D_ala_Dala.
Pfam; PF01820; Dala_Dala_ligas; 1.
TIGRPAM6; TIGR01205; D_ala_DalaTIGR; 1.
PROSITE; PS00843; DALA_DALA_LIGASE_1; 1.
PROSITE; PS00844; DALA_DALA_LIGASE_2; 1.
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ster than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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Human anti-factor
Novel human diagno
Propionibacterium
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Human novel polype
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ALIGNMENTS

Human anti-factor VIII antibody VH protein VH EL-14 CDR3

fragment.

23-MAR-2000 (first entry)

AAY50956;

AAY50956 standard; Protein; 21 AA.

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RESULT 1
ANY50956
ID ANY50956
XX ANY50956
XX ANY50
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XX Huma
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XX Huma
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XX 
New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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Best Local S
Matches 21
                                                     hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human antibody VIII antibody clone EL-14 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                         This invention
                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 4A; 6lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-053102/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Voorberg JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; VH gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-factor VIII antibody VH clone EL-14 encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY50948;
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ilarity 100.0%;
Conservative (
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Pred. No. 1.1e-11;
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymclectides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC afford supplement. (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC disorders involving aberrant protein expression or biological activity.
CC disorders for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Mote: The sequence data for this patent did not appear in the printed
CC at ftp.wipo.int/pub/published_pct_sequences.
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ABG00057
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Sequence
                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 30416; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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DB; AAS64244.
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   265
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Pred. No. 8.4e-11;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                  ion of mutations and to assess
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Query Match Best Local

Similarity

43.3%;

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22;

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Matches

9;

Conservative

2;

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RESULT 4
ANU43195
ANU
                                                           pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

C. P. acnes is also involved in infections of bone, joints and the central conervous system, however it is particularly involved in the inflammatory constituents associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a condition of the inflammatory conditions associated with a binding agent that binds to the proteins of the invention conditions agent that binds to the proteins of the invention conditions agent that binds to the proteins of the invention conditions agent that binds to the proteins of the invention conditions agent that binds to the proteins of the invention conditions agent that binds in the sample. The conditions are not polypeptides may be used as antigens in the production of antibodies conditions agents for ferming P. acnes polypeptides and conditions. The antibodies may also be used as conditions agents for determining P. acnes presence, for example, by conditions the square data for this patent did not form part of the printed conditions, but was obtained in electronic format directly from WIPO conditions.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID No 4390; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW,
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uveitis; endophthalmitis; bone; joint; central nervous system; inflammatory lesion; acne vulgaris; enzyme linked immunosorben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
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                                                    ftp.wipo.int/pub/published
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                                             _pct_sequences
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Query Match Best Local Similarity

42.9%; 71.4%;

Score Pred.

51.5; No. 3

DB 22;

Length 118,

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Sequences ABB31028-ABB35561 represent 4534 novel human proteins CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-CC ABN75887 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively collectively collectively proteins, proteins, polynucleotides at least 85% identical to the ORF1-ORF4534 (collectively collectively  And methods of screening for modulators of ORFX expression or collectively, and methods of screening individuals for a predisposition to an CC collectively collectively. The order collectively collectively collectively collectively. CC chemokinetic activity, haemostatic activity, thmoust inhibition activity, the collectively. CC collectively collectively, and may also be involved in the determination of boddily characteristics, fertility and behaviour. ORFX proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 1516; 2508pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; disbetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; neuroprotective; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerocic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABN77579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-106200/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leach MD,
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angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
thrombolytic; tumour inhibition; bodily characteristic; fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune modulation;
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itoring; cytokine; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-25825P.
27-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the esse
                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                              polynucleotides for the identification and development of biotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                               2001-611495/70
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                                                                                                                                      511pp; English
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC genes themselves and the encoded proteins. The prokaryotes used are CE Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC programmes. The antisense nucleic acid sequence for also useful to screen CC awide variety of organisms. The present sequence represents an CC awide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part CC format directly from WIDO at
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Best Local S
Matches
The present invention describes a method (M1) of evaluating the potential of a chemical entity (CE) to associate with a molecule or molecular complex comprising a binding pocket (BP) defined by specific structural coordinates (SC) of D-Ala-D-Ala ligase (I) E. coli amino acids Lys144, Glu180, Lys181, Leu183, Glu187, Asp257 and Glu270, by employing a computational unit to perform a fitting operation between CE and BP defined by SC and analysing the results of the fitting operation to
                                                                                                                                                                                             Evaluating association binding pocket defined computational unit for
                                                                                                                                                                                                                                                                                                  Navia MA,
Magee AS,
                                                                                                                                             Example 8; Fig 10; 115pp;
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co-ordinate data; D-Ala-D-Ala ligase inhibitor; antibacterial.
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Connelly PR,
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                                                                                                                                                                                    potential of chemical entity to complex having by structural coordinates, by employing entity-pocket fitting operation and analyzing
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           The present invention describes a method (M1) of evaluating the potential of a chemical entity (CE) to associate with a molecule or molecular complex comprising a binding pocket (BP) defined by specific structural coordinates (SC) of D-Ala-D-Ala ligase (I) E. coli amino acids Lys144, Glu80, Lys81, Leu183, Glu87, Asp257 and Glu270, by employing a computational unit to perform a fitting operation between CE and BP defined by SC and analysing the results of the fitting operation to quantify the association between CE and BP. Also described is a method (M2) for identifying a potential inhibitor of (I). M1 is useful for evaluating the potential of a chemical entity to associate with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quantify the association between CE and BP. Also described is a method (M2) for identifying a potential inhibitor of (I). M1 is useful for evaluating the potential of a chemical entity to associate with a molecule or molecular complex comprising a binding pocket. M2 is useful for identifying a potential inhibitor of D-Ala-D-Ala ligase. The methods are useful in the identification of key interaction in the active site of the enzyme, as well as the design and optimisation of inhibitors. The methods are also useful in the drug discovery methods, particularly for discovering new drugs that inhibit D-Ala-D-Ala ligase, an essential enzyme in the formation of bacterial cell walls. The present sequence represents a D-Ala-D-Ala ligase amino acid sequence given in an example
                                                                                                                                                                                                                                                                                                                   Magee
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data; D-Ala-D-Ala ligase inhibitor;
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by structural coordinates, by
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binding
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RESULT 9
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                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for identifying a potential inhibitor of D-Ala-D-Ala ligase. The methods are useful in the identification of key interaction in the active site of the enzyme, as well as the design and optimisation of inhibitors. The methods are also useful in the drug discovery methods, particularly for discovering new drugs that inhibit D-Ala-D-Ala ligase, an essential enzyme in the formation of bacterial cell walls. The present sequence represents a D-Ala-D-Ala ligase amino acid sequence given in an example
                                                                                                                                         neurodegenerative disorders,
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                                                                                                                                        disorders, and
                                                                                                                                                            New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer,
                                                                                                                                                                                                                                                                                           15-MAR-2001; 2001US-0810173
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T, Wang J,
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40.0%;
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1 R, Wang Z,
                                                                                                                                                  disorders,
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encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone

The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics,

degenerative disorders,

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disease,

fibrosis,

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RESULT 10
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XX TAO1;
KW D38;
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                                                                                           The present sequence represents rat TAO2 protein kinase, which is capable of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are completed for treating or preventing: (1) inflammation, completed for completed for completed for cancer and degeneration (inhibitors of phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders can meurodegeneration (enhancers of phosphorylation). TAO kinases are modulators and as immunoassay reagents for detecting TAO kinases, and (b) in the form of fragments, for detecting TAO kinase polynucleotides can be used: (a) for recombinant expression completed for the form of fragments, for detecting TAO completed for the form of fragments. Table completed for the form of fragments for detecting TAO completed for the form of fragments. Table completed for the form of fragments for detecting TAO completed for the form of fragments.
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Matches 10
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RESULT 12 ABG24835 ID ABG24 XX

ABG24835 standard; Protein; 564

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56 8 Matches Query Match Best Local :

Similarity 69.; 9; Conservative EGPLLEPRPDALD EPPXLQPGPDALD

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The present invention relates to the isolation of novel human enzyme CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences concerning them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolasses, lyases, CC diagnosis, treatment, prevention and/or prognosis of a wide range of the invention are useful in the CC disorders including hyperproliferative disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. Alzaelarer's disorders (e.g. arthritis), neurological disorders (e.g. Alzaelarer's disorders (e.g. asthma), cardiovascular disorders (e.g. atheroscience), CC (e.g. asthma), cardiovascular disorders (e.g. atheroscience), CC (e.g. asthma), cardiovascular disorders (e.g. atheroscience), CC (e.g. infertility) and infectious disorders (e.g. Inflammatory disorders (e.g. infertility) and infectious disorders (e.g. Inflammatory disorders (e.g. infertility) and infectious disorders (e.g. Inflammatory disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The CC (aANZ22915-AANZ23814 represent the novel human enzyme polypeptides of the
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 Sequence
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N-PSDB; AAS41213.
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2000US-0249217.
2000US-0249218.
2000US-0249244.
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Matches 7
            ABG24833
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                                    ABG24833 standard; Protein; 816
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO XXX
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                                             ABG04046;
                                                                    ABG04046 standard; Protein; 858
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13-FEB-2002

(first entry)

Novel

human diagnostic protein #4037

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supplement; medical imaging; diagnostic; genetic disorder.
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39 WYEAVVLAPQPETLPL 154
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CC Note: The sequence data for this patent did not appear in the printed content of the sequence of the invention.
Sequence
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Pred. No. 1.7e+02;
4; Mismatches 5
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Search completed: December 30, 2003, 10:54:32 Job time : 7.83882 secs

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Published Applications AA:*

1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARII
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43.5	44	44	44	44.5	45	46	47	47	47.5	50	50	50	50	50.5	Score
36.2	36.7	36.7	36.7	37.1	37.5	38.3	39.2	39.2	39.6	41.7	41.7	41.7	41.7	42.1	Query Match
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16825	Sequence 12356, A	Sequence 22963, A	Sequence 29, Appl	Sequence 11403, A	Sequence 11806, A	Sequence 44, Appl	Sequence 2, Appli	Sequence 748, App	Sequence 20793, A	Sequence 8003, Ap	Sequence 30, Appl	Sequence 31, Appl	Sequence 10772, A	Sequence 3841, Ap	Description

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US-10-177-293-94	US-10-205-823-76	US-09-826-752-6	US-10-042-417-52	US-10-081-872-40	US-10-369-493-23477	US-09-741-669-415	US-09-816-095-4	US-09-969-680A-31	US-09-965-529-31	US-09-738-626-5311	US-09-738-626-4654	US-10-101-482-16	US-09-864-761-42742	US-09-864-761-39151	US-10-297-022-20	US-10-297-022-15	•	US-10-340-578-22	US-09-355-815-3	US-10-320-769-2	US-10-261-049-2	US-08-556-422-2	US-09-738-626-6454	US-10-320-769-7	US-10-369-493-1856	US-09-764-891-3296	US-10-106-698-5387	US-09-917-340-71	00-03-303-604-403
94,	e 7	'n	տ		e 2	415	4	31,			Sequence 4654, Ap	Sequence 16, Appl	Sequence 42742, A	39151	20,		129	22	w	<u>ب</u>	e 2,	2, Ar	64	Sequence 7, Appli	e 18	e 3296,	e 5387,	Sequence 71, Appl	sequence 409, App

ALIGNMENTS

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
ITTLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITLE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION UNMBER: US 60/360,039
PRIOR APPLICATION ONMER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
INUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3841
LENGTH: 1427
TYPE: PRT
ORGANISM: Neurospora crassa
US-09-815-242-10772
, Sequence 10772, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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US-10-369-493-3841
                                                                                          RESULT 2
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Publication No. US20030233675A1
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Best Local Similarity 58.8
Matches 10; Conservative
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58.8%;
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Pred. No. 1.2e+02;
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR RILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 341
TYPE: DET
; LENGTH: 348
TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-186-886-31
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                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/10186886 Publication No. US20030119061A1
                                                                                                                         APPLICANT: Mage, Andrew S.
APPLICANT: Connelly, Patrick R.
APPLICANT: Connelly, Patrick R.
APPLICANT: Perola, Emanuele
TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
TITLE OF INVENTION: DRUGS
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 10283-014001
CURRENT APPLICATION NUMBER: US/10/186,886
CURRENT APPLICATION NUMBER: US 60/301,676
PRIOR APPLICATION NUMBER: US 60/301,676
RIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 52
CONTRADED FOR SEC 10.
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Best Local ?
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APPLICANT: Ala, Paul J.
APPLICANT: Griffith, James P.
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8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trawick, John D.
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Pred. No. 35;
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PUBLICATION NO. US20030119018A1

GENERAL IMFORMATION:
APPLICANT: IMFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHARKI, YOSHIYUKI
APPLICANT: SHARKI, YOSHIYUKI
APPLICANT: SHARKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
ITITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8003
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 10283-014001
CURRENT APPLICATION NUMBER: US/10/186,886
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/301,676
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 52
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 358
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Best Local Similarity 40.0%;
Matches 8; Conservative
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APPLICANT: Navia, Manuel A.
APPLICANT: Ala, Paul J.
APPLICANT: Griffith, James P.
APPLICANT: Ali, Janid A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40...
""" be 8; Conservative
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TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
TITLE OF INVENTION: DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 KEGOWVKGPLLTEKPASKDV
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Faerman, Carlos H.
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Connelly, Patrick R.
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; Pred. No. 35;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
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GENERAL ALL CONTROL GREGORY J.
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
INUMBER OF SEQ ID NOS: 47374
SEQ ID NO 748
LENGTH: 362
TYPE: PRT
ORGANISM: Escherichia coli
US-10-369-493-748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces avermitilis US-10-156-761-8003
Query Match
Best Local Similarity
Thes 7; Conserva
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; ORGANISM: Rhodopseudomonas palustris
US-10-369-493-20793
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Best Local Similarity
""" Conserv
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20793
LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 748, Application US/10369493
Publication No. US20030233675A1
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                    Conservative
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                    4; Mismatches
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Pred. No. 1e+02;
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                    <u>ت</u>
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                    Indels
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                  0
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      38.3%;
Best Local Similarity 45.0%;
Matches 9; Conservative
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CURRENT APPLICATION NUMBER: US/10/203,708
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
INUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence; PERTURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-808-880-2
                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-708-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-808-880-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/10203708
Publication No. US20030149238A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.1.c. TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GP50013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/106,100
PRIOR FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 30062-20029-0.0 CURRENT APPLICATION NUMBER: US/09/808,880 CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
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Local Similarity 56.2%; Pred. No. 1.1e+03;
les 9; Conservative 1; Mismatches 6; Indels
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Score 46; DB 12;
Pred. No. 1.3e+02;
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2; Mismatches

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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length: 2000000000
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Match Length
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Gapop 10.0 ,
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-454-196-8
US-08-454-196-17
US-08-454-196-17
US-09-064-033-17
US-09-064-033-17
US-09-291-046-18
US-09-291-046-17
US-09-107-532A-5920
US-09-060-410-4
US-09-107-532A-5920
US-09-252-991A-31355
US-09-252-991A-31355
US-09-252-991A-20263
US-09-252-991A-20263
US-09-252-991A-22518
US-09-252-991A-22518
US-09-252-991A-23201
US-08-456-422A-2
US-09-252-991A-30437
US-08-138-641-2
US-08-138-641-2
US-08-138-641-2
US-08-138-641-2
US-08-138-641-2
US-08-138-641-2
US-08-138-133-2
US-08-471-058-16
US-08-471-058-16
US-08-690-095-3
US-08-471-058-16
US-08-471-058-16
US-08-471-058-16
US-08-471-058-16
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                                                                                                                      Sequence 8, Appli
Sequence 17, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 11355, A
Sequence 11385, A
Sequence 1238, Ap
Sequence 7, Appli
Sequence 43, Appl
Sequence 23201, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 30437, A
Sequence 16, Appli
Sequence 16, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 16, Appli
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Sequence
Sequence
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US-08-454-
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42 35.0 43 1 US-07-661-610C-2 42 35.0 519 3 US-09-172-841-55 42 35.0 519 4 US-08-951-621-55 42 35.0 888 2 US-08-861-464-6 42 35.0 888 2 US-08-861-464-6 42 35.0 888 3 US-08-39-001-6 42 35.0 2710 2 US-08-68-459A-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 2710 2 US-08-487-8268-12 42 35.0 2710 2 US-08-487-8268-14 41 34.2 16 1 US-08-248-819A-50 41 34.2 16 2 US-08-248-819A-50 41 34.2 16 2 US-08-379-646A-68 41 34.2 16 2 US-08-379-646A-68 41 34.2 16 3 US-08-978-523-42 41 34.2 16 3 US-08-978-523-42 41 34.2 17 1 US-08-978-523-42 41 34.2 17 2 US-08-337-565-14	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	1
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US-07-661-610C-2 US-09-172-841-55 US-08-951-621-55 US-08-961-464-6 US-08-1861-464-6 US-08-1861-459A-12 US-08-1861-459A-12 US-08-1861-12 US-08-1861-12 US-08-1861-12 US-08-1861-14 US-08-248-819A-50 US-08-337-648A-68 US-08-337-548A-68	2	_	u	N	N	-	_	N	4	N	N	w	N	N	4.	w	_	•
	US-08-661-479-14	-08-333-565-1	-08-927-326-6	US-08-978-523-42				US-08-487-826B-14		US-08-487-826B-12		-09-323-433A-	•	-08-861-464	-08-951-621	-09-172-84	US-07-661-610C-2	
	, Appl	Appl	Appl	App1	Appl	Appl	Appl	, Appl	Appl	App1	Appl	Appli	Appli	Appli	, Appl	, Appl	Appli	

ALIGNMENTS

S-08-454-196-8 Sequence 8, Application US/08454196
GENERAL INFORMATION:
MICH
APPLICANT: BVERS, STEFAN
COURVALIN
OF INVENTION: BACTERIA
NUMBER OF SEQUENCES: 17
CE ADDRESS:
1755 S TERFERSON DAVIS HIGHWAY
CITY. ARITHGROUN DAVIS HIGHWAI, SUIIB 400
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MEDIUM TVDR: Florny Alak
OFERNITING SISTEM: FC-DUSYMS-DUS SOFTWARE: FC-DUSYMS-DUS
ATA:
APPLICATION NUMBER: US/08/454,196
CLASSIFICATION: 435
APPLICATION NUMBER: FR 92/15671
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
NAME: OBLON, NORMAN F.
TRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION: GOULTUI-O FCI
TELEPHONE: 703-413-3000
INFORMATION FOR SEO ID NO: 8:
••
LENGTH: 348 amino acids
STRANDEDNESS: not relevant
near
MOLECULE TYPE: protein

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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-196-17
RESULT 3
US-09-064-033-8
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Best Local S
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Best Local Similarity 40.0%; Pred. No. 9,
Matches 8; Conservative 5; Mismatche
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                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FR 93
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FR 9:
FILING DATE: 18-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN C
TITLE OF INVENTION: RESISTANC
TITLE OF INVENTION: BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ARTHUR, MICHEL APPLICANT: DUTKA-MALEN, SYLVIE APPLICANT: EVERS, STEFAN EVERS, STEFAN
                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 07-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OBLO
                                                            42 KDGQWVKGPLLSERPQNKEV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                             Similarity 41.7%; Score 50; 1 Similarity 40.0%; Pred. No. 9 8; Conservative
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5770361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN CONFERRING AN INDUCIBLE RESISTANCE TO GLYCOPEPTIDES, PAI
                                                                                                                                                                                                                                                                                                                                                                                                                                      FR 93/08356
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                                                                                                                          5; Mismatches
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                                                                                                                                                    DB 1; Length 348;
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US-09-064-033-17; Sequence 17, A; Patent No. 608
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Warches 8; Conserva
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; MOLECULE TYPE:
US-09-064-033-8
                                                                                                                      GENERAL INFORMATION:
APPLICANT: ARTHUR
APPLICANT: DUTKA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09064033 Patent No. 6087106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                              APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
NUMBER OF INVENTION: BACTERIA
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORM:
COMPUTER: IBM FORMS
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEIN OF TITLE OF INVENTION: RESISTANCE OF INVENTION: BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARTHUR, MICHEL APPLICANT: DUTKA-MALEN, SYAPPLICANT: EVERS, STEFAN APPLICANT: COURVALIN, PATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                          Application US/09064033
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1755 S.
                                                                                                                                         ARTHUR, MICHEL
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ilarity 40.0%;
Conservative
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Pred. No. 9.2;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     Length 348
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US-09-291-046-8
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Patent No. 6569622
GENERAL INFORMATION:
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FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-413-3000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,033
FILING DATE:
CLASSIFICATION:
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        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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     CURRENT
                                                                                                                                                                                                                                                COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCTBLE
RESISTANCE TO GLYCOPEPTIDES, PARTICULARLY IN GRAM-POSITIVE
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                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ARTHUR, MICHEL
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8; Conserv
                                                                                                                                 CITY: ARLINGTON
STATE: VA
                                                                                                                                                         STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 348 amino acids
amino acid
GY: linear
                                                                                                                   COUNTRY: USA
APPLICATION DATA:
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40.0%;
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Pred. No. 9.2;
5; Mismatches
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          Version #1.30
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i Sequence 17, Applicatio
Fatent No. 6569622
GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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RESULT 5

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INFORMATION FOR SEQ ID NO: 8:
                                                    APPLICATION NUMBER: US/09/291,046
FILING DATE: 14-Apr-1999
CLASSIFICATION: <URNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE: <UNKnown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/291,046
FILING DATE: 14-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/454,196
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-UUL-1993
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1755 S.
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
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TYPE: amino acid
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REGISTRATION NUMBER: 24,618
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EVERS, STEFAN
COURVALIN, PA
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40.0%; Pred. No. 9
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                       24,618
660-101-0 PCT
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                                      US-09-107-532A-5920
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
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Best Local
Query Match
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                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5920: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                      NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...370
SEQUENCE DESCRIPTION: SEQ ID NO: 5920:
                                                                                                              FEATURE
                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: YES
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TYPE: amino acid
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STATE: Massachusetts
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SOFTWARE: ASCII
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                ORGANISM:
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ilarity 40.0%;
Conservative
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41.7%; Score 50;
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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 DB 4;
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Length 370;
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US-09-060-410-4
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                              Sequence 4, Application US/09723458
Patent No. 6586242
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNMEER: 31,392
REFERENCE/DOCKET NUMBER: 8600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTI
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 993 amino acids
NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                           TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
                                                                                                    APPLICANT: Cobb, Melanie
                                                                                                                                                                                                                       888 GWVQGPVLTPVPE 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5<u>4</u>
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                                                                                                                                                                                                                                                                            40.0%;
Similarity 53.8%;
7; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (206) 622-4900
                                                                     Hutchinson, Michele
Chen, Zhu
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                                                            Kevin
                             THEREFOR
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                                                                                                                                                                                                                                                                                               Score 48; DB 3; Length 993; Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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APPLICANT: Belach, Mary C.

APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert

APPLICANT: Tang, Li

ITITLE OF INVENTION: RECOMBINANT CLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER APPLICATION NUMBER: 60/106,100

EARLIER APPLICATION NUMBER: 60/106,100

EARLIER FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1
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  Query Match
Best Local Similarity
                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 4150
                                                                 -09-428-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09428517 Patent No. 6251636
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Best Local
                                                                                OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-49
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888 GWVQGPVLTPVPE 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GWYEGPLLEPRPD 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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FILING DATE: 27-No. 6586242-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 993 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington COUNTRY: USA
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STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
                                                                                Description of Artificial Sequence: Recombinant Oleandolide PKS
    39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%; Score 48; DB 53.8%; Pred. No. 57;
Score 47;
Pred. No.
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DB 3; Length 4150 3.9e+02;
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                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-31355
                                                              Query Match
Best Local Similarity 36.0%;
Matches 9; Conservative 5
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US-09-252-991A-31355
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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SEQ ID NO 31355
LENGTH: 605
                                                                                                                                                                                                                                                                            APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31355, Applipatent No. 6551795
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bunkers,
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                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                 LENGTH: 76
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
27 RRDGGWIESIGYYNPLSEPKDIKID 51
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o. 6573361
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                              1 QQNGGW-----YEGPLLEPRPDALD 20
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                                                                             Score 44.5;
Pred. No. 1;
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Pred. No.
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RESULT 13

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20263
ENGTH: 396
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US-09-227-357-409
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: PCT/US98/13684
BARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20263, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER
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TITLE OF INVENTION: 123 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-252-991A-20263
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
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                                                                                                                                 ER APPLICATION NUMBER: 60/051,931
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,932
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,916
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,930
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,930
                                                                                                                                                                                                                                                                                                                                                                                                                            ER APPLICATION NUMBER: 60/051,929
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,803
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/052,732
ER FILING DATE: 1997-07-08
                                     APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919 FILING DATE: 1997-07-08
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FILING DATE: 1997-07-08
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Pred. No. 82;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-7
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US-09-227-357-409
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08556422A
Patent No. 6576754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 409
LENGTH: 35
                                                                                                         APPLICANT: FREEMAN, Gordon J.
APPLICANT: SCHULTZE, Joachim L.
APPLICANT: BOUSSIOTIS, Vassiliki
APPLICANT: NADLER, Lee M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
FILE REFERENCE: DFN-005CPA2
CURRENT APPLICATION NUMBER: US/08/556,422A
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEO ID NOS: 7
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Best Local Similarity
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EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,664
FILING DATE: 1997-09-12
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/056,360
FILING DATE: 1997-08-18
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PILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,723
PILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,948
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53.3%;
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Pred. No. 8.1;
1; Mismatches
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Query Match

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Length 425,

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Oy 1 QOGGEN-TEXPLIZERED 18
Db 180 OSHTANEWEVEXENCO 199
Search completed: December 30, 2003, 11:05:33
Job time: 3.21575 secs
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Minimum
Maximum
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1: pir1:*
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ALIGNMENTS

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Ig heavy chain V region - human
C;Species: Home sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26792
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7;
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26792
A;Status: preliminary
A;Accession: S26793
A;Bratus: preliminary
A;Residues: 1-131 <MOR>
A;Cross-references: EMBL:X61012; NID:932804; PIDN:CAA43346.1; PID:91335131
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C/Superfamily: immunoglobulin V region; immunoglobulin homology c/Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1 F;15-98/Domain: immunoglobulin homology <IMM> F;35-135/Region: complementarity-determining 1 F;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-132 <MAR>
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C.Species: Homo sapiens (man)
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C.Accession: PH0954
R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 933-991, 1992
A.Title: Evidence for somatic selection of natural autoantibodies.
A.Reference number: PH0952; MUID:92202880; PMID:1552291
A.A.Accession: PH0954
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D15R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Bate: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C;Accession: B72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, submitted to GenBank, March 1998
A;Bescription: Analysis of the complete coding sequence of DNA of alastrim vA;Reference number: A72150
A;Accession: B72175
A;Accession: B72175
                                                                                                                                        A; Notecube type: DNA
A; Molecule type: DNA
A; Residues: 1-1896 <SHC>
A; Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54796.1; PID:e1542752;
A; Cross-references: Strain Garcia-1986
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A;Cross-references: GB:X69198
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O A;Reference number: 948868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A;Accession: A36858
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                                                                                          Query Match
Best Local
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;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
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Best Local Similarity
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    variola virus (strain India-1967)

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                                   AYEDVWSGEYPEY 18
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                                                                    Conservative
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ilarity 56.5%;
Conservative
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                                                                                     39.6%;
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                                                                                                                                                                                                                                                                                         the complete coding sequence of DNA of alastrim variola minor
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                                                                                   Score 53;
Pred. No.
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Pred. No.
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                                                                                 58;
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37;
                                                                                                    DB 2;
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                                                                Indels
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C;Accession: T26908
R;McMurray, A.
Submitted to the EMBL Data L
A;Reference number: Z20285
A;Accession: T26908
                                          A;Map position: 4
A;Introns: 228/2; 261/3
C;Superfamily: Caenorhal
                                                                                                                                                                                                                                                                                                                                     hypothetical protein Y45F10A.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
                                                                                                      A; Gene: CESP:Y45F10A.1
                                                                                                                             C; Genetics:
                                                                                                                                     A;Cross-references: EMBL:AL021488; PIDN:CAA16365.1; GSPDB:GN00022; CESP:Y45F10A.1
A;Experimental source: clone Y45F10A
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-292 <WIL>
                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ohkuma, Y.; Hashimoto, S.; Roeder, R.G.; Horikoshi, M. Nucleic Acids Res. 20, 5838, 1992
A;Title: Identification of two large subdomains in TFIIE-alpha A;Reference number: S26646; MUID:93087200; PMID:1454543
A;Accession: S26646
                                                                                                                                                                                                                                                                                                                                                                                                               T26908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-433 <OHK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription factor IIE - African clawed frog
C;Species: Kenopus laevis (African clawed frog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
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S26646
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A;Title: Potential virulence determinants in terminal regions of variola smallpox viru A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28621
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A;Experimental source: strain Bangladesh 1975
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C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
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                                  Caenorhabditis elegans hypothetical protein Y45F10A.1
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    Score 50;
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Pred. No. 2
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Pred. No.
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  DB 2;
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Length
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
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; ORGANISM: homo sapiens
US-10-041-860-325
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-880-748-1674
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. SEQ ID NO 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1674, Application US/09880748 Publication No. US20030059937A1
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Best Local Similarity 78.9%;
                                                                                                                                                                                                                                                                                                    Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 252
TYPE: PRT
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Similarity 78.0%;
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                                                                                                  VWGQGTTVTVSS 132
                                                                                                                                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEY-PEYYAM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                          VWGQGTLVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVWGQGTTVTVSS 127
                                                                                                                                         AQKLQGRVTLTTDTSTSTAYMELRSLRSDDTAVYYCAR--
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                                                                                                                                                                                                                                                                                                Score 524; DB 11;
Pred. No. 3.2e-42;
7; Mismatches 16;
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Pred, No. 1.4e-42;
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                                                                                                                                                                                                                                                                                                                                        Length 252;
                                                                                                                                                                                                                                                                                                    Indels
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GENERAL INCURRENT.

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT EPILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1921

LENGTH: 251

TYPE: PRT

TYPE: PRT
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                                                        US-09-880-748-973
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US-09-880-748-1921
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                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                               SEQ ID NO 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1921, Application US/09880748 Publication No. US20030059937A1
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     Query Match
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                        LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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al Similarity 74.6%;
103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 BYYAMDVWGQGTTVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \mathbf{\mu}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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5. US20030059937A1
     73.3%;
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     Score 521
     B
Length 259;
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APPLICATION NUMBER: 60/276, 248
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 05/9/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PATENTIN Ver. 2.0
LENGTH: 253
TYPE: PRT
                                                                                                                                                                                                 RESULT 10
US-09-880-748-1778
                                                                                                                                      : Sequence 1778, Application US/09880748
: Publication No. US20030059937A1
: PUBLICATION: CONTROL INFORMATION:
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US-09-880-748-1777
; Sequence 1777, Application US/09880748
; US-09-880-748-1777, Application US/09880748
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US-09-880-748-1777
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Best Local S
Matches 100
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  APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  102;
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                                                                                                                                                                                                                                                                                                   VWGQGTTVTVSS 132
                                                                                                                                                                                                                                                                                                                                                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                        AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-GDFGDY-DILTGYYPVYYGMD 118
                                                                                                                                                                                                                                                                     VWGQGTMVTVSS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.1%; Score 520; DB 11; 75.8%; Pred. No. 7.8e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253;
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                                                                                                                                                                                                                                       ; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo s
US-09-880-748-1610
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEO ID NOS: 3239
SOPTWARE: PALENTIN VET. 2.0
SEQ ID NO 1610
SEQ ID NO 1610
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; ORGANISM: Homo sapiens
US-09-880-748-1778
                                                                                                                                                                   Matches
                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                   104;
                61
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                                                                                                  1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                           h 72.4%;
Similarity 77.0%;
04; Conservative
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                                                                          QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY 60
AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE---YY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                           6; Mismatches
                                                                                                                                                                               Score 514.5;
Pred. No. 2.7
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Pred. No. 2.0
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                                                                                                                                                                       ..7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.6e-41;
                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 248;
                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                             Length 257;
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BLyS

7;

Gaps

60 60

113

7;

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TITLE OF INVENTION. Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PFLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARP: DATASTTT VATOR OF SECULOR 
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
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US-09-880-748-1576
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; ORGANISM: Homo sapiens
US-09-880-748-1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1576, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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US-09-880-748-1425
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SOFTWARE:
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Best Local
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ruben et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 FDIWGQGTLVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
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                             PatentIn Ver.
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Similarity 76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 513; DB 11; Length 249; Pred. No. 3.6e-41;
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RESULT 15
US-09-880-748-1452
; Sequence 1452, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-1562
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1562
                                                                                                                                                                                                                                                                                                                                                                                                    Matches 101; Conservative
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Publication No. US20
GENERAL INFORMATION:
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Best Local Similarity 75.9%;
Matches 101; Conservative
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Best Local Similarity
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 251
                                                                                                                                                                                             121 VWGQGTTVTVSS 132
                                                                                                                                                                114 YWGQGTTVTVSS 125
                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                           OVOLVOSGABVKKVPGASVKVSCKASGYTPTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 510.5; DB 11; Length 251; Pred. No. 6.2e-41;
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Pred. No. 4.1e-41
8; Mismatches 2
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FILL OF INVENTION: Antibodies that Immunospecifically Bind BLys
CURRENT PILIKG AFE: US/09/880,748
CURRENT FILIKG AFE: 2001-06-15
PRIOR FILIKG DATE: 2000-06-15
PRIOR APPLICATION WUMBER: 60/212,210
PRIOR APPLICATION WUMBER: 60/212,210
PRIOR FILIKG DATE: 2000-01-01-17
PRIOR APPLICATION WUMBER: 60/277,379
PRIOR FILIKG DATE: 2000-01-01-17
PRIOR FILIKG DATE: 2001-03-12
PRIOR FILIKG
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        464
452.5
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476.5
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471.5
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.
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711
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| (GD12_6/ptodata/1/iaa/5A_COMB.pep:*
| (GD12_6/ptodata/1/iaa/5B_COMB.pep:*
| (GD12_6/ptodata/1/iaa/6A_COMB.pep:*
| (GD12_6/ptodata/1/iaa/6B_COMB.pep:*
| (GD12_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| (GD12_6/ptodata/1/iaa/backfiles1.pep:*
          QVQLLQSATEVKKPGASMKV.....YPEYYAMDVWGQGTTVTVSS 132
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Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                US-09-025-769B-36
US-09-025-769B-59
US-09-025-769B-22
US-08-264-093-3
US-08-561-521-45
US-08-561-521-45
US-08-561-521-45
US-08-955-01219-45
US-08-964-690-22
US-08-964-690-22
US-08-964-899-1105
US-08-964-899-1105
US-08-964-899-14
US-08-964-899-14
US-08-964-899-14
US-08-964-899-14
US-08-964-899-14
US-08-964-899-155-155
US-08-899-575-155
US-08-899-575-155
US-08-899-575-155
US-08-899-575-155
US-08-899-575-155
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Sequence 36, Appl Sequence 22, Appl Sequence 27, Appl Sequence 45, Appl Sequence 45, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 21, Appl Sequence 19, Appl Sequence 105, Appl Sequence 115, Appl Sequence 114, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 119, Appl Sequence 110, Appl Sequence 115, Appl Sequ
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	432 432	433	433	433.5	433.5	434.5	434.5	434.5	435.5	435.5	436.5	436.5	436.5	438	438	438	438
	60.8	60.9	60.9	61.0	61.0	61.1	61.1	61.1	61.3	61.3	61.4	61.4	61.4	61.6	61.6	61.6	61.6
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ALIGNMENTS	US-08-137-117D-112 US-08-436-717-112	US-08-436-717-100	US-08-137-117D-100	US-09-434-122-63	US-08-836-561-63	US-08-477-989B-94	US-08-472-281A-94	US-08-477-877B-94	PCT-US95-01219-12	US-08-561-521-12	PCT-US95-11235-65	US-08-931-645-65	US-08-300-386A-65	US-08-436-717-102	US-08-137-117D-102	PCT-US95-01219-41	US-08-561-521-41
	Sequence 112, App Sequence 112, App	100,	100,	63,			Sequence 94, Appl	-	Sequence 12, Appl		Sequence 65, Appl		Sequence 65, Appl	Sequence 102, App	Sequence 102, App	Sequence 41, Appl	Sequence 41, Appl

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RESULT 1
US-09-025-769B-36
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                             APPLICATION NUMBER: EP 95 11 3021.0 FILLING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
                                                                   TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James
STREET: 1251 Aven
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                 LENGTH: 120 amino TYPE: amino acid
                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09025769B
                                                                                                                                 120 amino acids
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Score 485; DB 4;
Pred. No. 5.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
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Matches Query Match

Local

l Similarity 96; Conserv

Conservative

Mismatches

12;

Gaps

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DB 4; Length 120; Indels

68.2**%**; 72.7**%**;

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US-09-025-769B-59
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GENERAL IN
                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., 1
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2121596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPPUTER: TEMPER PC-DOS/MS-DOS
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ADDRESSEE: James F. Haley, Jr., Esq.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 18-FEB
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 121 VWGQGTTVTVSS 132
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                                                                                                               QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                            AOKFOGRVIMITDISRRIAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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Ge, Liming
The Simon
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Ilag, Vic
                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                    protein
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72.7%;
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                                                                                                                                                                                                                                                                                                                 59:
                                                                                                                                                         7; Mismatches
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                                                                                                                                                      Score 485; DB 4; Length 120; Pred. No. 5.3e-39; 7; Mismatches 17; Indels
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US-09-025-769B-22
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
FENGTH: 117 amino acids
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                                                                                                                                                                                                     Matches
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
ANNEL: 17-EGG Halor: 17-EGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/09/025,769B
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: James F. Haley, Jr., REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
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109 YWGQGTLVTVSS 120
106
                     121 VWGQGTTVTVSS 132
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                                                                                                                                                                                                   96;
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                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY
                                                                                                                                                     OVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
YWGQGTLVTVSS 117
                                                               AQKFQGRVTMTRDTSISTAYMELSSLRSDDTAVYYCARDGDGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knappik, Achim
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                   68.1%;
72.7%;
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                                                                                                                                                                                                 Score 484.5; DB 4
Pred. No. 5.7e-39;
5; Mismatches 16
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                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                   Length 117;
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RESULT 4 US-08-264-093-3

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Sequence 3, Application US/08264093 Patent No. 5639863 GENERAL INFORMATION:

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US-08-561-521-45
Sequence 45, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                     GENERAL INFORMATION;
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
APPLICANT: Jones, S. Tarran
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TITLE OF INVENTION: HUWAN MONOCLONAL ANTIE
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 362-0823 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: M5H 2J7

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: WS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
                CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                               TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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California
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VENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
VENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canada
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72.0%; Pred. No. 2.2e-38;
ive 11; Mismatches 15
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                                                                                                                                                                                                                                                   APPLICANT: DO COUTO, FE.
APPLICANT: CERIANI, ROB
APPLICANT: ETERSON, JE.
TITLE OF INVENTION: REC
TITLE OF INVENTION: MC3
TITLE OF INVENTION: MC3
TITLE OF INVENTION: MET
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
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APPLICATION NUMBER: US/08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,539A FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/561,521 FILING DATB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                           STREET: 755 Page
CITY: Palo Alto
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lir
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                                                                                                                                                               COUNTRY:
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                                                                                                                                                               USA
                                                                                                                                                                                                                  755 Page Mill Road
                                                                                                                                                                                                                                                                                                          PETERSON, JERRY A.

VENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

VENTION: Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
                                                                                                                                                                                                                                                                                                                                                                CERIANI, ROBERTO L.
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                                                                                                                                                                                                                                                                          METHODS OF HUMANIZING ANTIBODY PEPTIDES 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.0%; Score 476.5; 71.4%; Pred. No. 3.7
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PCT-US95-01219-45
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
SEQUENCE 129 amino acids
LENGTH: 129 acid
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NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 2763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
SEQUENCE CHARACTERISTICS:
                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sir
                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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One Market Plaza, Steuart Tower, Suite 2000
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linear
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                                                                                                                                                                                                                                   UMBER: PCT/US95/01219
25-JAN-1995
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                                                                                          15270-14
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                                                                                                                  TELEPAX: 415-320 INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
FRACTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22,
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                   TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                      FEATURE:
                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                    TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                     LOCATION:
                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAULSON, James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHESNUT, Robert W. POLLEY, Margaret J.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.0%; Score 476.5; DB 5; 71.4%; Pred. No. 3.7e-38; ative 11; Mismatches 22;
/label= HUMAN_I
                                                                                                                                                                                                                                         14137-77
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US-08-964-690-22
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US-08-964-690-22
                                                      Best Local Similarity Matches 95; Conserv
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. GENERAL I
                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local (
                                                                                                                                                                                              MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0/
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rei
CURRENT APPLICATION DATA
APPLICATION NUMBER: US
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHESNUT, Robert W. APPLICANT: POLLEY, Margaret J. APPLICANT: PAULSON, James C. APPLICANT: JONES, S. Tarran APPLICANT: SALDANHA, Jose W.
                                                                                                                                      NAME/KEY: Protein LOCATION: 1.128 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
COMPUTER: I
                                                                                                                                                                                                                                                                                 ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION: Antibodies to P-Selectin and Their Uses
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                                                                                                                                                                                                                                                                            128 amino acids
                                                    Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                            protein
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                                        66.9%; Score 476; DB 3; Length 128; 71.4%; Pred. No. 4.1e-38; Live 11; Mismatches 21; Indels
                                                                                                                                  /label= HUMAN_I
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                                          Gaps
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APPLICANT: Taylor, Alexander H.

APPLICANT: Trulli Jr., Stephen H.

APPLICANT: Trulli Jr., Stephen H.

APPLICANT: Johanson, Kyung O.

ITILE OF INVENTION: Humanized Monoclonal Antibodies

FILE REFERENCE: 950860

CURRENT APPLICATION NUMBER: US/09/199,149

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
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US-08-652-816A-19
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US-09-199-149-3
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: OBbourn, JK
APPLICANT: OBbourn, JK
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/08652816A Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local !
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COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 125
TYPE: PRT
                                                                                                      STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
COUNTRY: United:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDG---GGGAYEDVWSGEYPEYY 117
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                                                                                                                                                     6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAQKFQGRVIMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVMSGEYPEYYAM 119
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                                                                                                                                                     Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 471.5; DB 3; Pred. No. 1.1e-37; 8; Mismatches 18
                                                                                                                                               Gerstein, Murray &
South Wacker Drive
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DB 3; 18;

Indels Length 125;

13;

Gaps

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RESULT 12
US-08-933-983-21
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US-08-652-816A-19
                                                                                                                                                                                                        Sequence 21
Patent No.
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATE: 01-JUN-157.
FILING DATE: 01-JUN-157.
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111
TELECOMMUNICATION: TELECOMMUNICATION: 312-474-6300
TELECOMMUNICATION: 19:
                                                                                                                                                                                          GENERAL INFORMATION:
                                       APPLICANT: REED, GUY L
APPLICANT: HARRIS, LINDA
APPLICANT: BAJORATH, JURGEN
APPLICANT: MATSUEDA, GARY
APPLICANT: MATSUEDA, GARY
APPLICANT: HSU, MEI-YIN
APPLICANT: NOVOTNY, JIRI
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING
TITLE OF INVENTION: FIBRINOLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
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APPLICATION NUMBER:
FILING DATE: 02-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 23-MAY-
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APPLICATION NUMBER:
FILING DATE: 07-DEC-
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FILING DATE: 23-MAY-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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5. 6114506
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STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                  ADDRESS
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02-DEC-1992
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23-MAY-1996
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07-DEC-1995
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23-SEP-1992
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71.2%;
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Pred. No. 5.2e-37;
5; Mismatches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 120;
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RESULT 13
US-08-545-809A-105
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                                                                                                                                                                                                                                                                                                                     Sequence 105, Application US/08545809A
Patent No. 6096878
                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CO

NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 06(
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    ADDRESSEE: Fish a ALL.
CTREET: 225 Franklin Street
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                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 19-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NEW
CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VWGQGTTVTVSS 132
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                                                                                                                                    Boston
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65.2%; Pred. No. 7.5e
tive 14; Mismatches
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APPLICANT:
APPLICANT:
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APPLICANT:
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Best Local Similarity
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acid
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-UUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithic Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
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REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                         STATE: New Jersey COUNTRY: U.S.A.
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/JP93/00603
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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TOPOLOGY: lino-
LECTRE
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVQLVQSGAEVKKÞGASVKVSCKASGYTFTSYGTSWVRQAÞGQGLEWMGWISAYNGNTNY 79
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Weiss, Martin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holcomb, Ryan
Hallett, William
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                                                                                                                                                                                                                                                                                                                                                       American Cyanamid Company
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Irwin
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                                     32,368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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RESULT 15
US-08-452-164A-19
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          Query Match
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                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REGISTRATION NUMBER: 32,368-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5877296
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.2
86; Conservative
                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: American
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TITLE OF INVENTION: Conjugate
TITLE OF INVENTION: Agents and

TOTAL OF STOTIENCES: 73
                                                               LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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LENGTH: 139 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: American Home Products Corporation One Campus Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08452164A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsou, Hwei-Ru
Weiss, Martin J.
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Hallett, William
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                                                                                                                                                                               201-683-2158
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63.0%; Score 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugates of Methyltrithio Antitumor Agents and Intermediates for Their Synthesis
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   DΒ
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Title:
Perfect score:
Sequence:
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No.
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Maximum
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     number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
BG
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     GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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A;Cross-references: EMBL:212316; NID:g32855; PIDN:CAA78186.1; PID:g32856 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Kupwords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

Query Match Local

Similarity

87.5**%**; 87.8**%**;

Length 98;

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-98 <TOM>

C;ACCEBBION: 826919 R;Tomlinson, I.M.; Walter, G.; Marks, J.D J. Mol. Biol. 227, 776-798, 1992 A;Title: The repertoire of human germline A;Reference number: \$26885; MUID:93021117 A;Accession: \$26919 A;Farus; preliminary	RESULT 1 S26919 Ig heavy chain V region C;Species: Homo sapiens C;Date: 22-Nov-1993 #sec		4 5	44	43	42	41	40	39	38	37	36	35	3 4	u u	32	31	30	
on: 826 on, I.M. ol. 22 the rep ie numb on: 826 on: 826	hain V Homo		367	367	369	369	370	372	376	377	377	377	377	378	379	380	381	382	
1.M.; Walter, 227, 776-798 repertoire of umber: S26885 S26919			70.4	70.4	70.8	70.8	71.0	71.4	72.2	72.4	72.4	72.4	72.4	72.6	72.7	72.9	73.1	73.3	
er, G. 798, 1 of hu 385; M	(DP-14) (man) quence_r		116	98	109	104	98	98	126	135	120	117	116	119	98	171	142	118	
3.; Ma 1992 human MUID	re 4)		N	N	N	N	N	N	N	N	N	—	N	N	N	N	N	N	
arks, J.D. germline :93021117;	jion (DP-14) - human (fragment) lens (man) #sequence_revision 10-Nov-1995	ALIGNMENTS	S31698	S26915	PH1668	PH1665	S26921	S24680	I44151	B32274	S31999	HVHU35	S31667	JN0295	PH0871	S23623	A32483	PH1666	
Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. 176-798, 1992 Dire of human germline V(H) sequences reveals about fifty groups of S26885; MUID:93021117; PMID:1404388	xagment) Nov-1995 #text_change 23-Jul-1999	MENTS	chain pr	chain	heavy chain	heavy chain V	heavy chain V-	heavy	heavy chain V	heavy chain V	Ig heavy chain V r								

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A;Residues: 1-129 <GRI>A;Cross-references: EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903
A;Cross-references: EMBL:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin homology <IMMs
                                                                                                                                                                                                                 C;Accession: S36260
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, CEMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36260
                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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S36260
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    Score 453;
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Pred. No. 1.7e-39;
4; Mismatches 8
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Length 129;
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A;Molecule type: mRNA
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
A;Residues: 1-40, 'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
A;Residues: EMBL:X61647; NID:937667; PIDN:CAA43828.1; PID:91335368
A;Note: the difference for residues 41-60 results from misplacement of 10;C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotettamer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, A;Reference number: $24442 A;Accession: $24442
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-124 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: By-passing immunization. Human antibodies from V-gene A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19665...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, J. Mol. Biol. 222, 581-597, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (alpha-phOx15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
                                                                                                                                                                                                                                                                                                                                   R;Jones,
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A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (clone alpha-THY-29) - human (fragment) C;Species: Homo sapiens (man) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999 C;Accession: S36271 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bve. J.M.; Embleton M.T. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-122 < GRI>
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S36271
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVIMTIDISRRTAYMELRSLRSDDTAVYYCA 97
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                               Similarity
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85; Conserv
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           Conservative
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87.6%;
                            86.4%;
86.7%;
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    Score 450; DB 2;
Pred. No. 9.1e-39;
3; Mismatches 10
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Pred. No. 7.1e-39;
4; Mismatches 8;
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3; Mismatches 9;
                                                                                                                                                                                                                                                                                                      October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.P.; McCafferty, J.; Griffiths, A.D.; Winter
                                             Length 124
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       Indels
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R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A;Title: Relationship of variable region genes expressed by a human B cell lymph, Reference number: PL0106; MUID:89235583; PMID:2541221

A;Reference number: PL0105

A;Rolecule type: mRNA

A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu C;Comment: The antibody is one of the cold agglutinins that preferentially bind C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: autoantibody; hemagglutinin

C;Keywords: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology 
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                                                                                                                                      F;118-131/Domain: D region <DRG>
F;132-144/Domain: J4 segment <JS
F;145-160/Domain: C region <CRG>
                                                                                                                                                                                                      F;49-54/Region: complementarity-determining 1
F;69-84/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C;Accession: PL0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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A;Accession: S21924
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C;Accession: S21924; S21923
R;Friedman, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X60505; NID:g33565; PIDN:CAA43025.1; PID:g33566; EMBL:X60504,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-131 <FRI>
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C;Species: Homo sapiens (man)
C;Date: 20-Peb-1995 #sequence_revision
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                                                                           Similarity
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Similarity 82.7%;
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                                                        Conservative
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                                                                           82.1%;
81.6%;
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                                          Score 428; DB 2; Length 160;
Pred. No. 2.1e-36;
6; Mismatches 12; Indels
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Pred. No. 6.5e-37;
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                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885, MUID:93021117; PMID:1404388
A;Accession: S26918
                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-98 < TOM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Genetics:
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A; Residues: 1-111 <FRI>
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A; Accession: S21925
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Best Local S
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77; Conserv
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                                                                  AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
                                                                                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAXNGNTHY
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78.6%;
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87.0%;
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Pred. No. 9.1e-36;
4; Mismatches 8; Indels
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S31600
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A; Residues: 20-117 < TOM>
                                                                                                                                             Query Match
Best Local Similarity
Matches 77; Conserv
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A; Residues: 1-117 <SHI>
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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 117
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                                                                                                                                             Conservative
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A;Molecule type: mRNA
A;Molecule type; mRNA
A;Residues: 1-136 <CUI>
A;CUIs
A;Crose'references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992 A;Description: Mechanisms that generate human immunoglobulin diversit. A;Reference number: S31585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
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A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin home C;Superfamily: immunoglobulin V region; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;1-19/Product: Ig heavy chain V region (VI-3b) #status F;20-117/Product: igheavy chain V region (VI-3b) #status
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Blol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26916
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If heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18553; S26916
C;Accession: S18553; S26916
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A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:
A;Reference number: $18551; MUID:92037524; PMID:1935893
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61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                              1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                               SOKFOGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR
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78.6%;
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78.6%;
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                                                                                                                                                                         Score 407; DB 2;
Pred. No. 2.4e-34;
9; Mismatches 12
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Pred. No. 2e-34;
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Ig heavy chain V region - human (fragment)
N;Alternate names: anti-cytomegalovirus glycoprotein B antibody
C;Species: Homo sapiens (man)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: S68170
R;Boeldicke, T; Hasse, B, Boecher, M.; Lindenmaier, W.
A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and r.
A;Reference number: S68170; MUID:96128166; PMID:8536681
A;Accession: S68170
A;Status: preliminary
A;Kolecule type: mRNA
A;Residues: 1-125 <BOE>
A;Cross-references: GB:S80750; NID:g1246061; PIDN:AAB35861.1; PID:g1246062
C;Superfamily: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                       RESULT
S31680
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Pate: 22-Nov-193 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C.Accession: S26938
R.FOmlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A.Fitle: The repertoire of human germline V(H) sequences reveals about fifty groups
A.Recession: S26938
A.Accession: S26938
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A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local S
Matches 75
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Best Local
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                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
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Pred. No. 6.8e-34;
7; Mismatches 15
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Pred. No. 3.5e-34;
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A;Title: Physical map of the 3' region of the human immunoglobulin A;Reference number: S18551; MUID:92037524; PMID:1935893
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S18551
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                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
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A; Residues: 1-117 <OLE>
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A; Residues: 1-117 <SHI>
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Description: Mechanisms that generate human immunoglobulin diversity operate from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A; Residues: 1-117 < CUI>
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A; Accession: S31680
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Best Local :
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Best Local
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                                                                                                                                                                                          Similarity
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                              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                          QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
AOKFOGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR 117
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llarity 77.6%;
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Pred. No. 8.2e-34;
7; Mismatches 15
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S49530

anti-Sm antibody VH chain (VHI/DK1 or DMI/JH4b) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: Ol-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Accession: S48797
A;Accession: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
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A;Cairns Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Cairns Molecular characterization of natural human anti-Sm autoantibodies.
A;Cairns Molecul
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(without alignments)
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	Query Match 73.5%; Score 383; DB 1; Length Best Local Similarity 75.5%; Pred. No. 1e-37; Matches 74; Conservative 7; Mismatches 17; Inde	SEQUENCE 117 AA;	NON_TER 117 117	CHAIN 20 117 IG HEAVY CHAIN V-I	SIGNAL 1 19	PROSITE; PS50835; IG LIKE;	SMART; SM00406; IGV	InterPro; IPR003596	InterPro; IPR003006	GO; GO:0006955; P:immune response; NAS.	GO; GO:0003823; F:antigen binding	HSSP; P01772; 2FB4.	EMBL; J00240; AAA52988.1; PIR: A02024: HVHTHG	or send an email to license@isb-sib.ch).	entities requires a license agreement (See http://	use by non-profit institutions as long as its	the European Bio	CC This SWISS-PROT entry is copyright. It is produced through	-!- SIMILARITY:	(VH) gene subgroups."; Proc. Natl. Acad. Sci II S & Soless Sci (1992)	"Evolutionary aspects of immunoglobulin heavy chain v	MEDLINE=83144028; PubMed=62987;	[1]	ia; Primates; Catarrhini; Hominidae;	Homo sapiens (Human).	Ig heavy chain V-I region HG3 pred	21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42 tagt sequence)	P01743;	SULT 1 1B HUMAN 1V1B HUMAN STANDARD: PRT	ALIGNMENTS	261.5 50.2 115 1	263 50.6 117 1 263 50.5 117 1	264 50.7 126 1	265.5 51.0 116 265 50.9 119	265.5 51.0 97 1	266 51.1 117 1	269 51.6 114 1	270 51.8 122 1 HV3.	370 61 8 122 1
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RESULT 3
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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GO; GG
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MEDLINE=88296408; PubMed=2841108;

Matsuda F., Lee K.H., Nakai S., S
Ohno H., Fukuhara S., Honjo T.;

"Dispersed localization of D segn
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01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
Ig heavy chain V-I region V35 precursor.
Homo saplens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          30; GO:0005576; C:extracellular; NAS.
30; GO:0003823; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
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HSSP; P01772; 2FB4.
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EMBO J. 7:1047-1051
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7; Mismatches 18
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Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

SMART; PS50835; IG LIKE; 1

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"""" y region; Sic
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat.
Ig heavy chain V region VH558 Al/A4 precurs
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS. GO; GO:0005876; C:extracellular; NAS. GO; GO:0003823; F:antigen binding activ GO; GO:0006955; P:immune response; NAS. InterPro; IPR0070110; Ig-1ike. InterPro; IPR0070106; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H., (In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.:
Marcel Dekker, New York (1978).
-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 immunoglobulin-like domain HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton
Bell L.O., Gould H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                      Score 359; DB 1;
Pred. No. 8.3e-35;
3; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V-I REGION ND IG-LIKE.
                                                                                                                                            PRT;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

precursor

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RESULT 5
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Best Local
      MEDLINE=71064027;
Gall W.E., Edelman
"The covalent stru
                                                     "The covalent structure of a human gamma acid sequence of heavy-chain cyanogen brobiochemistry 9:3161-3170(1970).
                                                                                                                                           Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      Cunningham B.A., Rutish Waxdal M.J., Edelman G.
                                                                                             MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U.,
                                      DISULFIDE BOND.
                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-I region EU.
                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                       HUMAN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produble the European Bioinformatics Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85099340; PubMed=2578321; Yancopoulos G.D., Alt F.W.; "Developmentally controlled and tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro;
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     W.E., Ede
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                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAYYYCAR 98
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                       PubMed=4923144;
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 human gamma
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Pred. No. 1e-32;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION VH558 A1/A4. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     8B0BC138856DFC9D CRC64;
                                                                                              Gall W.E.,
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                                                            nma G-immunoglobulin. VII. Amino
bromide fragments H1-H4.";
                                                                                                                                                                                            update)
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G-immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ong as its content is in
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InterPtc, IPRUC,
InterPro; IPRUC,
Pfam; PP00047; ig; 1.
SMART; SM000406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1
PROSITE; P850835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 66
                                                                PIR; A02022; GIMSAA.
HSSP; P01772; 2FB4.
InterPro; IPR0071110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                   Capra J.D., Nisonoff A.,
"Structural studies on induced antibodies with defined idiotypic specificities, VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse)
                                                                                                                           REGION SEQUENCE.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                    THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE
                                                                                                                                                                                                                                                                       SEQUENCE.
STRAIN=A/J;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                        MEDLINE=79195438; PubMed=109536;
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DISULFID
NON TER
SEQUENCE
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SMART; SM00406; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

DOMAIN

1 112

IG-LIKE.

PYRROLITHONE CARBOXYLIC ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).

-i- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A90563; G1HUEU.
HSSP; P01772; 2FB4.
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56; Conservative
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117
117 AA;
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117
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          IG-LIKE.
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Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID
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Best Local Similarity
Matches 59; Conserv
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Best Local
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MGD; MGI:96486; Igh-VJ558.
InterPro; IPR003710; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                          SIGNAL
                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@eisb-sib.ch).
                                                                                                                                                                                                                                                                                           EMBL; J00488; AAA38519.1; -. PIR; A02041; HVMS8A.
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81245215; PubMed=6789211; Givol D., Zakut R., Effron K., Rechavi "Diversity of germ-line immunoglobulin Nature 292:426-430 (1981) -!- SIMILARITY: Contains 1 immunoglobul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 108A precursor.
IGH-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 immunoglobulin-like domain.
                  80
                                     61
                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                  NOKEKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLQOSGAELVKAGSSVKMSCKATGYTFSSYELYWVRQADGQGLEDLGYISSSSAYPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTITADESTNTAYMELSSLRSEDTAVYFCA
                                                                                                                                        1
20
20
117
117
                                                                                              62.6%; Score 326; DB 1; larity 60.2%; Pred. No. 4.5e-31; Conservative 16; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                >117
                                                                                                                                                                           117
                                                                                                                                        12972 MW; 428CB44DF25D1BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12555 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                            IG HEAVY CHAIN V REGION 108A IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 326; DB 1;
Pred. No. 4.4e-31;
7; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DD8F0B6A69F4BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                             G., Ram D., VH genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                 Length 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                         J.B.;
                                                                                              <u>,</u>
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                                                                                             Gaps
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                                                     79
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RESULT 9
HV04 MOUSE
HV04 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
HV03_MOUSE
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: Contains 1 immu HSSP; P01789; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                             P01748;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
To heavy chain V region 23 precursor.
    antibodies: somatic mutation Cell 24:625-637(1981).
                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                         Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NON TER
SEQUENCE
                                             Baltimore D.;
                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Immunol. 12:1023-1032(1502).

-I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV03_MOUSE
P01747;
21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genetic basis of antibody production: the idiotype response of the strain A mouse."; Eur. J. Immunol. 12:1023-1032(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Creater,
21-JUL-1986 (Rel. 01, Last seq.
15-SEP-2003 (Rel. 42, Last anno
7- heavy chain V region 36-65.
   MISCELLANEOUS:
                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                2 VQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHYA
                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                        EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCAR
                                                                                                                                                                                                                                                                                             QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                120
120 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD,
   SIHT
                                                                                                                         ; Chordata; (; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                               120
13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                          62.6%;
  GERMLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybridoma
                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
                   contribution to the NPb evident in a gamma 2a va
                                                                                                                                                                                                                                                                                                                                                              Score 326; DB 1;
Pred. No. 4.6e-31;
B; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE
                                                                                                                       Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                   PRT;
  GENE
                                                                                                                                                                                                                 117
 BELONGS
                                                     Imanishi-Kari T.,
                                                                                                                                                                    update)
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SET OF CLOSELY
                    variable region.";
                                                                                                                                   Euteleostomi;
                                family of
                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                    120;
                                                     Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TO THE S
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THE FEET OF SOLUTION AND SOLUTION OF THE SOLUT
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HV02_M
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Best Local S
Matches 61
                                                                            EMBL; J00493; AAA38128
PIR; A94264; HVMSG7.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; I
      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
Pfam; PF00047; ig; 1
                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                               "Somatic mutation in genes for the variable portion immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=82152818;
Sims J., Rabbitts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATED GENES TH
PIR; A02030; HVMS23.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLLQSATEVKKPGASMKVSCWASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OVÓLOÓPGTELVKPGÁSVKLSCKÁSGYTFTSYMMHMVKORPGÓGLEMIGNINPGNGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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20
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55
69
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41
                                                                                                                                             AAA38128.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=6801765;
T.H., Estess P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THAT COULD ENCODE V REGIONS OF
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68
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117
115
115
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Pred. No. 9
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION 23.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325; DB 1;
No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPB ANTIBODIES
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                                                               Query Match
Best Local S
Matches 59
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Best Local
                                                                                                     DOMAIN
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          P01753, P11271;
P01753, P11271;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence upda:
15-JUL-1999 (Rel. 38, Last annotation up
15-JUL-1999 (Rel. 38, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybrid
SIGNAL 1 19
CHAIN 20 140
DOMAIN 20 139 IC
NON TER 140 140
SEQUENCE 140 AA; 15514 MW;
                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                  SIGNAL
CHAIN
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                         PIR; D90809; HVMS61.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                               antibodies: somatic r
Cell 24:625-637(1981)
                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                           InterPro; IPR003596;
                                                                                                                                                                                                    mmunoglobulin
                                                                                                                                                                                                                                                   InterPro; IPR007110;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                   Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable
                                                                                                                                                                                                                                                                                                                                            Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        MISCELLANEOUS: THIS GERMLINE GENE BELONGS RELATED GENES THAT COULD ENCODE V REGIONS
                         20
                                                                                                                                                                                                                       PF00047; ig; 1.; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                               59;
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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                                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMVGWISAYNGNTHY
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                                                                                                                                                                                                   PS50835; IG_LIKE; 1.
obulin V region; Sign
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50
55
69
86
41
                                                              Conservative
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                                                                                                                      49
54
68
85
117
117
                                                                                                12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                         ; Ig-like.
; Ig_MHC.
; Ig_v.
                                                                      61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15514 MW;
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                                                                                                                                                                                                   Signal
                                                             15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridoma; Signal
                                                                                                                          IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                    Score 319;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                   Reth M.,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                         Mismatches
                                                                                                                     SIMILARITY
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                                                         DB 1; I
2.9e-30;
nes 24;
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.5e-31;
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                                                                          Length 117;
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Best Local S
Matches 58
                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque)
15-JUL-1999 (Rel. 38, Last anno)
Ig heavy chain V region 102 pree
Mus musculus (Mouse)
Ebkaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                             HV06 MOUSE
P01750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dildrop R., Bovens J., Siek
"A V region determinant (id
lymphocytes is encoded by a
EMBO J. 3:517-523 (1984).
PIR; A02040; MHMS38.
HSSP; P01789; IMCP.
                                                       STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, 01-JAN-1988 (Rel. 06, 15-JUL-1999 (Rel. 38, 1g heavy chain V regimus musculus (Mouse)
"Heavy chain variable antibodies: somatic mu Cell 24:625-637(1981).
                                                                                                                                   SEQUENCE FROM N.A.
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NON_TER
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                                                                                                                                                                        NCBI_TaxID=10090;
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SMART; SM00406; IGv;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M.,
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NOKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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99
105
22
118
118 AA;
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(Rel. 01, Last sequence update)
(Rel. 38, Last annotation updat
ain V region 102 precursor.
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8 (Rel. 06, Last seq
9 (Rel. 38, Last ann
hain V region AC38 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
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V region.
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118
96
118
            le region contribution to the mutation evident in a gamma 2
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59.2%;
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annotation
38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 315; DB
Pred. No. 8.7e.
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evitz M., Beyreuther K., Rajewsky K.;
iotope) expressed at high frequency in B
large set of antibody structural genes.";
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                                                                                                                                                                                    Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                PRT;
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Sciurognathi; Muridae; Murinae; Mus.
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SEGMENT.
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                                                                   Imanishi-Kari T.,
                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                  Vertebrata; E
thi; Muridae;
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                ^{2a}
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                                  NPb family
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              variable
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; Murinae; Mus
                                                                   Rajewsky
                            of.
            region."
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AC PRINTER OF THE PRI
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              Query Match
Best Local S
Matches 57
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./erpro; IPR00.
./erpro; IPR00.
./erpro; IPR00300.
./erpro; IPR00390.
./erpro; IPR00390.
./erpro; IPR003596; .
./erpro; IPR003
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Dildrop R., Bovens J., Siekevitz M., B.
"A V region determinant (idiotope) exp.
lymphocytes is encoded by a large set of EMBO J. 3:517-523(1984).
PIR; A02037; MHMS15.
HSSP, P01810; 2FBJ.
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Best Local :
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 15.3.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain v rey
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DISULFID
NON TER
SEQUENCE
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DOMAIN
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SMART; SM00406; IGV;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
              1 Similarity
57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGMISAYNGNTHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÓKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYÝCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLQQPGAELVKPGASVKVSCKASGYTFTSYWYHWVKQRPGQGLEWIGRIHPSDSDTNYN
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obulin V region; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
117
           Conservative
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                                   60.3%;
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     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
Score 314; DB 1;
Pred. No. 1.2e-29;
6; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION 102. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
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) SEGMENT.
) SEGMENT.
3Y SIMILARITY.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                            914453F426F09834 CRC64;
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No. 1
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                                                    Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
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h frequency :
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RR SEQUEN
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Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; 1...
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                           DISULFID NON_TER
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ig heavy chain V region 3 precursor.
IGH-VJ558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01810; 2FBJ.
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                                                                                                                 58;
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                                                                                                                                       Similarity
QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                              117
117 AA;
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                                                                                                               Conservative
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54
68
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117
115
                                                                                                                                                                                                           13016 MW;
                                                                                                                               60.1%;
59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                            15;
                                                                                                 Score 313; DB 1; Length 117;
Pred. No. 1.5e-29;
5; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 3.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                      427C861C53975EDC CRC64;
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61 AQKFQGRVIMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Search completed: December 30, 2003, 10:55:49 Job time : 5.25426~Becs

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OM protein - protein search, using sw model
Run on:

December 30, 2003, 10:46:19; Search time 23.883 Seconds
(without alignments)

Title:
Perfect score: 521
Sequence:

1 QVOLLOSATEVKKPGASMKV........AYMELRSLRSDDTAVYYCAR 98

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:
830525 minimum Match 0%
Maximum DB seq length: 0
Maximum DB seq length: 23:*
1: sp_accheria:*
2: sp_hungan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_bage:*
10: sp_rodent:*
11: sp_rodent:*
11: sp_rodent:*
11: sp_rodent:*
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11: sp_bacteria:*
11: sp_bacteria:*
11: sp_rotens:*
11: sp_bacteria:*
11: sp_rotens:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

384 2 384 3 382 4 378 5 371 6 358 7 358 8 357 9 340 10 337 11 335 11 335 13 331 13 331 13 331 14 330 16 329	sult No. Score
73.7 73.7 73.3 71.3 68.5 68.5 64.3 64.3 64.3 63.3 63.3	% Query Match Length
125 119 500 124 614 6149 119 119 1497 116 147 147 116 147 150 1481 150 1481 150 1481 150 1481 159	
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Q9UL95 Q9UL95 Q9UL92 Q9UL92 Q9GA6 Q9UL92 Q9GA6 Q9GYZ2 Q9GYZ2 Q9GYZ3 Q91WT1 Q9Y298 Q9Y298 Q9Y298 Q9YUJ1 Q9Y214 Q8YUJ1 Q99LC4	SUMMARIES
O9u195 homo sapien O9u194 homo sapien O9brv0 homo sapien O9brv0 homo sapien O96ga6 homo sapien O96ga6 homo sapien O96ga6 homo sapien O96gs0 homo sapien O99gyz2 schistosoma O8wy24 homo sapien O90189 homo sapien O902583 mus musculu O91wr1 mus musculu O91wr1 mus musculu O99z98 homo sapien O8bv24 mus musculu O9d814 mus musculu O9d814 mus musculu O9d1c4 mus musculu	Description

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Q924r8	Q924r4	Q924r1	0924Q7	27413	202499	200400	2000	200	101000	2000414	2007450	77.400	000400	09340	092164	092582	084469	091467	092458	2000	204400	201271		700000	0 0		2017	084047	09247
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Query Match
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Matches 72
                          SEQUENCE FROM N.A.
TISSUE=prostate;
Strausberg R.;
Submitted (APR-2001) to the EI
EMBL; BC005951; AAH05951.1; -
HSSP; P01789; IMCP.
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Q9UL94;
Q9UL94;
Q9UL94;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 23, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                    Q9BRVO; PRELIMINARY;
Q9BRVO;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia, Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Liu B., Van der Merwe P.L.,
                                                                                                                                                  NCBI_TaxID=9606;
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SMART; SM00406; IGv;
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HSSP; P01810; 2FBJ
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Mammalia; Eutheria; Primates;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                         ACKFOGKVTMTKDTSISTAYMELSRLRSDDTAVYYCAR
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119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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         Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%; Score 384; DE 73.5%; Préd. No. 8.96 tive 10; Mismatches
                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                 PRT;
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                                                             databases
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Q9UL92
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Best Local S
Matches 72
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Best L
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                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW.
Q96GA6;
Q96GA6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL92;
Q9UL92;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1)
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MEDLINE-98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; I
InterPro; IPR003596; I
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. EMBL; AF035022; AAD56258.1; -HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                         AQXFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKKFOGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCAR 117
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 (TrEMBLrel.
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBLrel. 13, Created)
EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
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Primates;
                                                                                                                                                                                                                                                                                                                                            13580 MW;
                                                                                                                                                                                                                                                                                    72.6%;
73.5%;
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72.4%;
19,
                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                               Score 378; DB 4;
Pred. No. 4.3e-34;
10; Mismatches 16
 Created
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 382; DB 4;
Pred. No. 8.2e-34;
9; Mismatches 18
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                          1BAAACBD96ACD2A2 CRC64;
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                                                                                                                                                                                                                                                                   Indels
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RESULT OPERATE OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
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В
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Best Local S
Matches 69
                                                                                     Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBan EMBL; BC009851; AAH098511; -. Interpro; IPR000005; HTHAYSC. Interpro; IPR007110; Ig-like. Interpro; IPR007110; Ig-like. Interpro; IPR00306; Ig_MHC. Interpro; IPR003596; Ig_w. Pfam; PF00047; 1g; 5. SMART; SM00406; IGv; 1. PROSITE; PS00041; HTH ARAC_FAMILY_1; 1. PROSITE; PS000315; IG_LIKE; 5. PROSITE; PS000390; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96QS0 PRELIMINARY; PRT; 159 AA.
Q96QS0;
Q16QS0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Hypothetical protein.
                                                                                                                                                                                                                                                      "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY039025; AAK82649.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
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                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein sequence 614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tilson M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                 SEQUENCE
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                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                     QVOLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
  QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY
                                                                                                                                                                                 159
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                                                                                          Conservative
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                                                                                                                                                                                 : IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
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                                                                                                            69.7%;
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23,
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Last
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Pred. No. 1
                                                                                       Score 363; DB 4;
Pred. No. 2.6e-32;
3; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain
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Q8WY24;
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Song X.T., Feng Z.Q., Guan X.H.;

"Amplification, cloning and sequence analysis of the heavy
variable region gene of monoclonal anti-idiotypic antibody
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Bukaryota; Metazoa; Platyhelminthes;
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SMART; SM00406; IGv; 1.
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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                        Zheng S., Shao X., Cao J., Geng L., Pang Y., D
"Identification and Characterization of SNC66,
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL, AF283566; AAL36987.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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13567 MW;
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Best Local S
Matches 67
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Best Local S
Matches 65
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EMBL; AF035025; AAD56261.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
Pfam: PE00047; ig-1
                                    01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1 NON TER 1 16 NON TER 116 AA; 12605 MW
                                                                                                Q925S3;
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Q9UL89;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                       MRP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Yin R. Van der Merwe P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW;
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  musculus
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                                                                                                                                                                                                                                                                                                                                                                                    . Similarity 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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0 (TrEMBLrel. 13,
3 (TrEMBLrel. 23,
                                                                                                                    PRELIMINARY;
(Mouse)
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Primates;
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72.0%;
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                                                                                                                                                                                                                                                                                                                                                                           Score 340; DB 4; Lo
Pred. No. 6.3e-30;
8; Mismatches 18;
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Pred. No. 4.7e
14; Mismatches
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C8F9131DE13EA898 CRC64;
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                              sequence update)
annotation update)
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4.7e-31;
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Best Local S
Matches 62
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Best Local S
Matches 63
                                                                                            Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ day
EMBL; BC013490; AAH13490.1; -
InterPro; IPR003701; Ig-1ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_v.
Pfam; PP00407; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS0035; IG_HKE; 4.
PROSITE; PS00390; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463P65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the same strain.";

Int. J. Radiat. Biol. Relat. Sturent. J. InterPro; IPR003006; Ig. MHC. InterPro; IPR003596; Ig. J. SMART; SM00406; IG. J. SMART; SM00406; IG. J. SMART; SM00406; IG. J. SEQUENCE 147 AA; 16274 MM; 8
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SEQUENCE FROM N.A.
STRAIN=BALB/C;
PubMed=11819679;
Cui D., Zeng G., Ye
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91WT1
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91WT1;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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"Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
         62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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64.3%; Score 335; DB 11;
63.3%; Pred. No. 1.2e-28;
cive 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 337;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
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it with the
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                                           DB 11;
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.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          their precursors improving irradiation in mice.";
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                                                                                         CRC64;
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Murinae; Mus
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Best Local S
Matches 65
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SEQUENCE FROM N.A.
TISSUE=Breast tumor;
Strausberg R.;
                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, La
01-MAR-2003 (TrEMBLrel. 23, La
Similar to expressed sequence
Mus musculus (Mouse)
                                                                                                                                                                                                                                                 Q8K0Z4
                                                                             NCBI_TaxID=10090;
                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
NON TER
SEQUENCE
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InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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MEDLINE=98322155; PubMed=9657749;

Jacquemin M.G., Vander Elst L.P.L.;

"Mechanism and kinetics of factor VIII inactivation: study with an IgG4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ224083; CAA11829.1; -. HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                        AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                                                                                                                                                                                                                                                                                                                                            AREFOGSVIMTADISTDIAYMELSSLRSDDTAVYYCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
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67.08;
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Last sequence update)
Last annotation updat
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Pred. No. 4e-2
8; Mismatches
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Catarrhini;
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Best Local S
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Best Local :
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SEQUENCE 123 AA; 13
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Interpro; IPR007110; Ig-like.
Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig-c1.
Interpro; IPR003596; Ig-MC.
Interpro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 4.
SMART; SM00409; IG; 3.
SMART; SM00400; IGc1; 3.
SMART; SM00406; IGv 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG-MHC; 2.
SEQUENCE 480 AA; 51645 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                         Wloch M.K., Alexander A.L., Pippen A.M., PiBetsky D.S., "Differences in V kappa gene utilization and VH CDR3 sec anti-DNA from C3H-lpr mice and lupus mice with nephritis Eur. J. Immunol. 26:2225-2233(1996).

EMBL; U59154; AAB02916.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Anti-DNA heavy chain (Fragment).
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01-MAR-2002
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                                                                                                                                                                                                                   Similarity
                                                                                                            1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                        AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
SOKFKDKATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR
                                                                                                    EIQLQQSGTEL
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                                                                                                                                                                                      63.3%;
llarity 60.2%;
Conservative 1:
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                                                                                                                                                                                                                                                                                 13806 MW;
                                                                                   VKPGASVKI ŚCKAŚGYSFTGYNMNWVKQSHGKSLEWVGDI NPYYGGTRY
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                                                                                                                                                                            Score 330; DB 11;
Pred. No. 8.6e-29;
9; Mismatches 20
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Sciurognathi; Muridae; Murinae; Mus
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98
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RESULT 15
QOBBLA
ID QOBBL
AC QOBBL
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DT 01-JU
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DT 01-JU
DT 01-WA
DE 18100
GN IGH-1
OS MUB mi
OC EMARA
OC Mamma
OX NCBIL
RA KAWAI
RA KAWAI
RA AIZAW
RA KAGOtt
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
Functional annotation of a full-length mouse cDNA collection.";
RT. Weiter Angels, School of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00306; Ig_V.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUR-2003 (TrEMBLrel. 23, Last annotation update)
1810060009Rik protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00229; IG_MHC; 1.

SEQUENCE 473 AA; 51699 MW;
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                                                                                                                                                                                 20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                                                                                                                                                                   1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                Ch 63.3%; Score 330; DB 11; Length 473; Similarity 61.2%; Pred. No. 4.3e-28; 60; Conservative 17; Mismatches 21; Indels
                                                                                                                                       PRELIMINARY;
                                  December 30, 2003, 11:01:02
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-79002) were isolated and cloned from a series of cosmid constructs; Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are
                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment comprising human immur production of human immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-1994
 15-JUN-2001; 2001WO-US19110.
                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                         19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NISB )
                                                      WO200202641-A1
                                                                                                                            systemic
                                                                                                                                                                                                                                                                     ABP45461;
                                                                                                                                                                                                                                                                                                 ABP45461 standard; Protein;
                            10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1995-006791/01.
)B; AAQ78956.
                                                                                  sapiens.
                                                                                                                                                                                                           BLyS binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Page 54-55; 130pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in producing human immunoglobulin in mammalian hosts.
ed on 25-MAR-2003 to correct PN field.
                                                                                                              variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                      AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                            lupus
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                                                                                                                          erythematosus;
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                                                                                                             :rythematosus; rheumatoid arthritis; CVID; AIDS;
immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                              BCFV SEQ ID 1472.
                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%;
87.8%;
                                                                                                                                                                                                                                                                                                 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASC. DB 16;
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bulin in mammalian
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Search completed: December 30, Job time: 32.6089 secs

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                                                                                                                                                                                                                  This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell tumour necrosis factor (TNP) super family and induces B cell cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be immunostity such as cancer, immune, and autoimmune disorders and conditionacy (e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVD) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the inventor.
                                                                                                                                Query Match
Best Local
                                                                                                                     Matches
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2159-2160; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
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                                                                                                                                                                             Sequence
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CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                  Similarity
                                                                                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
                                                                                                                     Conservative
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                                                                                                                                  87.5%;
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                                                                                                                     4
                                                                                                                  Score 456; DB
Pred. No. 5.6e
4; Mismatches
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                                                                                                                                  DB 23;
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RESULT 13
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AC ABB40
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AC ABB40
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DT 04-FE
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DE Pept:
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                                                                                                                                                                                                                                                                                                                                                      measuring human gene expression in a sample derived from human adult cliver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high cliver (1) may be used for predicting, measuring and displaying gene cexpression in samples derived from human adult liver. The genes clientified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which clients associated with coronary heart disease. A89/7348-A855930 represent cliver the sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly crom wife at firp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023459.

04-OCT-2000; 2000GB-0024263.
Peptide #8044 encoded by human foetal liver single exon probe.
                                      04-FEB-2002
                                                                    ABB40538
                                                                                            ABB40538 standard;
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157273-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2003
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                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful sing gene expression in human adult liver -
                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                            AQKLQGRVIMTIDISTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                                  ÓVÓLVÓSGAEVKKPGÁSVKVSCKÁSGYTFTSYGISMVRÓAÞGÓGLEMMGMÍSÁYNGNTNY
                                                                                                                                                                                                                                    QVQLLQSATEVKKPGASMKVŚCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 34543; 658pp; English.
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                                   (first entry)
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                                                                                         Peptide;
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                                                                                            104
                                                                                                                                                                                                                                                                               Score 456; DB 22;
Pred. No. 2.2e-39;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                         Length 104;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                          Gaps
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RESULT 14
AAR66311
ID AAR66
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Best Local S
Matches 86
                                                     Primer; cosmid;
       W09426895-A1
                                                                               Human immunoglobulin variable heavy chain #17.
                             Homo sapiens
                                                                                                             25-MAR-2003
03-AUG-1995
                                                                                                                                                AAR66311;
                                                                                                                                                                   AAR66311 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 33173; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SG,
                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                           86;
                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                     j...4
                                            PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pUB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                          AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101
                                                                                                                                                                                                                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                      QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                                                                                                                                                                                                                                                                                                                                                                           104 AA;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-023639.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DK,
                                                                                                                                                                                                                                                                                                                                   87.5%;
87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank
                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                      Score 456; DB 22;
Pred. No. 2.2e-39;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                             Length 104;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                               The invention relates to an isolated epitope present on cancer cells and comportant in physiological phenomena such as cell rolling, metastasis and important in where the epitope is capable of being bound by an antibody, it is antigen-binding fragment or its complex comprising at least one cantibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune continuous or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for concreasing mortality of tumour or leukaemia cells, for increasing the concreasing mortality of diseased cells to damage by anti-disease, anti-cancer concreasing cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseases concer, leukaemia, autoimmune diseases, cardiovascular diseases such as myocardial confiarction, retinopathic diseases and other diseases mediated by abnormal concrete concrete interactions and diseases caused by sulphated tyrosine-dependent in reparations.
                                                                                                                                            Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                 fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 246-247; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lazarovits J, Hagai Y, Szanthon E, Richter T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-2000; 2000US-258948P.
29-DEC-2000; 2000US-0751181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-DEC-2001; 2001WO-US49442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200253700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOT-) BIO-TECHNOLOGY GEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human antibody fragment #46
     61
                                      61
                                                                                                                                              96;
                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody;
AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                               QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISMVRQAPGQGLEMMGWISAYNGNTNY
                                                                                 OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWTSAYNGNTHY
                                                                                                                                     87.5%;
milarity 87.8%;
Conservative
                                                                                                                                                                                                               86
                                                                                                                                                                                                                                             tein interactions. This sequence represents a human
                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plaksin D, Vogel T, Amit B, Kooperman L,
                                                                                                                                 Score 456; DB 23
Pred. No. 2e-39;
4; Mismatches
                                                                                                                                                                   DB 23;
                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nimrod A,
,, Peretz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interaction.
98
                                                                                                                                                                   Length
                                                                                                                                     Indels
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Levanon
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                                                                                                                                 Gaps
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RESULT 11 ABG78171

RESULT 12 ABG55895

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ABG55895

standard; Peptide;

104

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The invention relates to a peptide or polypeptide comprising an Fv CC molecule, a construct or fragments or a construct of a fragment with CC enhanced binding characteristics which selectively and/or specifically CC binds to a target cell in favour of other cells, where binding is CC primarily determined by a first hypervariable region and Fv is a single CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a CC pharmaceutical agent, is useful in the manufacture of a medicament, where CC the medicament has activity against a diseased cell, preferably a cancer CC (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, CC (myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a CC composition for use in inhibiting the growth of a diseased or cancer CC cell. This sequence represents a human Fv molecule hypervariable region ver
                                                                                                                                 Matches
                                                                                                                                                               Query Match
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptide/polypeptide for cancer therapy has Fv molecule, or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favoucells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plaksin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2000; 2000US-0751181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-2001; 2001WO-US49440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fv molecule hypervariable region related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200259264-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG78171 standard; Protein; 98
                                                                                                                                                 Local
      61
                              19
                                                                   ш
                                                                                                 ш
                                                                                                                                 86;
                                                                                                                                              Similarity
                    AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                          QVQLVQSGAEVKXPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 169; 232pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lazarovits J,
                                                                                                                                                                                             86
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peretz T;
                                                                                                                                                                                             A
K
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                                                                                                                                           87.5%;
87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guy R,
                                                                                                                             4.
                                                                                                                        Score 456; DB 2:
Pred. No. 2e-39;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipschitz O,
                                                                                                                                                      23;
                                                                                                                        8
                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Szanton
98
                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell in favour of other
                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Levanon A;
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Matches 87
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ABP45584
                                                                                                                                                                                                                                  This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have entirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. The antibodies bind to Blogical samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases. As a surfamic limina everthematical rhammarked arthritis.
                                                                                                                                                                         diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-2000; 2000US-212210P.
17-0CT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAMB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; tumour necrosis factor; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45584 standard; Protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP45584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM,
                                                                         87;
                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLyS
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TI
OVÓLVÓSAABVKKPGÁSVKVSCKÁSGYTFTSYGISMVROAPGOGLEMMGWISAYNGNTNY
                    QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                       250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding scrv SEQ ID 1595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2306-2307; 3148pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTIBODY TECHNOLOGY.
                                                                                    88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choi GH,
                                                                 Score 460; DB
Pred. No. 2.2e.
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF superfamily; human; cytostatic; proliferation; B cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaughan T,
                                                                 DB 23;
2.2e-39;
1es 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hilbert
                                                                                                Length
                                                                 Indels
                                                                                                250;
                                                               0,
                                                             Gaps
 60
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XSXE Ĭ

standard;

Protein;

86

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04-DEC-2002 ABG91862; ABG91862

(first entry)

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RESULT 9
AAY50952
ID AAY50952
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Huma
XX Huma
XX Hom

ABG91862
                         RESULT 10
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Best Local S
Matches 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has breasence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody clone DP-14 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 4B; 6lpp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-053102/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anti-factor VIII antibody VH clone DP-14 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                      QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMVGWISAYNGNTHY
                                                                                      AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain; antibody; factor VIII; hemostatic;
; VH gene.
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                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                       Score 456; DB 2
Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-27739P.
25-MAX-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                            88;
                                                                                                                                                                                                                      invention
                                                                                                                         Similarity 89.8
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMBRIDGE ANTIBODY
                  AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                        QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 2264-2265; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                        88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TECHNOLOGY.
                                                                                                                      Score 463; DB 23;
Pred. No. 1.1e-39;
3; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for immune disorders -
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98
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                                                                                                                                                  Length
                                                                                                                       Indels
                                                                                                                                                       250;
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                                                                                                                                                             This invention describes novel antibodies that immunospecifically bind to CB Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, can rirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and conditions are common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC of the antibodies and fragments of the antibodies described in the method cc of the invention.
                                                                                                 Query Match
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Matches 87
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                                                                                                                                                              Sequence
                                                                                                                                                                                        of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2476-2477; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
(CAMB-) CAMBRIDGE ANTIBODY TO
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                                                                                               Similarity
87; Conserv
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AQXFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                       QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGI
                                                   QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against B Lymphocyte Stimulating
                                                                                                                                                             251
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                                                                                                 Conservative
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                                                                                                               88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                              Score 463; DB 23;
Pred. No. 1.1e-39;
3; Mismatches 8
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

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Best Local S
                                                                                                                                                                                                                                                                                                          presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilla A patients. This sequence represents the humanti-factor VIII antibody VH EL-25 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 presence of neutralizing antibodies against factor VIII \boldsymbol{a} treatment of hemophilia A patients with these antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for
                         ABP45105;
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 4B; 61pp; English
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19-AUG-2002
                                                ABP45105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hemophilia A;
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                                                                                                                                                                                                                                                                                                invention
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                                                standard;
                                                                                                                                                                QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                                                                                                                       98 AA;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain; antibody; factor VIII; hemostatic;
(first
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                                                Protein;
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                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                Score 469; DB 21;
Pred. No. 9.4e-41;
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tumous inscreence; immunoscrimence; autoimmune disoruer, antiAIDS; vaccine; cancer; immune; autoimmune disoruer, antiAIDS; vaccine; cancer; immune; autoimmune disoruer, antiAIDS; eystemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; eystemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; eystemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; eystemic lupus erythematosus; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-2000; 2000US-212210P.
17-JUN-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                   WPI; 2002-114799/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blymphocyte stimulator; TNF superfamily; human; cytostatic; r necrosis factor; B cell proliferation; B cell differentiation; sometiments of memoration; antirheumatic; immunostimulant; immunomodilatory; antirheumatic; IDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                              Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLyS binding
                                                                                                                                                                                                                                                                                                                                                                    CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCFV
                                                                                                                                                                                                                                                                                                                                            Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID 1116.
                                                                                                                                                                                                                                                                                                                                            Vaughan
                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                            Hilbert
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -

Claim 1; Page 1734-1735; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypoptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell cumour necrosis factor (TNP) super family and induces B cell correct the invention and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antibit the expression and activity of BLyS. The antibodies bind to BLyS in CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS cand so may be used to detect and quantitate the presence of BLyS in CC indibit the expression and activity of BLyS. They may also be associated with aberrant expression of BLyS. They may also be communicated to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and cquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC from antibodies and fragments of the antibodies described in the method invention.

Sequence 247 ž

Query Match Best Local :

Similarity

Length 247;

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ABP45549
ID ABP455
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          ABP45549 standard; Protein; 250
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                                                                                                           1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                           QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                         AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                  Conservative
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Matches 96
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This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
                                                                                                                                                                                 New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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                                                                                                                                                                                                                                                                              Voorberg
                                                                                                                                                                                                                                                                                                                                             08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50953 standard; Protein; 132
                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                              (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-factor VIII antibody VH protein VH IT-2.
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                                                                                                                                                      4; Fig
                                                                                                                                                                                                                                                                               JJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain; antibody; factor VIII; hemostatic;
; VH protein.
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Pred. No. 4.5e-45;
1; Mismatches 1;
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                                                                                                                                                                                                                                                   This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody clone IT-2 protein which is used in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, polypeptide and presence of neutralizing antibodies treatment of hemophilia A patients v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human anti-factor VIII antibody VH clone IT-2 encoded protein.
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Pred. No. 1.1e-43;
2; Mismatches 2;
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Pred.
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                                                                                                                 490; DB 2
No. 9e-43;
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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                         is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
        98.1
95.8
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Gapop 10.0 ,
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521
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:
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Copyright (c) 1993 - 2003 Compugen Ltd
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(without alignments)
493.415 Million cell updates/sec
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  AAY50954
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          Human anti-factor
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Human anti-factor
Human BLyS binding
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anti-factor
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ALIGNMENTS

23-MAR-2000 (first entry)

AAY50954;

AAY50954 standard; Protein; 98 AA

RESULT 1
AAYS0954
ID AAY5
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Homo
CX Homo
CX Homo
XX H New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -WPI; 2000-053102/04 08-MAY-1998; 07-MAY-1999; Human anti-factor VIII antibody VH protein VH EL-5. Voorberg JJ, (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING. WO9958680-A2 Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; VH protein. 18-NOV-1999. Homo sapiens. Van Den Brink EN, 98EP-0201543 99WO-NL00285. Turenhout EAM;

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

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15: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US108 PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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1	463	98.9	247	11	US-09-880-748-1116	Sequence 1116,
2	463	88.9	250	11	US-09-880-748-1560	Sequence 1560,
IJ	463	88.9	251	11	US-09-880-748-1738	
4.	460	88.3	250	11	US-09-880-748-1595	
υī	456	87.5	98	12	US-10-041-860-2	Sequence 2, Appli
ტ	456	87.5	98	12	US-10-041-860-324	Sequence 324, A
7	456	87.5	98	12	US-10-041-860-326	Sequence 326, A
80	456	87.5	98	12	US-10-041-860-355	u
9	456	87.5	98	12	US-10-041-860-356	356,
10	456	87.5	98	12	US-10-308-817-44	Sequence 44, App
11	456	87.5	98	15	US-10-194-975-4	Sequence 4, Appli
12	456	87.5	104	9	US-09-864-761-47285	Sequence 47285, A
13	456	87.5	117	12	US-10-041-860-206	Sequence 206, App
14	456	87.5	125	12	US-10-041-860-42	Sequence 42, Appl
15	456	87.5	125	3	115-10-041-860-303	20

45	44	3	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	10
446	446	446	447	447	448	449	450	450	451	452	452	452	453	453	453	453	453	453	456	456	456	456	456	456	456	456	456	456	400
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251	251	251	259	257	248	253	254	251	257	251	251	248	251	250	250	249	247	123	259	255	251	251	251	248	127	127	127	126	122
11	11	11	11	11	11	11	11	11	11	11	11	11	11	1	11	11	11	15	11	11	11	11	11	11	12	12	12	12	Ü
-748-186	-09-880-74	-748-93	-09-880-748-97	-09-880-748-1	-09-880-748-1	9-880-748-1	-09-880-748-1	-09-880-748-	-09-880-748-157	-09-880-748-	-09-880-	-09-880-748-	-09-880-74	-880-748-15	-09-880-748-15	-09-880-	-09-880-748	US-10-269-805-51	-09-880-748	-09-880-748	-09-880-748-1	0-748-	9-880-748-1	-880-748-147	-10-041-860-32	-10-041-860-24	-10-041-860-3	-10-041-860-	3
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3339
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1116
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1116
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Publication No. US20030059937A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                            Local
61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                        1 QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEMMGWISAYNGNTNY
                                                                                                                                                                                 ch 88.9%; Score 463; DB 11; Length 247; Similarity 89.8%; Pred. No. 6.9e-40; 88; Conservative 3; Mismatches 7; Indels
                                                                                                           1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEMVGWISAYNGNTHY 60
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOTTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 2000-06-15
PRIOR PRIOR PRILING DATE: 2000-06-15
PRIOR PRILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                            ; ORGANISM: Homo sapiens US-09-880-748-1738
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Best Local
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GENERAL INFORMATION:
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Publication No. US20030059937A1
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Query Match
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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                                                                                             TYPE: PRT
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nilarity 89.8%;
Conservative
88.98;
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Pred. No. 7e-40;
3; Mismatches
Score 463;
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DΒ
11;
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Length 251;
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; ORGANISM: Homo sapiens
US-09-880-748-1595
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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Best Local S
Matches 87
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SEQ ID NO 1595
LENGTH: 250
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APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10041860 Publication No. US20030157109A1
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                                            APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                 CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377
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                                                                                                                                                                                        APPLICANT:
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SOFTWARE: FastSEQ for Windows Version 4.0
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3; Mismatches
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APPLICANT: CORVAIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
             Sequence 326, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTER
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LENGTH: 98
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ORGANISM: homo sapiens
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CANT: Bezabeh, Binyam
OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
OF INVENTION: THEREOF
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Similarity 87.8%;
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Pred. No. 1.3e-39;
4; Mismatches 8;
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Pred. No. 1.3e-39;
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GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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RESULT 9
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 98
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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 326
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Best Local
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Best Local Similarity
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APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
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Pred. No. 1.3e-39;
4; Mismatches 8
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Pred. No. 1.3e-39;
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US-10-041-860-356
Sequence 356, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: COTVALAN, JOSE R.F.

APPLICANT: APPLICANT: APPLICANT:

Jia, Xiao-Chi

Feng, Xiao Yang, Xiao-Chen, Franc

Francine Xiao-Dong

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RESULT 10
US-10-308-817-44
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 356
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Best Local S
Matches 86
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CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 98
TYPE: PAT
ORGANISM: human
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Publication No. US20030219861A1
GENERAL INFORMATION:
                                                             Sequence 4, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: FOOte, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
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TYPE: PRT
ORGANISM: homo sapiens
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87.8%;
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Pred. No. 1.3e-39;
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Pred. No. 1.3e-39;
4; Mismatches 8;
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RESULT 12
US-09-864-761-47285
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4
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SOFTWARE: PatentIn version
SEQ ID NO 4
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Best Local Similarity
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APPLICANT: Rank, David R.
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT FILING DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                   PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                              APPLICATION NUMBER: PCT/USG1/00661 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00670
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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                                                                                                                 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
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APPLICANT: COTVAIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTHEODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377
                                                                     RESULT 14
US-10-041-860-42
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
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FEATURE:
FEATURE:
FEATURE:
FOTHER INFORMATION: MAP TO AB019440.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
OTHER INFORMATION: EST_HUMAN HIT: AW403728.1, EVALUE 4.00e-45
US-09-864-761-47285
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US-10-041-860-206
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APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi APPLICANT: Feng, Xiao APPLICANT: Yang, Xiao-Dong
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TYPE: P
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Local Similarity 87.8%;
hes 86; Conservative
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Pred. No. 1.6e-39;
4; Mismatches 8;
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Pred. No. 1.4e-39;
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Sequence 207, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGRIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 207
LENGTH: 125
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 125
TYPE: PRT
ORGANISM: homo sapiens
Search completed: December 30, Job time : 21.0171 secs
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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Local Similarity 87.8%;
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Weber, Richard
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87.8%;
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Pred. No. 1.7e-39;
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Pred. No. 1.7e-39;
4; Mismatches 8;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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Match Length
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-545-809A-105
US-08-264-093-3
US-08-264-090-22
US-08-964-690-22
US-08-561-521-45
US-08-555-539A-76
US-08-565-521-94
US-08-565-521-91
US-09-025-769B-22
US-08-561-521-10
US-09-025-769B-59
US-09-025-769B-59
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US-08-137-117D-102
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                                           Sequence 105, Appli Sequence 22, Appli Sequence 22, Appli Sequence 45, Appli Sequence 45, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 41, Appli Sequence 41, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 102, Appli Sequence 102, Appli Sequence 102, Appli Sequence 102, Appli Sequence 103, Appli Sequence 104, Appli Sequence 104, Appli Sequence 106, Appli Sequence 107, Appli Sequence 108, Appli Sequenc
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87. 1 llarity 87. Conservative	T 1 1 1 1 20 -545-809A-105 1 2 -645-809A-105 1 2 -6096878 APPLICANT: HONJO, TASUKU APPLICANT: HONJO, TASUKU APPLICANT: HONJO, TASUKU APPLICANT: HONJO, TASUKU APPLICANT: HONJO, SEGMENTS CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardso STREET: 225 Franklin Street COMPUTER PEALORBLE FORM ACOUNTRY: US ZIP: 02110-2804 COMPUTER REALORBLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FASESEQ for Windo CURRENT APPLICATION NUMBER: US/08/5 FILING DATE: 27-MAR-1996 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 096 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070 TELEFAX: 617-542-5070	.0 110 .0 117 .0 119 .0 119 .7 236 .5 117 .5 135 .5 135 .1 123 .3 123 .3 123 .3 123 .9 1140 .9 1140 .9 1140 .9 1108
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456; DB 3 No. 4.4e-4 smatches	FRAGMEN 2.0	-09-899-896-5 -08-545-809A-91 -08-561-521-13 -08-561-521-13 -09-049-672A-13 -09-049-672A-13 -09-089-896-3 -08-137-117D-112 -08-436-717-112 -08-477-878-94 -08-477-9898-94 -08-477-9898-94 -08-477-9898-94 -08-513-968-38 -09-899-896-1 -08-579-378A-8 ALIGNMENTS
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117; s 0;	7HB	Sequence 9 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 6 Sequence 9 Sequence 9 Sequence 6 Sequence 6 Sequence 6 Sequence 1 Sequence 1 Sequence 1 Sequence 6 Sequence 6 Sequence 1
Gaps 0;	SAME	5, Appli 13, Appl 13, Appl 13, Appl 13, Appl 128, App 1128, App 112, Appl 112, Appl 94, Appl 94, Appl 63, Appl 63, Appl 63, Appl 63, Appl 63, Appl 63, Appl 63, Appl 63, Appl

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US-08-264-093-3
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                                                                                                    Sequence 22
Patent No.
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                                                                  APPLICANT: CHESNU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NO
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
                                   APPLICANT:
   APPLICANT:
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STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY. 7-7-1
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette - 3.5 in COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor
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ZIP: M5H 2J7
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                                                                                                    22, Application US/08202047
5. 5800815
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CHESNUT, Robert ...
POLLEY, Margaret J.
PAULSON, James C.
TONES, S. Tarran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    not applicable
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82.7%;
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                                                                                                                                                                                                                                                                                                                                                Score 436; DB 1;
Pred. No. 6.6e-40;
9; Mismatches 8
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RESULT 4
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                                                                                                                                                                                                                                                                                   Sequence 22, Appli
Patent No. 6033667
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APPLICANT: CHESNU
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
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TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
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                                                                                                                                APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
COMPUTER READABLE FORM:
                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Palana
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OTHER INFORMATION:
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ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                             COUNTRY:
                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                         61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                 94105
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One Market Plaza, Steuart Tower,
                                                                                                                                                                                                                                                                                                   Application US/08964690
                                                                                E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 amino acids
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                                                                                                                                                                                 PAULSON, James C.
JONES, S. Tarran
SALDANHA, Jose W.
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                                 USA
                                                                                                                                                                                                                                  CHESNUT, Robert W. POLLEY, Margaret J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 5.4e-38;
8; Mismatches 10
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Suite 2000
                                                                                  Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                     and Their Uses
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OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-561-521-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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Patent No.
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
RIOR APPLICATION DATA:
                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 128 amino acids
TYPE: amino acid
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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80; Conserv
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                                                                                                                                                                                                     USA
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linear
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IBM PC compatible
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80.8%; Pred. No. 5.4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DO COUTO, F
APPLICANT: CERIANI, RC
APPLICANT: PETERSON, J
TITLE OF INVENTION: RE
TITLE OF INVENTION: MC
TITLE OF INVENTION: ME
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS: MORRISON
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TELEPHONE: 415-543-9600
                                                                                         TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William L. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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DO COUTO, FERNI
TORTANI, ROBERTO J
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JERRY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERNANDO J.R.
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Pred. No. 5.5e-38;
                                                                                                                                                                                                                                                                                                                     Version #1.30
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GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                      Query Match
Best Local Similarity 80.8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Une .... CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 80.3%;
Local Similarity 80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/01219 FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                     YAQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                  QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAY-NGNTH 59
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YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR
                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN
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Pred. No. 5.5e-38;
                                                                                                                                                     Score 418.5; DB 5
Pred. No. 5.5e-38;
                                                                                                                                        Mismatches
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RESULT 9
US-08-545-809A-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT AFFILIANTIAN INMBER: US/09/UZ3,/VJAPPLICATION NUMBER: US/09/UZ3,/VJAPPLICATION NUMBER: EP 95 11 3021.0 APPLICATION NUMBER: EP 95 11 3021.0 FILLING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
NAME: James F. Haley, Jr., Esq.
NAME: James F. Haley, Jr., Esq.
                                                  Sequence 96, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22,
Patent No. 6
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SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: MC
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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 ADDRESSEE:
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Ilag, Vic
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Fish & Richardson,
                     ADDRESS:
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80.6%;
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Pred. No. 9.1e-38;
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RESULT 10
US-08-561-521-10
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APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
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                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
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OPERATING SYSTEM: WINDOWS95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TELEFAX: 200154
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CLASSIFICATION:
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CITY: Boston
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77; Conservative
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424
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; ORGANISM: Artificial Sequence ; FEATURE; OTHER INFORMATION: Description of Artificial Sequence: Variable ; OTHER INFORMATION: region of heavy chain of human antibody (M17750) US-09-438-954-41
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 41
                                                                                                                                                                      Matches
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Sun
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yuil
APPLICANT: KOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
FILE REFERENCE: 1303-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver: 2.1
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Best Local :
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INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
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STRANDEDNESS: sir
TOPOLOGY: linear
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es 77; Conserv
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                                                                                                      1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                  78.1%;
l Similarity 78.6%;
77; Conservative
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                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
SOKFOGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR 98
                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
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78.6%;
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                                                                                                                                                                  Score 407; DB 4; Length 119; Pred. No. 8.7e-37; Indels
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RESULT 12 PCT-US95-01219-10

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US-09-025-769B-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                            Sequence 36, Application US/09025769B Patent No. 6300064
                                                                                                                              GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Pecer
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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APPLICANT: JONES, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/1 FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION: NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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                                                        APPLICANT: Moroney,
APPLICANT: Plueckth
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 amino acids
3: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
                                                                  Plueckthun, Andreas
VENTION: Protein/(Poly)peptide libraries
                                                                                                            Ge, Liming
Moroney, Simon
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78.6%;
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Pred. No. 8.7e-37;
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US-09-025-769B-59
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
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MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                              STATE:
                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                      10021
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                                                                                                                                                                                                            New York
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Pack, Peter
Ilag, Vic
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(212)596-9090
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78.6%;
                                      US/09/025,769B
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                                                                            Version #1.30 (EPO)
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TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUEENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TYPE: protein
US-09-025-769B-59
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US-08-652-816A-19
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                                                                                                                                                    COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-MBR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19,
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APPLICANT: OSBOURD, JK
APPLICANT: Alen, DJ
APPLICANT: MCCafferty, JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United Stat
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 9: FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: Specific binding members, materials and ITLE OF INVENTION: methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 S
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: James F. Haley, Jr., I
REGISTRATION NUMBER: 27,794
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5872215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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78.6%;
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Best Local Similarity 80.4%;
Matches 78; Conservative
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APPLICATION NUMBER: US 08/244,597

FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: DAVId M. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/3330:
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312-474-630
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 120 amino acids
TYPE: amino acid
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                                                                                60 AQKFQGRVTMTTDTSTSTAYMELRSLRSEDTAVYYCA 96
                                                                                                   61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
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Pred. No. 1.3e-36;
6; Mismatches 12;
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A;Cross-references: E C;Superfamily: immuno C;Keywords: heterotet F;15-98/Domain: immun R;Griffiths, A.D.; Ma EMBO J. 12, 725-734, A;Title: Human anti-e A;Reference number: S A;Accession: S36260 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-129 -GR Ig heavy chain V regi C;Species: Homo sapie C;Date: 03-Feb-1994 # C;Accession: S36260 R;Tomlinson, I.M.; Wa J. Mol. Biol. 227, 77 A;Title: The repertoi A;Reference number: S A;Accession: S26919 C; Species: Homo sapic C; Date: 22-Nov-1993 # C; Accession: \$26919 A;Cross-references: E C;Superfamily: immunc C;Keywords: heterotet F;15-98/Domain: immun A;Status: preliminary A;Molecule type: DNA A;Residues: 1-98 <TON Ig heavy chain V regi 61 AQKFQGE 1 QVQLLQS 1 Similari 87; Cons QVQLVQS AQKLQGE Cons .:Z18851; NID:g33124; PIDN:CAA79303.1; PID:g939903 bulin V region; immunoglobulin homology er; immunoglobulin obulin homology [vist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, \
)3 TTDTSRRTAYMELRSLRSDDTAVYYCAR 98 /ative .:212316; NID:g32855; FIDN:CAA78186.1; FID:g32856 bulin V region; immunoglobulin homology ner; immunoglobulin cobulin homology <IMM> /98, 1992
of human germline V(H) sequences reveals about fifty groups
85; MUID:93021117; PMID:1404388 nucleic acid sequence not shown [uence_revision 03-Feb-1994 #text_change 23-Jul-1999 HTTDTSTSTAYMELRSLRSDDTAVYYCAR 98 VRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY r, G.; Marks, J.D.; Llewelyn, M.B.; Winter, puence_revision 10-Nov-1995 #text_change 23-Jul-1999 antibodies with high specificity from phage display libraries. 56; MUID:93178448; PMID:7679990 (DP-14) - human (fragment) (man) VKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY (man) (clone alpha-CEA4-8A) - human (fragment) 89.1%; 88.8%; 4 Score 460; DB Z; L. Pred. No. 1.5e-38; Length 98; Indels 0 ດ Gaps 60 60

88.6%;

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36271
A;Accession: S36271
A;Cross-references: EMBL: Z18832; NID:933115; PIDN:CAA79284.1; PID:g939895
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (alpha-phOx15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Date: 0.19165; S24442
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. McCafferty, J. McCafferty, J. McCafferty, J. McCafferty, J. McCafferty, J. McCafferty, McCafferty, J. McCafferty, McCa
                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118,'T', 120-124 <JON>
A; Residues: 1-40, 'GLSGWDGSALTMVTQSILDK', 61-118,'T', 120-124 <JON>
A; Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g1335368
A; Note: the difference for residues 41-60 results from misplacement of 10 l
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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submitted to the EMBL Data Library,
A;Reference number: S24442
A;Accession: S24442
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A; Residues: 1-124 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on A;Reference number: S19663; MUID:92085276; PMID:1748994
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   Score 454; DB 2;
Pred. No. 7.6e-38;
3; Mismatches 9
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C;Species: Homo sapi
C;Date: 20-Feb-1995
C;Accession: S21924;
R;Friedman, D.F.
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F;34-117/Domain: imm
F;49-54/Region: comp
F;69-84/Region: comp
F;118-131/Domain: D
F;132-144/Domain: J
F;145-160/Domain: C
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A; Accession: S21924
A; Status: preliminar
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A; Residues: 1-160 <S
A; Note: the authors
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J. Exp. Med. 169, 16
A;Title: Relationshi
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A; Residues: 1-131 <F
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C; Keywords: autoanti
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C;Accession: PL0105
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923
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quence_revision 20-Feb-1995
1923
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      EVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                                                                                                                                      ion <DRG>
                                                                                                                                                                                                                                                                                                                                                                                                      equence #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quence_revision 31-Mar-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .EVKKPGASVKVSCKASGYTFTSFGISWVRQAPGQGLEWMGWISVYNGDTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTTDTSTSTAYMELRSLRSDDTAVYYCVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable region genes expressed 06; MUID:89235583; PMID:2541221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 444; DB 2;
Pred. No. 7.8e-37;
                                                                                                    Score 443; DB 2;
Pred. No. 1.2e-36;
                                                                        Mismatches
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Gaps

EMBL: X60504;

preferentially bind

red 5

Gaps

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human

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cell lymphoma

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C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <FRI>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S21923
A; Accession: S21925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Friedman, D.F. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Speciés: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                  Query Match
Best Local
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Best Local (
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                                                                                                                                           QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTA 92
                                                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                    AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
                                                                                                                                                                                              Conservative
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82.7%;
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Pred. No. 6.2e-35;
Pred. No. 6.2e-35;
                                                                                                                                                                                                              Score 423; DB 2;
Pred. No. 6.8e-35;
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             C;Species: Homo Bapi,
C;Date: 03-Mar-1994,
C;Accession: S31680
R;Cuistnier, A.M.; G,
Submitted to the EMBI
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 A; Description: Mecha:
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                                                                                                                                           RESULT 11
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A; Note: the nucleotic
C; Superfamily: immun
C; Keywords: heterote
F; 15-98/Domain: immu
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C;Species: Homo sapi
C;Date: 22-Nov-1993
C;Accession: S31600
R;Cuisinier, A.M.; G
submitted to the EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: .
C;Superfamily: immun.
C;Keywords: heterote.
F;34-117/Domain: imm
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R;Tomlinson, I.M.; W
J. Mol. Biol. 227, 7
J. Title: The reperto
                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-98 <TO
A;Cross-references:
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A; Accession: S26938
A; Status: preliminar
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AQKFQG
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bbulin V region; immunoglobulin homology
ner; immunoglobulin
jlobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ns that generate human immunoglobulin diversity operate 585
                                                                                                                                                                                                                                    7:214071; NID:932969; PIDN:CAA78451.1; PID:932970 sequence was submitted to the EMBL Data Library, July 1992 bulin V region; immunoglobulin homology ner; immunoglobulin

    12.7, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
    198, 1992
    of human germline V(H) sequences reveals about fifty groups
    185; MUID:93021117; PMID:1404388

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                                                                                          ;VRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                                                                                                                                                                                   cobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        puence_revision 17-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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TRDTSISTAYMELSRLRSDDTAVYYCAR
                  ||TTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Pred. No. 3.3e-34;
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Pred. No. 1.9e-34;
                                                                                                                                           Mismatches
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98
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                                                                                                                                         Gaps
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nier, L.; Boubli, L.; Fougereau, M.; Tonnelle, ta Library, June 1992

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from

puence_revision 10-Nov-1995 #text_change 23-Jul-1999

(man)

is that generate human immunoglobulin diversity operate

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A;Reference number: S3158
A;Accession: S31680
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <CUI>
A;Cross references: EMBL:
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglob
C;Keywords: heterotetrame
F;34-117/Domain: immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region precursor (VI-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18551; S23625
R;Shin, E.K.; Matsuda, F: Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG> F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92136804; PMID:1740665 A;Accession: S23625
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anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - C;Species: Homo sapiens (man) C;Date: 01-Feb-1995 #sequence_revision 12-May-1995
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C; Superfamily: :
C; Keywords: hete
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A; Residues: 1-117 <OLE>
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A; Residues: 1-117 <SI
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Matches 80
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    12-May-1995 #text_change
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S34014
Ig heavy chain V rec
C; Species: Homo Bap.
C; Date: 02-Dec-1993
                                                               C;Accession: 334014
R;Mariette, X; Tsa;
Eur. J. Immunol. 23
A;Title: Nucleotidi:
A;Reference number:
A;Accession: S34014
A;Status: prelimina;
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A; Residues: 1-127 <
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          A;Cross-references:
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A.; Brouet, J.C.

quence_revision 10-Nov-1995

#text_change 16-Aug-1996

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C;Accession: S49530
R;Mahmoudi, M.; Edwa
submitted to the EMF
A;Description: Molec
A;Reference number:
A;Accession: S49530
A;Status: prelimina;
A;Molecule type: mRN
A;Residues: 1-135 </
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EMBO J. 12, 725-734,

A;Title: Human anti-

A;Reference number:

A;Accession: S36265
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C;Date: 03-Feb-1994
C;Accession: S36265
R;Griffiths, A.D.; b
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S36265
Ig heavy chain V rec
C; Species: Homo sapi
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C;Keywords: heterote
F;15-98/Domain: immu
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C; Superfamily: immun
F; 34-117/Domain: imn
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A;Molecule type: mR:
A;Residues: 1-118 <(
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MTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                           (lobulin homology <IMM>
                                                                                                                                                                                L:218846; NID:g33121; PIDN:CAA79298.1; PID:g939900 obulin V region; immunoglobulin homology mer; immunoglobulin
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.93
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Pred. No. 5.1e-34;
7; Mismatches 12
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AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR

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P01744;
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16-OCT-2001
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAEDLINE=88296408; PubMed=2841108;
MAESUGA F., Lee K.H., Nakai S., Sato T.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in
heavy-chain locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV1G_HUMAN
P23083;
                                                                                                                                                                                                                                                                                                           Immunoglobulin
SIGNAL 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
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                                                                                                                                                                                                                                                                                                                                     PROSITE;
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SMART; SM00406; IGv; 1.
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-NOV-1991 (Rel. 20, Last sequence up-
-NOV-1991 (Rel. 42, Last annotation
heavy chain V-I region V35 precurso
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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S00476; HVHU35.
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117 AA;
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78.6%;
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 sequence
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NCBI_TaxID=9606;

SEQUENCE

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Chordata;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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GO; GO:0005576; C:extracellular; NAS.
GO; GO:000553; F:antigen binding activity;
GO; GO:0005953; F:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                  HVIA HUMAN STANDARD; PRT; 1
P01742;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-I region EU.
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Eukaryota; Metazoa;
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SIGNAL
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton
Bell L.O., Gould H.J.;
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Ig heavy chain V-I region N
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                                                                                                                                                                                                                                                                      SEQUENCE
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APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAK 117
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bbulin_V region; S:
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11; Mismatches
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VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                          "Parcopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific unrearranged VH gene segments.";
Cell 40:271-281(1985).
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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15-JUL-1999
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P06327;
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SMART; SM00406; IGv; 1.
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Waxdal M.J., Edelman G
                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                             MEDLINE=85099340; PubMed=2578321;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=10090;
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Immunoglobulin V region; Pyrrolidone carboxylic
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Cunningham B.A., F
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heavy chain V region VH558 Al/A4 precursor
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hemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         covalent structure of a human gamma G-immunoglobulin. VII. Amino
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117 AA;
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody)
Mus musculus (Mouse)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                    PIR; A02022; G1MSAA.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=79195438; PubMed=109536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SMART; SM00406; IGv;
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                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
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                           PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
DOMAIN 1 106
                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 immunoglobulin-like domain
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THE IGG1 SUBCLASS. THERE
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IPR003006;
IPR003596;
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Ig_MHC.
Ig_v.
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Pred. No. :
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REMANORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.

FRAMEWORK-3.

FRAMEWORK-3.

BY SIMILARITY.
                              IG-LIKE
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21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region 186-1 precursor.
Mus musculus (Mouse).
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NON TER
SEQUENCE
                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Sign
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RELATED GENES THAT COULD
PIR; D90809; HVMS61.
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                                                                                          OVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                          NEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                 VKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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                                                                                                                                                                                IG HEAVY CHAIN V REGION 186-1. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. BY SIMILARITY.
                                                                                                                    Score 330; DD -. Pred. No. 4.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 339; DB 1;
Pred. No. 3.7e-32;
4; Mismatches 17
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21-JUL-1986 (Rel. 01, Las
15-SEP-2003 (Rel. 42, Las
Ig heavy chain V region 3
Mus musculus (Mouse)
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN 1 111 IG-LII
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
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InterPro; IPR007110;
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                                                                                                 immunoglobulin heavy chain Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV02_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Pa
                                                                                                                     "Somatic mutation in genes for the immunoglobulin heavy chain.";
                                                                                                                                                                                     Sims J., Rabbitts
                                                                                                                                                                                                            MEDLINE=82152818;
                                                                                                                                                                                                                            STRAIN=A/J
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                          -!- SIMILARITY: Contains 1 immunoglobulin-like
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SIMILARITY: C
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region 36-65.
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T.H., Estess P.
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Pfam; PF00047; 1g; 1.
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MGD; MGI: 96486; Igh-VJ558.
InterPro; IPR0037110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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P01758;
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                 EMBL; J00488; AAA38519.1; PIR; A02041; HVMS8A.
                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       use by non-profit institutions as long as its omedified and this statement is not removed. Usage
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi
"Diversity of germ-line immunoglobulin
Nature 292:426-430(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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profit institutions as long as
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RESULT 11
HV06_MOUSI
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Best Local S
Matches 62
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Best Local S
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P01750;
P01750;
21-JUL-1986 (Rel. 01, Createu,
21-JUL-1986 (Rel. 01, Last sequence upd
15-JUL-1999 (Rel. 38, Last sequence voice of the control of t
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Immunoglobulin V
SIGNAL 1
CHAIN 20
DOMAIN 20
NON TER 117
SEQUENCE 117
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NON TER
SEQUENCE
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                        signal :
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SMART; SM00406; IGv; 1.
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HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltimore D.;
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62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AOKFOGRVIMITDISRRIAYMELRSLRSDDTAVYYCAR 98
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 QKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                    VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNYN
                                                                                                                                                                                                                                                                                                                                                                                               PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR 117
                                                                        VQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDYA
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117 AA;
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117
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38, Last annotation update)
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                                                                                                           Score 321; DB
Pred. No. 4.5e
L2; Mismatches
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Pred. No. 1.2e-30
                                                                                                                                                                                                                                         FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                           .; DB 1; Le
. 4.5e-30;
cches 22;
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                                                                                                                                              Length 117;
                                                                                                                                                                                        CRC64;
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RESULT 12
HV04_MOUSE
ID HV04_M
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HV07_MOUSI
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Best Local S
Matches 61
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DOMAIN
                                           HV07_MOUSE STANDARD; PRT; 139 AA.
P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation update)
15 heavy chain V region B1-8/186-2 precursor.
                                                                                                                                                                                                                                                                                        DISULFID
NON TER
SEQUENCE
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21-JUL-1986
                                                                                                                   MOUSE
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HSSP; P01810; 2FBJ.
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Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
NCBI_TaxID=10090;
                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                        DOMAIN
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-JUL-1999 (Rel. 38, Last annotation
heavy chain V region 23 precursor.
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larity 62.2%;
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5; IG LIKE;
7 region; Si
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annotation update)
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                                                                                                                                                                                                                                              Score 319; DB 1;
Pred. No. 7.7e-30;
5; Mismatches 22
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION 23.
FRAMENCR-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                   Craniata; Veri
Sciurognathi;
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ODE V
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                    Vertebrata;
thi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
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2a variable region.";
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                                                                                                                                                                                                                                                 Indels
                     Euteleostomi; 
; Murinae; Mus
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RESULT 14
HV51 MOUSE STANDARD
AC P06330;
DT 01-JAN-1988 (Rel. 06, C
DT 01-JAN-1988 (Rel. 06, L
DT 15-JUL-1999 (Rel. 38, L
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Best Local S
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                                                  Ig heavy chain V regi
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bothwell A.L.M., Paskind M., Reth M., Baltimore D.;
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as love modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies: somatic n
Cell 24:625-637(1981)
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STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1A6U; 27-MAY-98.

PDB; 1A6W; 15-JUL-98.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00529; AAA38170.1; -. PIR; A90809; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz
                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSITE; PS50835;
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                                                                                                                                                                                           QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
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                                                    Chordata;
Rodentia;
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62.2%;
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Pred. No. 1.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION B1-8/1 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                    205.12.
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                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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MBL outstation -
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RESULT 15
HV12_MOUSE
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P01756;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15 Heavy chain V region MOPC 104E.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 59; Conserv
Query Match
Best Local Similarity
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Immunoglobulin V region.
DOMAIN
DOMAIN
DOMAIN
199 104
DOMAIN
105 118
DISULFID
122 96
NON TER
118 118
SEQÜENCE 118 AA; 12934 MW;
                                                                                            Immunoglobulin 1
DOMAIN 1
DISULFID 22
CARBOHYD 55
NON TER 117
SEQÜENCE 117 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete amino acid sequence of a mouse mu chain: homology heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.

!- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR; A02039; MINGS4E.

HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF PROTEIN HAS ALSO BEEN DETERMINED.
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   60.7%;
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IG-LIKE.
BY SIMILARITY.
N-LINKED (GLCN)
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BY SIMILARITY.
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Pred. No. 2.
Score 313; DB 1;
Pred. No. 3.8e-29;
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                                                                                                   3CF8ACE4BE447E41 CRC64;
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                                Length 117;
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              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                         Gaps
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Search completed: December 30, 2003, 10:55:50 Job time: 5.25426 secs

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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                SPTREMBL 23:*

1: sp archea:*
2: sp bacteria
3: sp fungi:*
4: sp human:*
5: sp inverteb
6: sp mammal:*
7: sp mhc:*
8: sp organel!
9: sp phage:*
10: sp phage:
11: sp rodent:*
12: sp virus:*
13: sp_vertebr
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516
1 QVQLLQSAAEVRKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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                                                                                                                             sp_organelle:*
sp_phage:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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16	15	14	13	12	11	10	ø	00	7	6	v	4	ω	N	1	Result
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64.9	65.1	65.1	65.5	65.7	66.3	66.5	68.4	71.5	72.3	72.7	73.3	75.8	77.1	77.3	77.5	Query Match
463	480	473	481	613	150	147	116	119	159	497	614	124	500	119	125	Query Match Length
11	11	11	11	1	4.	11	4	տ	4	4.	4	4	4	4.	4	BB
Q99LC4	Q8K0Z4	Q9D8L4	Q91WT1	Q8VCX7	Q9Y298	Q925S3	Q9UL89	Q9GYZ2	096080	Q8WY24	Q96GA6	Q9UL92	Q9BRV0	Q9UL94	Q9UL95	ID
Q91C4 mus musculu		Q9d8l4 mus musculu	Q91wt1 mus musculu	Q8vcx7 mus musculu	Q9y298 homo sapien	Q925s3 mus musculu	Q9ul89 homo sapien	Q9gyz2 schistosoma	Q96qs0 homo sapien	Q8wy24 homo sapien	Q96ga6 homo sapien	Q9ul92 homo sapien	homo	Q9ul94 homo sapien	homo	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
316	316	317	318	318	318	318	318	318	318	318	318	318	318	318	318	318	319	320	321	321	322	323	325	325	326	326	327	331
61.2	61.2	61.4	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.8	62.0	62.2	62.2		62.6		63.0	63.2	ω.	•	64.1
484	139	170	146	146	146	145	145	145	145	145	145	143	143	141	140	137	109	143	143	118	142	142	168	120	241	123	143	157
11	11	1	11	11	11	11	11	11	11	11	11	11	11	11	1	11	11	11	11	11	11	11	11	11	11	11	11	4.
Q99LA6	Q924R5	Q925S2	Q924Q8	Q924Q3	Q924R8	Q924R4	Q924R1	Q924Q7	Q924R3	Q924Q9	Q924Q6	Q924R0	Q924Q5	Q924Q4	Q924R2	Q924R6	Q9JL75	Q91V67	Q924Q0	Q9Z1C4	Q924Q1	Q924Q2	Q8VDC9	Q920E8	Q921A6	Q8VIJ1	Q924P9	095978
		Q92582 mus musculu	Q924q8 mus musculu	Q924q3 mus musculu	mue	Bum	Bru		Bru		Bum	mue		mue	BTI	Q924r6 mus musculu	mue	Q91v67 mus musculu	Bru	Q9z1c4 mus musculu	mus	Bru	8nm	Q920e8 mus musculu	8nm	mu8	8nm	095978 homo sapien

ALIGNMENTS

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RESULT 1
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Best Local Similarity
Matches 76; Conserv
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NON_TER
SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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Q9UL95;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MLX., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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125 AA;
                                                                                                                     Conservative
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13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                   77.5%;
77.6%;
                                                                                                                 Score 400; DB 4; Length 125;
Pred. No. 1e-37;
8; Mismatches 14; Indels
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Matches 76
                        TISSUE-Prostate;
Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL94;
01-MAY-2000
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HSSP; P01810; 2FBJ
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Mammalia; Eutheria;
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                                                                                                                                                                                                                             NCBI_TaxID=9606;
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119 AA;
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Primates;
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                                                                                      EMBL/GenBank/DDBJ
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Pred. No. 1.
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Best Local S
Matches 76
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Best Local (
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Q9UL92;
01-MAY-2000
01-MAY-2000
01-MAR-2003
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NON_TER
SEQUENCE
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EMBL; AF035022; AAI
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
      Q96GA6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                             Q96GA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus."
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124 AA;
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      (TrEMBLrel.
                                                                PRELIMINARY;
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PRT;

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Pfam; PF00047; ig; 4.

SMART; SM00406; IOv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                              AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCAR
AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54154 MW;
                                                                                                                                                                               13580 MW;
                                                                                                                                 75.8%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 398; DB
Pred. No. 9.5e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
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                                                                                                                    Score 391; DB Pred. No. 1.1e 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                               1BAAACBD96ACD2A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                            in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                         Kalis
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Best Local S
Matches 69
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Best Local :
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
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Q8WY24;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF283666; AAL36987.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50035; IG_LIKE; 4.

PROSITE; PS00259; IG_MIC; 1.

SEQUENCE 497 AA; 53665 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNC66 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 614 AA; 67921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00041; HTH ARAC FAMILY 1; PROSITE; PS50835; IG_LIKE; 5. PROSITE; PS00290; IG_MHC; 3.
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01-MAR-2003
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OBQLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMNPQTGNTEF
                                                     QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AOKFODRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR 117
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                                                                                                                                             Conservative
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23,
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23,
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Last
                                                                                                                                      Score 375; DB
Pred. No. 3.9e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 2.3e-34;
2; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata;
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                                                                                                                                                                                                                                                                             F24D08DFA5A663E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fang Y., Dong Q.;
n of SNC66, a Ig-like
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                                                                                                                  DB 4,
3.9e-34;
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                                                                                                                                                                                                      Length 497;
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Best Local S
Matches 71
**A Song X.T., Feng Z.O., Guan X.H.;

**Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma Japonicum.";

**Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.**

**EMBL; AP282622; AAG01452.1; -.

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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 159 AA; 17497 MW; 5
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY039025; AAK82649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9GYZ2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GYZ2;
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"Homo sapiens putative microfibrillar protein with Ig-like "Homo sapiens putative microfibrillar protein with Ig-like "Amount (Marrix Cell Adhesion Molecule-3, Mat-CAM 3).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Schistosoma.
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Best Local S
Matches 71
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Best Local :
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EMBL; AF035025; AAD56261.1; -.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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P6FF: P6F0047; ig. 1
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01-MAY-2000
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria; Primates;
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119 F
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116 AA;
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(TrEMBLrel.
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                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                              68.4%;
75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12605 MW;
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                                       19,
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                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 353; DB 4;
Pred. No. 2.1e-32;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8F9131DE13EA898 CRC64;
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                                       annotation update)
                                                           sequence update)
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RESULT 11
Q9Y298
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  Query Match
Best Local :
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EMBL, AP240166; AAK43731.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cui D., Zeng G., Yan X., Li X., Su C.; "Cloning of mouse genes related to repairing of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after world J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c;
PubMed=11819679;
Cui D., Zeng G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 147 AA; 16274 MW;
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                                                                                                                                                                                                                             Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII
IgG4 monclonal antibody derived from a
inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                           Blood 92:496-506(1998).
EMBL; AJ224083; CAA11829.1;
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                      Homo вapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Y298;
01-NOV-1999
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                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                    MEDLINE=98322155; PubMed=9657749;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                          PROSITE;
                                                                                                     InterPro;
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                                          PS50835;
                                                                                                   IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor
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                                     IG_LIKE;
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Rodentia;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stud.
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    POTENTIAL
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                                                                                                                                                                                                                                                        inactivation: study with an hemophilia A patient with
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3.8e-31;
hes 21;
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RESULT 13
Q91WT1
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AC Q91WT
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Best Local S
Matches 64
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OBVCX7

OBVCX7;

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T 01-MAR-2003 (TrEMBLrel. 23, Le

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Matches
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InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
                                         Q91WT1
Q91WT1;
Q91WT1;
Q91WT1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00
Hypothetical
SEQUENCE 61
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 SEQUENCE
                  NCBI_TaxID=10090;
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                               AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                          QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                                                                                                                                                                                                  QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                                                                                                                                                 65.7%; Score 339; DB 11; 65.3%; Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
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Pred. No. !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                     41A9384DD4C22862 CRC64;
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thi; Muridae; Murinae; Mus
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                                                                            update)
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RESULT 14
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boitelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hyynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hyynshayaki Y.,
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Best Local (
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                                          EMBL; AK007918; BAB25349.1; -.
EMBL; K007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR0077110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013490; AAH13490.1; -.
                Pfam; PF00047; ig; 4. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                            Nature 409:685-690(2001)
                                                                                                                                                                                             Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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llarity 65.3%;
Conservative 1
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                IGv; 1.
                                                                                                                                         BAB25349.1; -.
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Last annotation update)
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Pred. No. 6.1e-30;
1; Mismatches 23
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Sciurognathi; Muridae;
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                                                                                                                                                                            collection.";
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PS50835;

IG_LIKE;

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Q8K0Z4
ID Q8K0Z
AC Q8K0Z
AC Q8K0Z
AC Q8K0Z
DT 01-QC
DT 01-MA
DE Simil
OS Mus m
OC ELKar
OC Mamma
OC NCB1
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RRD SEQUE
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Search completed: December 30, Job time: 24.883 secs
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Best Local S
Matches 61
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C TISSUE-Breast tumor;

A Strausberg R.;

A Strausberg R.;

A Strausberg R.;

A Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

I Interpro; IPR003599; Ig.,

I Interpro; IPR003199; Ig.,

INTERPRO; IPR003199; Ig.,

INTERPRO; IPR003196; Ig.,

R Interpro; IPR003196; Ig.,

R Interpro; IPR003196; Ig.,

R Interpro; IPR003196; Ig.,

R SMART; SM00409; IG; 3.

RR SMART; SM00409; IG; 3.

RR SMART; SM00409; IGC1; 3.

RR SMART; SM00406; IGC1; 1.

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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
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SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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|||| ||   |:  ||||  ||:|||||  ||:||  |||:||  ||||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  |||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  ||:||  
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                                                     2003, 11:01:03
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             A Geneseq 19Jun03:*

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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460	460	464	467	467	471	491	500	504	Score
89.1	89.1	89.9	90.5	90.5	91.3	95.2	96.9	97.7	Query
98	98	250	250	247	98	132	132	98	Query Match Length DB
23	21	23	23	23	21	21	21	21	BB
ABG91862	AAY50952	ABP45584	ABP45549	ABP45105	AAY50954	AAY50950	AAY50953	AAY50955	ID
Human antibody fra	Human anti-factor	Human BLyS binding	Human BLyS binding	Human BLyS binding	Human anti-factor	Human anti-factor	Human anti-factor	Human anti-factor	Description

New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
449	4	449	450	450	450	451	451	451	451	451.5	452	453	454	454	455	455	456	456	456	457	457	457	457	457	458	460	460	460	460	460	460	460	460	460	460
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23	23	22	23	23	23	23	23	23	21	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	16	22	22	23
ABP45441	P456	•	ABP45858	572	ABP44919	ABP44962	59	71	95	518	8	ABP45953	39	ABP45544	ABP45568	ABP45767	ABP45859	ABP45575	ABP45860	ABP45867	ABP45582	ABP45550	41	ABP45862	ABP45727	534	517	ABP45910	586	ABP45551	ABP45461	631	053	ABG55895	817
Human BLyS binding		Ω	BLyS		BLyS	BLyS	BLyS-	BLyS	anti	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	_	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	BLyS	Human BLyS binding	Human immunoglobul	Peptide #8044 enco		ecul

ALIGNMENTS

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RRESULT 1
AAY50952
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ID AAY50952
AC AAY5
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                                                                                                                                                                                                                                                          Voorberg
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; VH protein.
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XX AAY5
XX Huma
XX Huma
XX Hemc
XX Hemc
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH EL-25 protein which is used in the method
This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; heavy hemophilia A;
                                                                                                                                                                                                     New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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                                                                                                                                                                                                                                                                                                           Voorberg
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; VH protein.
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RESULT 3
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Matches 94
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Matches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anti-factor VIII antibody VH clone IT-2 encoded protein.
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                                                                                                                                                                                                                                                    invention.
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                                                                                                                          95.2%;
94.9%;
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Pred. No.
                                                                                                                          Score 491; DB 21;
Pred. No. 2.3e-41
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RESULT 5
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     19-AUG-2002
                                                       ABP45105;
                                                                                                         ABP45105 standard; Protein;
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                                                                                                                                                                                                                                         AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA;
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89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 471; DB 21; Pred. No. 1.7e-39;
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  RESULT 6
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                                                                                                                                                                                                                                 This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypoptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell ctumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, can tirheumatic and antiAlDS activity and land be used in vaccines to chibit the expression and activity of BLyS. The antibodies bind to BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be caministered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and conditions of the sumunodeficiency (c.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                 Query Match
Best Local (
                                                                                                                     Matches
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16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2002.
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                                                                                                                                                                                                                        of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1734-1735; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001;
              61
                                                                                  ب
                                                                                                                   , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                     Similarity
                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                     247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-212210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCFV SEQ ID
                                                                                                                                 90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH,
                                                                                                                   <u>س</u>
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                                                                                                                 Score 467; DB 23;
Pred. No. 1.1e-38;
3; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilbert
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                                                                                                                                                Length 247;
                                                                                                                   Indels
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                                                                                                                   Gaps
                                                60
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ABP45549 standard; Protein; 250

61

AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR

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                                                                                                                                                                                                                                                                                                                                                                                                      B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell tumour necrosis factor (TWF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in complete and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be caministered to treat diseases associated with aberrant BLyS expression cand activity such as cancer, immune, and autoimmune disorders and ciseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (ruf) and cacquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-2000;
17-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001WO-US19110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Page 2264-2265; 3148pp; English.
51
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                                                                                                       بر
                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                             \vdash
                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME
CAMBRIDGE ANT
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEMMGWISIYSGNTDY
                            AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                       QVQLLQSAAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
  AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                 250 AA;
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                                                                                                                                                                                                                       Conservative
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2000US-240816P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTIBODY
                                                                                                                                                                                                                                              90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TECHNOLOGY.
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                                                                                                                                                                                                                    Score 467; DB 23;
Pred. No. 1.1e-38;
3; Mismatches 6
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                                                                                                                                                                                                                                                                        23;
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  86
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ABP45584

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ABP4

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                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                    Matches
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16-MAR-2001;
21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BLyS binding scFv SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
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                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies and fragments of the antibodies described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Page 2306-2307; 3148pp; English
            61
                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                  Similarity
                                                                                                                    QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
            ACKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                               250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-240816P.
2001US-276248P.
2001US-277379P.
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                                                                                                                                                                                                 Score 464; DB 23;
Pred. No. 2.2e-38;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaughan
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                   98
                                                                                                                                                                                                                                                           Length 250;
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RESULT 9
ABG91862
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AAY50952
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Best Local
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          Human antibody fragment #46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                       ABG91862 standard; Protein;
                                                                                                                                                                                                                                                                                                                                          of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-053102/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-1998;
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                                                                                                                                                                                                                                                            l Similarity 88.8
87; Conservative
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                                                                                                                                                                                                                          QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                         QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                      AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                 98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Brink EN,
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                                                                                                                                                                                                                                                                        89.1%;
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                                                                                                                                                                                                                                                           Score 460; DB 21;
Pred. No. 2.1e-38;
4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turenhout EAM;
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                                                                                                                                                                                                                                                                                     Length 98;
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                                                                                                                                                                                                               The invention relates to an isolated epitope present on cancer cells and comportant in physiological phenomena such as cell rolling, metastasis and comportant in physiological phenomena such as cell rolling, metastasis and comportant in physiological phenomena such as cell rolling, metastasis and composition, where the epitope is capable of being bound by an antibody, comparishing at least one comparishing and treation of the comparishing and comparishing and comparishing and comparishing and comparishing diseases unch as cancer, leukaemia cells, for increasing the comparishing diseases unch as cancer, leukaemia cells, for increasing the comparishing diseases and other diseases mediated by abnormal comparishing diseases caused by sulphated tyrosine-dependent comparishing the inventions. This sequence represents a human antibody confirment of the inventions.
                                                                                                                                         Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardic diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                             Sequence
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29-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 246-247; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-674776/72.
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Szanthon E, Richter
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61
                    AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                       QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                  the invention.
                                                                                                                                         Conservative
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2000US-0751181.
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                                                                                                                                                       Score 460; DB 23;
Pred. No. 2.1e-38;
                                                                                                                                         Mismatches
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Peretz T,
98
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ABG78171 standard;

Protein;

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RESULT 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-2001; 2001WO-US49440
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Human liver peptide,
                               25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2000; 2000US-0751181
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                                                                                           ABG55895 standard; Peptide; 104
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               peptide of the invention.
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                                                                                                                                                                                                                                     QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY 60
                                                                                                                                                                          AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                (first entry)
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SEQ ID No 34543
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                                                                                                                                                                                                                                                                                                                 Score 460; DB 23;
Pred. No. 2.1e-38;
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Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
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analysing
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03-AUG-2000;
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hypercholesterolaemia; coronary heart disease.
             Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                         Peptide #8044
                                                                                                                           ABB40538 standard; Peptide;
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                                                                                                   ABB40538
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                                                                                                                                                                                                                                                                                                                al Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for sing gene expression in human adult liver -
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                                                                                                                                                                                                                                                                        1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
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                                                                                                                                                                                                                                                         QVQLVQSGAEVKXPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 34543; 658pp;
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                                                                                                                                                                                                                                                                                                                                                                         104 AA;
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; 2000US-0236359.
; 2000GB-0024263.
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                    (first entry)
                                         encoded by
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                                         human
                                                                                                                               104
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                                                                                                                                                                                                                                                                                                               Score 460; DB 22;
Pred. No. 2.2e-38;
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                                         foetal liver single exon
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RESULT 13
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exonucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
03-AUG-1995
                                                                               24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunoglobulin variable heavy chain #17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
10-MAY-1993;
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87; Conserv
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                                                                                                                                                                                                                                                                                                                    placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                              PCR; amplify; human; immunoglobulin; variable; heavy
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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(first entry)
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Pred. No. 2.2e-38;
4; Mismatches 7;
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RESULT 14
ABP45461
PRX PXX PNX SXX XXX XXX XXX ID
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                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunoscory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                               Human BLyS binding scrv SEQ ID 1472.
                                                                                                                                                                                                                                                                                                                                                                                                    ABP45461 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                  19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-006791/01.
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     248
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Pred. No. 2.5e-38;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human immunoglobulin heavy
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16-JUN-2000; 2000US-212210P 17-OCT-2000; 2000US-240816P

15-JUN-2001; 2001WO-US19110

WO200202641-A1

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RESULT 15
ABP45551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the Ct tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell ctumour necrosis factor (TNF) super family and induces B cell trumour necrosis factor (TNF) super family and induces B cell ctumour necrosis factor (TNF) super family and induces B cell the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, and interpretation and activity and can be used in vaccines to chinibit the expression and activity of BLyS. The antibodies bind to BLyS in the service of the service of BLyS. They may also be associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and condition of the service of the 
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Best Local (
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                                                                                                                                                                                                 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antirheumatic; antirheumatic; cancer; immune; autoimmune disorder; immunodeficie; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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15-JUN-2001;
                                           10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv SEQ ID 1562.
                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP45551;
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                                                                                                                                                                                   common variable
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87; Conserv
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CAMBRIDGE ANTIBODY TI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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2001WO-US19110
                                                                                                                                                                                 immunodeficiency; acquired immunodeficiency syndrome
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88.8%;
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Pred. No. 5.5e-38;
4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilbert
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                                                                                                                                                                                                                                   immunodeficiency;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                  cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and activity such as cancer.
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                           diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                       the invention.
                                                                                                                                                                                                                                                                                                          antibodies and fragments of the antibodies described in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Page 2267-2268; 3148pp; English
    61
                       61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                        μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                     Similarity
                                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                           QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
AQKLQGRVIMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                 251 AA;
                                                                                                                                                                Conservative
                                                                                                                                                                                   89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
                                                                                                                                                                  4.
                                                                                                                                                                                     Score 460; DB 23;
Pred. No. 5.6e-38;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides, useful for 
immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilbert
      98
                                                                                                                                                                                                           Length 251;
                                                                                                                                                                     Indels
                                                                                                                                                                  0
                                                                                                                                                                  Gape
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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Bd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US0 NEW PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US0 NEW PUB.pep:*
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516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   724715 seqs, 199017464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQSAAEVRKPGASVKV.....AYMELRSLRSDDTAVYYCAR 98
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	80	7	ი	S	4.	w	N	_	Result No.
460	460	460	460	460	460	460	460	460	460	460	460	464	467	467	Score
89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.9	90.5	90.5	Query Match
125	125	125	117	104	98	98	98	98	98	98	98	250	250	247	Query Match Length DB
15	12	12	12	9	15	12	12	12	12	12	12	11	1	11	DB
US-10-269-805-45	US-10-041-860-207	US-10-041-860-42	US-10-041-860-206	US-09-864-761-47285	US-10-194-975-4	US-10-308-817-44	US-10-041-860-356	US-10-041-860-355	US-10-041-860-326	US-10-041-860-324	US-10-041-860-2	US-09-880-748-1595	US-09-880-748-1560	US-09-880-748-1116	ID
Sequence 45, Appl	Sequence 207, App	Sequence 42, Appl	Sequence 206, App	Sequence 47285, A	Sequence 4, Appli	44,	Sequence 356, App	Sequence 355, App	Sequence 326, App	Sequence 324, App	Sequence 2, Appli	Sequence 1595, Ap	Sequence 1560, Ap	Sequence 1116, Ap	Description

45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
451	451	ū	451.5	ū	453	ū	454	ū	ū	456	ū	ū	ū	457	457	457	S	457	S	460	6	460	460	6	σ	460	σ	460	
87.4	7.	7.	7.	7.	87.8	8	8	8	8	8	8	8	8		8	8	8	8	8	9	9	89.1	9	9	9	89.1	9	9	
259	257	247	246	248	253	254	251	257	248	251	251	248	251	250	250	249	247	123	251	259	255	251	251	251	248	127	127	127	
11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	15	11	11	11	11	11	11	11	12	12	12	
-09-880-748-97	-09-880-748-16	-09-880-	9-880-748-119	-09-880-74	8-196	-09-880-748-14	55	-09-880-748-157	8-177	-09-880-7	-09-880-748-158	48-187	-09-880-748-187	US-09-880-748-1593	-09-880-748-156	-142	US-09-880-748-1873	US-10-269-805-51	9-880-748-173	8-13	US-09-880-748-1190	US-09-880-748-1921	87	US-09-880-748-1562	48-147	-10-041-860-32	-10-041-860-24	-10-041-860-	
15			,,,	.,	Sequence		w	Sequence		w	U	10	ø	w	Φ		Seguence	10			•••	w		æ		Sequence	10	Sequence	
Ü	-	1726,	1192,	1877,	g	1405,	1555,	1579,	1778,	1870,	1586,	1871,	1878,	1593,	1561,	1425,		51, A	1738,	1356,	1190,	1921,	1872,	1562,	1472,	•	۳	31, A	
App	Ą	Ą	Αp	Ąp	Ą	Ą	Ą	Ąp	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	pp1	Ą	Ą	Ą	¥	Ą	Ą	Ą	App	App	pp1	

ALIGNMENTS

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APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/270,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
SEQ ID NO 1116
TENCTURE 2011
SEQ ID NO 1116
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                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-880-748-1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1116, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                          Matches
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                       LENGTH: 247
TYPE: PRT
                                                                                                                                                                                            Match 90.5%;
Local Similarity 90.8%;
61 AQKFQGRVIMITIDISRRTAYMELRSLRSDDTAVYYCAR 98
                                                                       89;
                                                                                                                                                                          Conservative
                                                                                                                                                                     Score 467; DB 11; Length 247; Pred. No. 1.8e-40; 3; Mismatches 6; Indels
                                                                                                                                                                        0
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/24,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/273,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/273,499
PRIOR APPLICATION NUMBER: 60/293,499
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                                               ; TYPE: PRT; ORGANISM: Homo sapiens US-09-880-748-1595
                                                                                                                                                                                                                      FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-25

PRIOR FILING DATE: 2001-05-25
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US-09-880-748-1560
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GENERAL INFORMATION
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Best Local Similarity
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                                                                                                                         SEQ ID NO 1595
LENGTH: 250
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                              Patentin Ver.
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  89.9%;
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Pred. No. 1.9e-40;
  Score 464;
  BB
  11;
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  Length 250;
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APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10041860 Publication No. US20030157109A1
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                                                                                                                                                                                                                                                                                                                         Sequence 324, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local S
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                                                                                                                                                                                                                                               APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
                            CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                    APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
                                                                                                                                                                                               APPLICANT:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
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                                                                                                                                                                                                               Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
                                                                                                                                                                                                                                                                                                                         Application US/10041860
DS20030157109A1
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; Mismatches 6;
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Pred. No. 3.6e-40;
4; Mismatches 7
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Sequence 355, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDO
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Meber, Richard
APPLICANT: Bezabeh, Bilyam
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                 US-10-041-860-355
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 98
TYPE: PRT
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/041,860
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ORGANISM: homo sapiens
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Similarity 88.8%;
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88.8%;
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Pred. No. 3.6e-40;
4; Mismatches 7;
                                                          PDGFD AND USES
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APPLICANT: Peng, Xiao
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDX
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENT, 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
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                                                                                                                          Sequence 44, Application US/10308817 Publication No. US20030219861A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 98
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NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 355
LENGTH: 98
TYPE: PRT
ORGANISM: homo sapiens
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Best Local 9
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             APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: homo sapiens
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Pred. No. 3.6e-40;
4; Mismatches 7;
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Pred. No. 3.6e-40;
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LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44
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US-10-194-975-4
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PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Matches
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Publication No. US20030039649A1
GENERAL INFORMATION:
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SEQ ID NO 44
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Matches 87; Conserv
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Best Local
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TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
                                                                                       FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                              PRIOR
                                           PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 98
FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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88.8%;
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Pred. No. 3.6e-40;
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Sequence 206, Application US/1004
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
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US-10-041-860-206
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Best Local :
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: -2001-01-30
PRIOR FILING DATE: -2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
               APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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ABGENIX.051A
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EXPRESSED IN ADULT LIVER, SIGNAL = 0.42

EXPRESSED IN FETAL LIVER, SIGNAL = 0.8

SWISSPROT HIT: P23083, EVALUE 2.00e-39

EST_HUMAN HIT: AW403728.1, EVALUE 4.00e-45
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Pred. No. 3.8e-40;
4; Mismatches 7
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                                                   PDGFD AND
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
                                                                                                                                            RESULT 14
US-10-041-860-207
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                                                                                          Sequence 207, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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US-10-041-860-42
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 206
SEQ ID NO 206
SEQ ID RO 206
ORGANISM: homo sapiens
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                                             APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
               APPLICANT:
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ORGANISM: homo
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87; Conserv
Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Gazit, Gadi
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Pred. No. 4.4e-40;
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RESULT 15

US-10-269-805-45

US-10-269-805-45

Sequence 45, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OP INVENTION: ANGIOPOIETIN-2 SPECIFIC BII
FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR APPLICATION NUMBER: US 60/328,604
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Best Local Similarity
Whiches 87; Conserve
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                                                                                                                                                                                          ; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-45
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CURRENT APPLICATION NUMB
CURRENT FILING DATE: 20
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Wi
SEQ ID NO 207
LENGTH: 125
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
                                                                                                                          Query Match 89.1%;
Best Local Similarity 88.8%;
Matches 87; Conservative
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                    61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
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Conservati
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                                                                                                                          Score 460; DB 15;
Pred. No. 4.7e-40;
4; Mismatches 7;
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Pred. No. 4.7e-40,
4; Mismatches
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 98
                                                                                                                                                          Length 125;
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Search completed: December 30, 2003, 11:45:23 Job time: 22.0171 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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425.5
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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             QVQLLQSAAEVRKPGASVKV.....AYMELRSLRSDDTAVYYCAR 98
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Copyright (c) 1993 - 2003 Compugen Ltd.
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         DB
   US-08-545-809A-105
US-08-264-093-3
US-08-265-769B-22
US-08-964-690-22
US-08-964-690-22
US-08-545-539A-75
US-08-545-809A-96
US-09-025-769B-59
US-09-05-1521-10
US-08-561-521-10
US-08-561-521-11
PCT-US95-01219-11
PCT-US95-01219-11
US-08-561-521-41
PCT-US95-01219-41
US-08-661-521-41
PCT-US95-01219-41
US-08-477-877B-94
US-08-477-877B-94
US-08-477-281A-94
US-08-477-281A-94
US-08-477-175-102
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Sequence 105, Appli Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 45, Appli Sequence 46, Appli Sequence 46, Appli Sequence 36, Appli Sequence 37, Appli Sequence 39, Appli Sequence 39, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 41, Appli Sequence 94, Appli Sequence 102, Appli Seq
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1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60

Query Matc Best Local Matches	INTLE OF INVENT: NUMBER OF ESQUEN CORRESPONDENCE A ADDRESSEE: Fi STREET: 225 F CITY: BOSION STATE: MA COUNTRY: US ZIP: 02110-28 COMPUTER READABLE MEDIUM TYPE: MEDIUM TYPE: MEDIUM TYPE: MOPERATING SYSTI SOFTWARE: Fast CURRENT APPLICATION NU FILING DATE: PRIOR APPLICATION NU FILING DATE: 10 ATTORNEY/AGENT IN REFERENCE/DOCK TELEFAEN: 617- TELEFAEN: 617- TELEFA: 200154 INFORMATION FOR SEE SEQUENCE CHARACT LENGTH: 117 a TYPE: MAINO MOLECULE TYPE: US-08-545-809A-105	Ж.Ю О № Г О № Г О В В В В В В В В В В В В В В В В В В В
Match ocal Sim	NUMBER OF ENUMERS CORRESPONDENCE ADDRESSE: F STREET: 225 CITY: BOSION STATE: MA COUNTRY: US ZIP: 02110-2 COMPUTER READAR MEDIUM TYPE: COMPUTER: IS OPERATING SYS SOFTWARE: FA CURRENT APPLICATION N FILING DATE: PRIOR APPLICATION N FILING DATE: PRIOR APPLICATION N FILING TO BATE: PRIOR APPLICATION N FILING TO BATE: APPLICATION N FILING TO BATE: APPLICATION N FILING TO BATE: TELENCE JOC TELETAX: 617 TELETAX: 20015 FORMATION FOR S SEQUENCE CHARAC LENGTH: 117 TYPE: -545-809A-105	28 401 29 401 307 31 397 31 397 32 397 33 397 33 397 33 395 39 395 39 395 39 395 44 393 45 395 44 395 44 395 44 395 45 395 47 395 48 39
h Similarity 87; Conservat	NUMBER OF ENCHRICS: LEGERN'S NUMBER OF SEQUENCES: 1445 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardso STREET: 225 Franklin Street CITY: BOSTON STATE: WA COUNTRY: US ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FASTSEQ for Windo CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/5 FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/UP9 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: Freeman, John W. REGISTRATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 06 REFERENCE/DOCKET NUMBER: 07 REFERENCE/DOCKET NUMBER: 06 REFERENCE/DOCKET NUMBER: 06 REFERENCE/DOCKET NUMBER: 06 REFERENCE/DOCKET NUMBER: 06 REFERENCE/DOCKET NUMBER: 07 REFERENCE/DOCKET NUMBER: 07 REFERENCE/DOCKET NUMBER: 07 REFERENCE/DOCKET NUMBER: 07 REFERENCE/DOCK	401 77.7 401 77.7 397 76.9 397 76.9 396 76.7 396 76.7 395 76.6 395 76.6 397 76.2 393 76.2 393 76.2 393 76.2 393 76.2
89.1 88.8 ive	ESS: ESS: ESS: Richa Richa Richa Rette mpatibl Windo O for W DATA: US/ MAR-199 ATA: RE PCT RR	108 4 U 117 3 U 1121 1 U 121 3 U 122 3 U 135 1 U 135 2 U 135 3 U 139 3 U 117 3 U 119 2 P 119 2 P 119 3 U 119 3 U 119 3 U 119 3 U 119 4 U 139 3 U 139 4 U 139 5
\$; Score 460; DB 3; Length\$; Pred. No. 1.2e-41;4; Mismatches 7; Inde	SAND DNA FRAGMENTS 3507, P.C. 35	S-09-899-896-3 S-08-545-809A-128 S-08-202-47-23 S-08-137-117D-110 S-08-137-117D-112 S-08-545-809A-91 S-08-545-809A-91 S-08-545-809A-91 S-08-545-809A-91 S-08-253-877C-19 S-08-253-877C-19 S-08-603-024-18 S-08-603-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-693-024-18 S-09-049-672A-13 ALIGNMENTS ALIGNMENTS
117; ls 0;	E E	Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 1
Gaps 0;	K.	3, Appli 128, App 23, Appl 23, Appl 100, App 112, Appl 112, Appl 113, Appl 13, Appl 14, Appl 14, Appl 14, Appl 15, Appl 16, Appl 17, Appl 17, Appl 18, Appl 19, Appl 11, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18, Appl

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                                             Sequence 22, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5639863
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette - 3.5 ir
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: NO.
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ridout &
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADURESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY. -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/264,093 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Canada
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Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                        not applicable
                                                                                                                                                                                                                                                                                                                                           85.3%;
83.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 5639863 applicable
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Pred. No. 1.7e-39;
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RESULT 4
US-08-202-047-22
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                              APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIO, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                STREET: One manusco
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY
                                                          94105
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                                                                                              California
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 amino acids
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(212)596-9090
                                                                                                                                                                                                                                                                                         POLLEY, Margaret J. PAULSON, James C.
                                                                                                                                                                                                                                                                                                                               CHESNUT, Robert W.
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 431; DB 4; Length 117; Pred. No. 1.5e-38;
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; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22
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Best Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
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NAME: SMICH, WILLIAM M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 424
                                                                                    CLASSIFICATION:
                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..128
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                               COUNTRY:
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n Release #1.0,
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Pred. No. 6.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/561,521
FILING DATE:
CLASSIFICATION A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-CAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
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Best Local Similarity
Matches 82; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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OTHER INFORMATION: /label= HUMAN_I
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
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                    ENGTH:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                  129 amino acids
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Leger, Olivier J.
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Pred. No. 6.2e-38;
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US-08-525-539A-77
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APPLICANT: DO COUTO, FERNANDO J
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                          Query Match
Best Local
                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 2763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 129 amino acid
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TOPOLOGY: line
MOLECULE TYPE: [
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                       TELEFAX: 15.
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                          Local Similarity
                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77, Application US/08525539A
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                60 YAQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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                                                                             1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQGLEWMGWISIY-SGNTD 59
                                                                                                                            82;
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
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                                                                                                                                                                                                                                                      129 amino acids
                                                                                                                                                                                                                                                                                                                  (415) 494-0792
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                                                                                                                            Conservative
                                                                                                                                                                                                    linear
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                                                                                                                                          82.5%;
82.8%;
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Pred. No. 6.2e-38;
                                                                                                                                          Score 425.5; DB 4
Pred. No. 6.2e-38;
                                                                                                                                                        DB 4;
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RESULT 8
PCT-US95-01219-45
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                                                                                                                                                  Sequence 96, Application US/08545809A Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                  GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/
FILING DATE: 25-JAN-1995
CLASSIFICATION: DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Soldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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ADDRESSEE:
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Fish & Richardson,
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Pred. No. 6.2e-38;
8; Mismatches 8;
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P.C.
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225 Franklin Street

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09025769B Patent No. 6300064
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Knappi
APPLICANT: Pack, I
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 96:
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             SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueskthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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CITY: B
STATE:
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SOFTWARE: FASTSEC
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                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                  CITY: New York
STATE: New York
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TOPOLOGY: linear
FILING DATE:
                                                                                                                                                                                                                                           ADDRESSEE:
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: MA
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                                                                                                                                                                                                                       E: James F. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 amino acids
                                                                                                                                                                   USA
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Ilag, Vic
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18-FEB-1998
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82.7%; Pred. No. 1e-37;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                                          APPLICATION NUMBER: EP 95 11
FILING DATE: 18 AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: James F: Haley, Jr., ES
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 95 11
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ER
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 36:
                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1251 Ave
CITY: New York
STATE: New York
                                       TELEPHONE: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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1251 Avenue of the Americas
120 amino acids
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Moroney, Simon
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Plueckthun, Andreas
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                                                                         (212)596-9000
                                                                                                                                                                                   UMBER: EP 95 11 3021.0
18-AUG-1995
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82.7%;
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                                                                                                             MORPHO/5
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                                                                                                                                            Esq.
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; TYPE: amino ; ; TOPOLOGY: li; ; MOLECULE TYPE: US-09-025-769B-59
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US-08-652-816A-19
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Best Local Similarity
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 9206310.

APPLICATION NUMBER: GB 9206312.6

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 23-SEP-1992

PRIOR APPLICATION NUMBER: GB 9525004.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652 P1/2

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STRET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                     APPLICATION NUMBER: GB 95
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 96
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CFILING DATE: 02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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82.7%;
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Pred. No. 1.7e-37
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RESULT 13
US-09-199-149-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
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Patent No. 6096878
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Patent No. 6160091
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Best Local Similarity
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: P50860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 125
TYPE: PRT
ORGANISM: Kabat VH subgroup
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                          ADDATEST: STREET: BOSTON
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Local Similarity 83.5%;
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                            COUNTRY: US
ZIP: 02110-2804
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                                                                                                                                                                                                                                           Application US/08545809A
                                                                                      225 Franklin Street
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Diskette
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RESULT 15
US-08-561-521-10
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TELEX: 200154
INFORMATION FOR SEO ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08561521 Patent No. 5840299
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Best Local Similarity
           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Admensized Antibodies Against Leukocyte
TITLE OF INVENTION: Admension Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTENC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
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                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Freeman, John W. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                    FILING DATE:
REFERENCE/DOCKET NUMBER: 15270-14
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Best Local Similarity 79.6%;
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TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
61 SQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCAR 98
                   61 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                 78;
                                                                                            1 QVQLLQSAAEVRKPGASVKVSCKASGYPFTSYDISWVRQAPGQCLEWMGWISIYSGNTDY 60
                                                                      QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                        single
                                                                                                                                             Score 411; DB 2; Length 119; Pred. No. 2e-36; 8; Mismatches 12; Indels
                                                                                                                                             0
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Search completed: December 30, 2003, 11:05:32 Job time : 10.0346 secs

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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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120
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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     QQNGGWYEGPLLEPRPDALDI 21
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
44	44	44.5	44.5	44.5	44.5	45	45	45	45	45	45	45	45	45	45
36.7	36.7	37.1	37.1	37.1	37.1	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5
239	147	644	275	76	76	1756	1472	1175	555	395	383	376	302	255	255
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T16159	H71016	AD3471	B49394	G64663	C71852	T02599	A84470	D85089	T45351	T43892	B87579	G95949	JQ1878	H97360	AI2578
hypothetical prote	hypothetical prote	adenylyl-sulfate k	translation elonga	ribosomal protein	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote	ferredoxin [import	translation elonga	hypothetical prote	probable oligopept	hypothetical 33.4K	hypothetical prote	conserved hypothet

ALIGNMENTS

RESULT 2 A49171 A49171 translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis N;Alternate names: 14-nm filament-associated protein C;Species: Tetrahymena pyriformis C;Species: Tetrahymena pyriformis C;Species: A19171; B49171 C;Accession: A49171; B49171 R;Kurasawa, Y; Numata, O; Katoh, M.; Hirano, H.; Chiba, J.; Watanabe, Y. Exp. Cell Res. 203, 251-258, 1992 A;Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation A;Reference number: A49171; MUID:93049915; PMID:1385189 A;Accession: A49171 A;Molecule type: mRNA A;Residues: 1-435 «KUR» A;Cross-references: GB:D11083; NID:9217407; PIDN:BAA01856.1; PID:9217408 A;Note: sequence extracted from NCBI backbone (NCBIN:117509, NCBIP:117510)	A;Experimental source: adult testis; clone DKFZp434L194 C;Comment: This protein enhances a temperature-sensitive mutant RCC1-stimulated nucleot C;Genetics: A;Note: DKFZp434L194.1 C;Superfamily: mitotic control protein dis3 Query Match Best Local Similarity 69.2%; Pred. No. 11; Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0; Qy 4 GGWYEGPLLEPRP 16 Qy 4 GGWYEGPLLEPRP 16 Db 40 GGAHEGPALEPQP 52	RESULT 1 JEO110 mitotic control protein dis3 homolog - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 02-Nov-2001 C;Accession: JEO110; T12542 R;Shiomi, T.; Fukushima, K.; Suzuki, N.; Nakashima, N.; Noguchi, E.; Nishimoto, T. J. Biochem. 123, 883-890, 1998 A;Title: Human Dis3p,which binds to either GTP- or GDP-Ran, complements Saccharomyces (A;Title: Human Dis3p,which binds to either GTP- or GDP-Ran, complements Saccharomyces (A;Reference number: JEO110 A;Recession: JEO110 A;Recession: JEO110 A;Molecule type: mRNA A;Residues: 1-1000 <shi> R;Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999 A;Reference number: Z17524 A;Accession: T12542 A;Status: preliminary A;Molecule type: mRNA A;Cross-references: EMBL;AL080158</shi>

Jak

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A;Accession: B49171
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 2-21 <KU2>
C;Genetics:
A;Genetics:
A;Genetic code: SGC5
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homo
C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F;2-435/Product: translation elongation factor EBF-1 alpha chain #status experimental
F;9-157/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;15-98/Region: GTP binding #status predicted
F;154-157/Region: GTP binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, July 1999
A;Reference number: Z21598
A;Accession: T37174
                                                                                                                                                                                                                                                                                                                      C; Species: Brugia pahangi
C; Date: 13-Jan-1995 #sequ
C; Accession: S26854
                                                                                                                                                                                                                                                                                                                                                              micofilarial sheath protein, major component - C;Species: Brucia nahano:
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A; Residues: 1-164 <SEE>
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A;Accession: S26854
A;Status: preliminary
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C;Genetics:
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                                                                                                                                                                                                                                                                                                         R;Selkirk, M.
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A; Residues: 1-205 <SEL>
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Best Local :
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Best Local
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QNGGWYEGPLLEPRPDA 18
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52.9%;
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50.0%;
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                                                           Score 50; DB:
Pred. No. 3.7;
1; Mismatches
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Pred. No. 2.9;
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Pred. No. 6.1;
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R;Selkirk, M.B.; Yazdanbakhsh, M.; Freedman, D.; Blaxter, M.L.;
J. Biol. Chem. 266, 11002-11008, 1991
A;Title: A proline-rich structural protein of the surface sheath
A;Reference number: A40525; MUID:91250404; PMID:1710216
A;Accession: A40525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-403 < KAW>
A; Cross-references: DDBJ: AP000061;
A; Cross-references: Strain K1
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Recession: H72634
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A40525
                                       R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proline-rich sheath protein Mf22 precursor - nematode (Brugia pahangi)
C;Species: Brugia pahangi
C;Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 27-Jan-1995
C;Accession: A40525; S18744
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                                                                                                                                                                                              probable dehydrogenase YPO1556 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
                    A; Reference number: AB0001; A; Accession: AG0189
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A; Residues: 1-205 <SEL>
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                                                                                                                                                                                                                                                                                                                                                         QTPGWTPGPPLTPKPTA
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Aa, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
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A/Gene: EF-la; aEF-lalpha
C/Superfamily: translation elongation factor Tu; translation elongation factor Tu
C/Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F/7-155/Domain: translation elongation factor Tu homology <ETU>
F/13-20/Region: nucleotide-binding motif A (P-loop)
F/152-155/Region: GTP-binding NKXD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Tanniciello, G.; Gallo, M.; Arcari, P.; Bocchini, V. Biochem. Mol. Biol. Int. 33, 927-937, 1994
A;Title: Organization of a Sulfolobus solfataricus gene cluster homologous to A;Reference number: Z17331; MUID:95078778; PMID:7527264
A;Accession: T11747
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A;EXperimental source: ATCC 49255 / MT-4
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A; Residues: 1-435 <IAN>
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A;Note: this sequence has been revised in R;Arcari, P.; Gallo, M.; Ianniciello, G.;
Nucleic Acids Res. 21, 3920, 1993
A;Reference number: S37631
A;Contents: erratum
A;Accession: S37631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X70701; NID:g395380; PIDN:CAA50033.1; PID:g395381 R;Arcari, P.; Gallo, M.; Ianniciello, G.; dello Russo, A.; Bocchini, V. Nucleic Acids Res. 21, 1666, 1993
A;Title: Primary structure of the elongation factor 1-alpha in Sulfolobus A;Reference number: S33718; MUID:93241951; PMID:8369039
A;Accession: S33719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change (c;Accession: S43507; S33719; S37631; T11747 R;Arcari, P.; Gallo, M.; Ianniciello, G.; Russo, A.D.; Bocchini, Biochim. Biophys. Acta 1217, 333-337, 1994 A;Title: The nucleotide sequence of the gene coding for the elong A;Reference number: S43507; MUID:94198299; PMID:8148382 A;Accession: S43507
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 'H', 2-13,'Q', 15-435 <ARC2>
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A; Residues: 1-13,'Q',15-435 < ARC1>
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A; Residues: 1-435 <ARC>
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A;Cross-references: GB:AL590842; PIDN:CAC90378.1; PID:g15979597; GSPDB C;Genetics:
A;Gene: YPO1556
A;Gene: YPO1556
C;Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology
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                                                                                                                                   Similarity
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                   ENMKWYNGPTLEEYLDQLEL 224
                                                              ONGGWYEGPLLEPRPDALDI 21
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                                                                                                              Conservative
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s: GB:AL590842; PIDN:CAC90378.1; PID:g15979597; GSPDB:GN00175
                                                                                                                              40.8%;
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                                                                                                                                                 Score 49;
                                                                                                         Pred. No. 12;
3; Mismatches
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Pred. No. 10;
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                                                                                                                                                    DB 2;
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                                                                                                                                                    Length 435;
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hypothetical protein 25 - Methanobacterium phage paiM2
C;Species: Methanobacterium phage psiM2
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A;Cross-references: GB:AL591985; pIDN:CAC48799.1; pID:g15140272; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble:
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, F.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                              A;Gene: SMb20413
A;Genome: plasmi
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935891
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSyn
C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                       A; Contents: annotation
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A; Residues: 1-75 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Rccession: G95891
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-435 <KUR>
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A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: H90162
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                                                                                                   Matches
                                                                                                                        Query Match
Best Local Similarity
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RSGGERNGIPLLSPRPDA
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                                                                                              Conservative
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C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 05-May-2000 C; Accession: T12741 R; Pfister, P; Wasserfallen, A.; Stettler, R.; Leisinger, T. submitted to the EMBL Data Library, May 1998 A; Description: Archaeophage PsiM2 complete genomic DNA. A; Reference number: Z17578 A; Reference number: Z17578 A; Accession: T12741 A; Status: translated from GB/EMBL/DDBJ A; Residues: 1-354 <PFI>A; Residues: 1-354 <PFI
A; Residues:
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A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-362 <BLAT'>
A;Cross-references: GB:AE000165; GB:U00096; NID:g1786808; PIDN:AAC7370 A;Experimental source: strain K-12, substrain MG1655 C;Genetics: C;Genetics: A;Gene: ybdH C;Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology
                                                                                                                                                                                                                                                            R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64793
                                                                                                                                                                                                                                                                                                                                                                                                                              glycerol dehydrogenase (EC 1.1.1.6) ybdH - Escherichia coli (strain K-12) C;Specias: Escherichia coli (C;Specias: Escherichia coli (C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 C;Accession: E64793 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; 1
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A;Molecule type: DNA
A;Residues: 1-362 <HAY>
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C;Keywords: oxidoreductase; transmembrane protein F;9-354/Domain: lactaldehyde reductase homology <LAR> F;109-125/Domain: transmembrane #status predicted <TM
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                       A;Cross-references: GB:AE005174; NID:g12513492; PIDN:AAG54934.1; A;Experimental source: strain O157:H7, substrain EDL933
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable oxidoreductase ybdH [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (C;Species: Escherichia coli (C;Datc: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (C;Datc: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (C;Datc: Becref)
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                                                                                                                                                          C; Superfamily: glycerol dehydrogenase; lactaldehyde
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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;Date: 18-Jul-2001 #seque
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O9y211 homo sapien
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[5] SEQUENCE OF 297-928 SEQUENCE OF 297-928 TISSUE=Testis; Wambutt R., Heubner Submitted (JUN-1999) -!- FUNCTION: COMPOI	A N.A. and Peripheral bloo book pubMed=11935316 Vahteristo P., Sand Vahteristo P., Haralds Nigam S., Golberger Stephan D.A., Baile srkardottir R.B., Nev DP.; 6-Mb region a identification and c	SEQUENCE FROM N.A. TISSUE=Brain; MEDLINE=99246063; PubMed=10231032; MEDLINE=99246063; PubMed=10231032; Nagase T., Ishikawa KI., Suyama Miyajima N., Tanaka A., Kotani H., "Prediction of the coding sequence The complete sequences of 100 new for large proteins in vitro."; DNA Res. 6:63-70(1999).	"Human dia3p, which binds to either Saccharomyces cerevisiae dis3."; J. Biochem. 123:883-890(1998). [2] ERRATUM. Shiomi T., Fukushima K., Suzuki N., Nishimoto T.; J. Biochem. 124:250-250(1998). [3]	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Crania Mammalia; Euthería; Primates; Catarr NCBI TaxID=9606; [1] Euthería; Primates; Catarr NCBI TaxID=9606; Euthería; Pubmed=9567621; Shiomi T., Pukushima K., Suzuki N., Nishimoto T.;	SULT 1 RR44 HUMAN STANDARD; PRT; RR44 HUMAN STANDARD; PRT; Q9Y2LI; Q8WW12; Q9UG36; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence 15-SEP-2003 (Rel. 42, Last annotatio) Exosome complex exonuclease RRP44 (B) processing protein 44) (DIS3 protein DIS3 OR RRP44 OR KLAAN1008.	34 42 35.0 324 1 B3G2 RAT 35 42 35.0 419 1 GLPB_ECOLI 36 42 35.0 420 1 EF1A_HALMA 37 42 35.0 457 1 GAL8_KLULA 38 42 35.0 457 1 FADE_ECO57 40 42 35.0 814 1 FADE_ECOLI 41 42 35.0 814 1 FADE_ECOLI 41 42 35.0 814 1 FADE_ECOLI 42 35.0 814 1 FADE_SALTY 43 42 35.0 824 1 JIP2_HUMAN 44 42 35.0 888 1 YGB4_YEAST 45 42 35.0 1550 1 GLTB_SYNY3 46 42 35.0 1550 1 GLTB_SYNY3
ıssenhuber J., Wiemann S.; k/DDBJ databases. 3->5 EXORIBONUCLEASE COMPLEX.	d leukocytes; ; berg T., Bergthorsson J.T., son K., Johannsdottir H.K., N., Robbins C., Pak E., Dutra A., y-Wilson J., Juo SH.H., Kainu T., anlinna H., Borg A., t 13q21-q22 implicated in cancer haracterization of candidate genes.";	M., Kikuno R., Hirosawa M., Nomura N., Ohara O.; s of unidentified human genes. XIII. cDNA clones from brain which code	GTP- or GDP-Ran, complements Nakashima N., Noguchi E.,	Vertebrata; E; Hominidae; ; Hominidae; shima N., Nog	928 AA. update) n update) SC 3.1.13) (Ribosomal RNA n homolog).	Q9z137 rattus norv P13033 escherichia P16018 haloarcula Q06433 kluyveromyc P24126 burkholderi Q8x7r2 escherichia Q47146 escherichia Q47146 escherichia Q8z937 salmonella Q8z937 salmonella Q13387 homo sapien P25339 saccharomyc P55037 synechocyst

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InterPro; IPR004539; EF7 Trbbind.
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InterPro; IPR004161; EFTU D2.
Pfam; PF00009; GTP_EFTU D2; 1.
Pfam; PF03144; GTP_EFTU D3; 1.
Pfam; PF03143; GTP_EFTU D3; 1.
TIGRRAMS; TIGR00483; EF-1 alpha; 1
PROSITE; PS00301; EFACTOR_GTP; 1.
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                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 49255 / DSM 5833 / MT
MEDLINE-93241951; PubMed-8369039;
Arcari P., Gallo M., Ianniciello (
"Primary structure of the elongat:
solfataricus.";
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NP_BIND 13
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MEDLINE=94198299; PubMed=8148382; Arcari P., Gallo M., Ianniciello G., Dello Russo A., Bocchini V.; "The nucleotide sequence of the gene coding for the elongation fall alpha in Sulfolobus solfataricus. Homology of the product with
                                     STRAIN=ATCC 49255
MEDLINE=94198299;
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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EMBL; A3312397; CAC42886.1; -.
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PIX; H90162; H90162.
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PDB; 1JNY; 23-JAN-02.
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-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN PROMOTEIN
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Biochim. Biophys. A.
[3]
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Pfam; PF03144; GTP EFTU D2; 1.
Pfam; PF03143; GTP EFTU D3; 1.
PFINTS; PR00315; ELONGATNECT.
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InterPro; IPR004539; EFI alpha.
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InterPro; IPR004161; EFTU_D2.
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MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arcari P., Masullo M., Bocchini V.;
"The nucleotide sequence of the gene encoding the elongation factor 1 alpha from the archaeon Sulfolobus solfatarious isolate MT3."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION
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Best Local :
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HAMAP; MF 00118; -; 1.
InterPro; IPR0004539; EFT alpha.
InterPro; IPR0004539; EF GTPbind.
InterPro; IPR0004509; EF GTPbind.
InterPro; IPR0004161; EFTU D2.
Pfam; PF00009; GTP EFTU, D2.
Pfam; PF03143; GTP EFTU D2; 1.
Pfam; PF03143; GTP EFTU D3; 1.
PRINTS; PR0315; ELONGATNFCT.
IGREAMS; TIGR00483; EF-1 alpha; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
YBDH_ECOLI
P45579; P77632;
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01-AUG-1990 (Rel. 1
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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STRAIN-ATCC 33909 / NCIB 11770 / DSM 639;

Auer J., Spicker G., Mayerhofer L., Puehler G., Boeck A.;

"Organisation and nucleotide sequence of a gene cluster comprising the translation elongation factor 1-alpha from the extreme thermophilic archaebacterium Sulfolobus acidocaldarius: phylogenetic implications.";
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P17196;
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Sulfolobus acidocaldarius.
Tenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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FUNCTION: THIS PROTEIN PROMOTES TH
AMINOACYL-TRNA TO THE A-SITE OF RI
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13 20 GTP (BY SIM)
90 94 GTP (BY SIM)
152 155 GTP (BY SIM)
435 AA; 48200 MW; A012AF5646
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                       STANDARD;
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THE GTP-BINDING ELONGATION
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Pred. No. 8.9;
1; Mismatches
                       PRT;
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EMBL; AE000165; AAC73700.1; -.
EMBL; U82598; AAB40800.1; -.
EMBL; D90701; BAA53229.1; -.
EMBL; X52904; -; NOT_ANNOTATED_C
PIR; E64793; E64793.
ECOGene; EG12692; ybdH.
InterPro; IPR001670; Fe-ADH.
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    "Detection of new genes in a bacterial genome using three gene classes.";
Nucleic Acids Res. 23:3554-3562(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yano M., Horiuchi T., TA 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage markets. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H.,
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                MEDLINE=96032851;
                                                                                                                                                                                                                                                                                                                                                               J. Mol. Biol. 218:129-140(1991).
                                                                                                                                                                                                                                                                                                                                                                                      "Molecular and functional characterization gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 282-362
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01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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Enterobacteriaceae; Escherichia.
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FAMILY. STRONG, TO BACTERIAL GLYCEROL DEHYDROGENASE.
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InterPro; IPR000795; EF GTPbind.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004161; EFTU D2.
Pfam; PF00009; GTP EFTU D2; 1.
Pfam; PF03144; GTP EFTU D3; 1.
PFam; PF03143; GTP EFTU D3; 1.
PRINTS; PR00315; ELONGATNECT.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Elongation factor 1-alpha C (EF-1-alpha).
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PROSITE; PS00913; ADH_IRON_1; 1.

PROSITE; PS00060; ADH_IRON_2; FALSE_NEG.

Hypothetical protein; Oxidoreductase; Complete proteome Hypothetical protein; Oxidoreductase; Complete Proteome SEQUENCE 362 AA; 39091 MW; C28BBBB4F8F247AE2 CRC64;
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Eukaryota; Rhodophyta;
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01-OCT-1996
                                                                                                                                                                      TIGREAMS; TIGR00483; EF-1 alpha; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
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DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SPOROPHYTE AND GAMETOPHYTE
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No.
    N 46;
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                                                                                       Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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                       Length 449;
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RESULT 10
FPRB_MYCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Probable ferredoxin/ferredoxin--NADP reduct
FPRB OR ML2134 OR MLCB57.39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-I- CATALYTIC ACTIVITY: Reduced ferredoxin + N
                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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Bacteria; Actinobacteria;
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      DOMAIN
DOMAIN
METAL
METAL
METAL
                                                                                                                                 PRINTS; PR00354; 7FE8SFRDOXIN.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                          InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR000813; 7Fe_ferredoxin.
InterPro; IPR000759; Adrindx_reductase.
InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00037; fer4; 2.
                                                                                                                                                                                                                                                                                               EMBL; Z99494; CAB16679.1; -. EMBL; AL583924; CAC31089.1;
                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                           PROSITÉ; PS00198; 4FE4S_FERREDOXIN; 1.
Oxidoreductase; Flavoprotein; NADP; FAD;
Iron-sulfur; 4Fe-4S; Complete proteome.
DOMAIN 1 83
                                                                                                                                                                                                                                                                  HSSP; P55907; 1XER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                Leproma; ML2134; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE FERREDOXIN FAMILY. SIMILARITY: IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: FAD; PROBABLY BINDS | SIMILARITY: IN THE N-TERMINAL,
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PERREDOXIN--NADP REDUCTASE.
IRON-SULFUR 1 (BY SIMILARITY).
IRON-SULFUR 1 (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY)
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY)
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                                                                                                       Electron
                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                     . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FERREDOXIN
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O THE BACTERIAL
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RESULT 12
RS16_HELPY
ID RS16_H
AC P56023
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., I Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iv Tummino P.J., Marberg D., Mills S.D., Jiang Q., Taylor D.E.,
RS16_HELPY
P56023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrance sequence comparison of two unrelated isolates of the human Nature 39:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ZK63;
30-MAY-2000
30-MAY-2000
28-FEB-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                                                                                                                                                                    protein;
76 AA;
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555
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updatal protein S16.
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               STANDARD;
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8985 MW; FC0FB21B58E230C8 CRC64;
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36.0%;
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32.1%;
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                                                                                                                                                                                           Score 44.5; D
Pred. No. 4.6;
5; Mismatches
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          PRT;
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IRON-SULFUR 2 (4FE-4
IRON-SULFUR 1 (BY S)
IRON-SULFUR 1 (BY S)
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(4FE-4S) (BY SIMILARITY).
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Carmel G.,
'N., Ives C.,
Vovis'
                                                                                                                                                                                           Indels
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RESULT 13
Y14D_BPT4
ID Y14D
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Best Local S
Matches
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TICR; HP151; -. 1.

HAMAP; MF 00385; -; 1.

HAMAP; MF 00385; -; 1.

InterPro; IPR000307; Ribosomal S16; 1.

ProDom; P900398; Ribosomal S16; 1.

ProDom; P9003791; Ribosomal S16; 1.

TICRFAMS; TICR000002; S16; 1.

R PROSITE; PS00732; RIBOSOMAL S16; 1.
                                                        Hypothetical 14.7 kDa pro
1410 OR PRD 2.
Bacteriophage T4.
Viruses; dsDNA viruses, 1
T4-like viruses.
    SEQUENCE FROM N.A. Poglazov A.B., Mes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
28-FEB-2003 (Rel. 41, L
30S ribosomal protein S
RPSP OR HP1151.
Helicobacter pylori (Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pylori.";
Nature 388:539-547(1997).
-1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.

Cotton M.D., Weidman J.M., Fujii C., Bownan C., Watthey L., Wallin Bayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000621; AAD08199.1; PIR; G64663; G64663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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9; Conserv
 A.B., Mesyanzhinov
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36.0%;
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Pred. No. 4.6;
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                                                                      вtage;
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                                                                                                          frd-Gp32 intergenic region
Kutter E.M
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                                                                  Caudovirales; Myoviridae;
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RESULT 14
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15-JUL-1999 (Rel. 4
16-OCT-2001 (Rel. 4
Hypothetical 14.8 k
FRD: 2 OR FRD2.
                                                                                                                                                                                Pfam; PF03197; FRD2;
Hypothetical protein.
SEQUENCE 128 AA; 1
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poglazov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.; "DNA Sequences of the frd region in T4-related bacteriophages."; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           EMBL; L46846; AAA74669.1; -.
                                                                                                                                                                                                                           InterPro; IPR004885; Fro
Pfam; PF03197; FRD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses,
T4-like viruses.
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15-JUL-1999
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EMBL; AF158101; AAD42579.1; -
InterPro; IPR004885; Frd2.
Pfam; PF03197; FRD2; 1.
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Pred. No. 9.6;
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Matches 7
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R HSSP; P07862; 11CM.

R HAMAP, MF 00047; -; 1.

R InterPro; IPR005905; D_ala_ Ijg_van.

R InterPro; IPR005905; D_ala_ Ijg_van.

R InterPro; IPR00291; Dala Ijgas; 1.

R Pfam; PF01820; Dala Dala Ijgas; 1.

R TIGRPAMS; TIGR01205; D_ala_ DalaTIGR; 1.

R PROSITE; PS00843; DALA_DALA_LIGASE 1; 1.

R PROSITE; PS00844; DALA_DALA_LIGASE 2; 1.

SEQUENCE 358 AA; 40128 MW; 225CF998AOA979F1 CRC64;
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Q47827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Evolution of structure and substrate specificity in D-alanine:D-alanine ligases and related enzymes.";
J. Mol. Evol. 42.706-712(1996)
-i- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-i- CURALITIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the D-alanine--D-alanine ligase
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
D-alanine-D-alanine ligase (EC 6.3.2.4) (D-a.
(D-Ala-D-Ala ligase).
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-!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
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MEDLINE=96270057; PubMed=8662022;
Canadewall B., Charles M., Dutka-Malen S.,
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
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sp_phage:*
sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
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096979 paranophrys
0968f5 homo sapien
Q8kbc1 chlorobium
000032 brugia paha
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ALIGNMENTS

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ID 056579

PRELIMINARY; PRT; 408 AA.

AC 096979; PRELIMINARY; PRT; 408 AA.

AC 096979

DT 01-MAX-1999 (TrEMBLrel. 10, Created)

DT 01-MAX-1999 (TrEMBLrel. 21, Last amoutation update)

DT 101-JUN-2002 (TrEMBLrel. 21, Last amoutation update)

DE franslation elongation factor 1-alpha (Fragment).

GN TEF1.

CS Paramophrys carnivora.

CS Elwaryota; Alveolata; Ciliophora; Oligohymenophorea; Scuticociliatia;

CC Philasterida; Orchicophryidae; Paranophrys.

CX NCBI TaxID=85900;

RN PEDLINE=99152616; PubMed=10028290;

RN MEDLINE=99152616; PubMed=10028290;

RN MIDLINE=99152616; PubMed=10028290;

RN MIDLINE=99152616; PubMed=10028290;

RN MEDLINE=99152616; PubMed=10028290;

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BA555G22.1.
Homo sapiens (Human).
Homo sapiens (Chordata; Chordata; Chordata; Chordata; Primates;
                                                                                                                                                                              Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M., Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H., Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F., Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey I Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune I Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.; The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium."; Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2001) to the
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2002 (TrEMBLrel. 22, Last annotation
BA555G22.1 (Hypothetical protein KIAA1008)
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STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDLINE=22103685; PubMed=12093901;
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01-OCT-2002
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                                                                                               SEQUENCE
                                                                                                                            Hypothetical
                                                                                                                                                             TIGR; CT1868; -.
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                                                                                     al protein;
175 AA; 19
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? (TrEMBLrel. 22, I)
al protein CT1868.
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19661 MW; 3C87FFF6C5A7E930
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2; Mismatches
Score 51;
Pred. No.
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01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
Hypothetical 38.6 kDa protein.
Methanobacterium wolfei.
Archaea; Euryarchaeota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91250404; PubMed=1710216;
Selkirk M., Yazdanbakhsh M., Free
Jenkins R.E., Willams S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                               "A proline-rich structural protein of Brugia filarial nematode parasites.";
J. Biol. Chem. 266:11002-11008(1991).
EMBL; X58063; CAA41094.1;
                                                        Submitted (AUG-2000) to the EMBL/Gen EMBL; AF301375; AAG39973.1; -. InterPro; IPR001993; Mitoch carrier. PROSITE; PS00215; MITOCH CARRIER; 1.
                                                                                                                                 Luo Y., Pfister P., Leisinger T., Wasserfallen A.;
"The Genome of Archaeal Prophage PsiM100 Encodes the Lytic Responsible for Autolysis of Methanothermobacter wolfeii.";
J. Bacteriol. 183:5788-5792(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Onchocercidae; Brugia.
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                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21429258; PubMed=11544247;
                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteria;
Methanobacteriaceae; Methanothermobacter
NCBI_TaxID=145261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6280;
                                                                                                      Luo
                                        SEQUENCE
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                                                                                                              SEQUENCE FROM N.A.
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         Local
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                                       al protein.
343 AA; 3
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the micofilarial sheath.
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          Score 50; DB
Pred. No. 20;
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                                        61D20A47A28905D3 CRC64;
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                    Length 343;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1674
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US-09-880-748-1674
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
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APPLICANT: Ruben et al.
APPLICANT: INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: pF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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Best Local :
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                                     121 VWGQGTTVTVSS 132
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78.0%;
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78.9%;
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Pred. No. 1.4e-42;
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RESULT 7

Query Match

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; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-973
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILLING DATE: 2001-03-21
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1921
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                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 973
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
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Local Similarity 74.6%;
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112 -YYGMDVWGRGTTVTVSS 128
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Pred. No. 4e-42;
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GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: pF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/270,399

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTMARAPE: DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                          RESULT 10
US-09-880-748-1778
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US-09-880-748-1777
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US-09-880-748-1777
Sequence 1778, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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Best Local S
Matches 100
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8; Mismatches 18
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US-09-880-748-1610
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Best Local S
Matches 104
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TYPE: PRT
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les 100; Conserv
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,348
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PACENTIN VET: 2.01
SEQ ID NO 1610
LENGTH: 257
TYVE: DET
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PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
VIMBER OF SEQ ID NOS: 3239
SOPTMARE: Patentin Ver. 2.0
SEQ ID NO 1778
                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-880-748-1610
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ORGANISM: Homo sapiens
US-09-880-748-1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind FILE REFERENCE: PF523
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                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPE---YY 117
                                                                                     QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTKY
                                                                                                                       QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
AQELQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDTLG---YDILTG-YPPPPYYYY 116
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Conservative
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75.8%;
                                                                                                                                                                                Score 514.5; DB 1
Pred. No. 2.7e-41;
6; Mismatches 18
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Pred. No. 2.6e-41;
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US-09-880-748-1576
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US-09-880-748-1425
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US-09-880-748-1425
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/2793,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1576, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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SEQ ID NO 1425
LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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NUMBER OF SEQ ID NOS: 3239
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
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76.9%;
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: pF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-6
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-1452
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576
Sequence 1452, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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SEQ ID NO 1562
LENGTH: 251
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Best Local Similarity 75.9%;
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Local Similarity 76.5%;
les 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIYSGNTDY 60
                                                                                                                                                                                                                                                                                                      AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                                                                                                                                        AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR-----MEYDILTGYYGGYF--D 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510.5; DB 11; Length 251; Pred. No. 6.2e-41; 7; Mismatches 17; Indels 7;
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Pred. No. 4.1e-41;
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FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
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PRIOR PILING DATE: 2001-03-16
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PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-16-12
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2007-03-16
PRIOR PILING DATE
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Result
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Listing first 45 summaries
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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416.677 Million cell updates/sec
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-025-769B-59
US-09-025-769B-22
US-08-264-093-3
US-08-561-521-45
US-08-562-539A-77
PCT-US95-01219-45
US-08-964-690-22
US-08-964-690-22
US-08-964-890-22
US-08-964-890-105
US-08-852-186A-19
US-08-852-186A-19
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US-08-652-816A-19
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US-09-035-769B-35
US-09-035-769B-35
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36, Appl
22, Appl
3, Appl
45, Appl
45, Appl
45, Appl
22, Appl
22, Appl
3, Appl
3, Appl
105, Appl
116, Appl
117, Appl
118, Appl
114, Appl
117, Appl
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119, Appl
110, Appl
110, Appl
111, Appl
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112, Appl
113, Appl
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115, Appl
115, Appl
116, Appl
117, Appl
118, Appl
118, Appl
118, Appl
119, Appl
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Query Match Best Local Similarity Matches 96; Conservat	RESULT 1 US-09-025-769B-36 Sequence 36, Application Patent No. 6300064 GENERAL INFORMATION: APPLICANT: Hack, Pet APPLICANT: Ge, Limin APPLICANT: Pluckth TITLE OF INVENTION: APPLICANT: Pluckth TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: James F STREET: 1251 Avenu CITY: New York STATE: New York STATE: New York COUNTRY: USA ZIP: 10021 COMPUTER READABLE FOR MEDIUM TYPE: Flopp COMPUTER: IBM PC COPERATING SYSTEM: SOFTWARE: Patentin CURRENT APPLICATION NUMBER: FILING DATE: 18-FE PRIOR APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 18-FE PRIOR APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 18-FE PRIOR APPLICATION NUMBER: FILING DATE: 18-AU ATTORNEY/AGENT INFORM NAME: James F. Hal REGISTRATION NUMBER: REFERENCE/DOCKET NU TELECOMMUNICATION INF TELEPAX: (212)59 TILEFAX: (212)59 TILEFAX: 120 amino SEQUENCE CHARACTERIST LENGTH: 120 amino TYPE: amino STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: prote	28 438 61.6 1 29 438 61.6 1 30 438 61.6 1 31 436.5 61.4 1 32 436.5 61.4 1 33 436.5 61.3 1 34 435.5 61.3 1 36 435.5 61.3 1 37 434.5 61.1 1 38 434.5 61.1 1 39 434.5 61.1 1 39 434.5 61.0 1 40 433.5 61.0 1 41 433.5 61.0 1 42 433.60.9 1 43 43 60.9 1 44 43 60.8 1 45 60.8 1
2%; Score 485; DB 4; Length 7%; Pred. No. 5.3e-39; 7; Mismatches 17; Inde	ALIGNMENTS ;/09025769B im Andreas Andreas Atain/(Poly)peptide libraries ;3 (aley, Jr., Esq. c/o Pish & Neav ,f the Americas ,f the Americas (aley, Jr., Esq. c/o Pish & Neav ,f the Americas ,f the Ame	2 US-08-561-521-41 5 PCT-US95-01219-41 15 PCT-US95-01219-41 10S-08-137-117D-102 2 US-08-30-386A-65 1 US-08-30-386A-65 5 PCT-US95-1123-65 5 PCT-US95-01219-12 1 US-08-477-8778-94 2 US-08-477-8788-94 2 US-08-477-8988-94 3 US-08-477-9898-94 3 US-08-436-717D-100 2 US-08-137-117D-100 2 US-08-137-117D-112 2 US-08-436-717-112
n 120; els 12; Gaps 1;	Neave	Sequence 41, Appl Sequence 102, App Sequence 102, App Sequence 65, Appl Sequence 65, Appl Sequence 65, Appl Sequence 12, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 94, Appl Sequence 63, Appl Sequence 63, Appl Sequence 100, Appl Sequence 112, Appl Sequence 112, Appl Sequence 112, Appl

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US-09-025-769B-59
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-59
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Best Local S
Matches 96
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APPLICANT: Knappik, Achi
APPLICANT: Fack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
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                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moroney, Šimon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 18-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
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                                                       AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCARDGGGGAYEDVWSGEYPEYYAMD 120
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                                                                                                                                                                                               68.2%;
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                                                                                                                                                                            Score 485; DB 4; Length 120; Pred. No. 5.3e-39; Mismatches 17; Indels
                                                                                                                                                                              12;
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STRANDEDNESS:
; TOPOLOGY: lin
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US-09-025-769B-22
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US-09-025-769B-22
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              RESULT 4
US-08-264-093-3
; Sequence 3, Application
; Patent No. 5639863
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OPERATING SYSTEM:
SOFTWARE: PATENTI
CURRENT APPLICATION
APPLICATION NUMBER
FILING DATE: 18-F
PRIOR APPLICATION DATE
APPLICATION NUMBER
FILING DATE: 18-A
ATTORNSY/AGENT INFOR
NAME: James F. Ha
REGISTRATION NUMBER
REFERENCE/DOCKET 
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GENERAL INFORMATION:
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APPLICANT:
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MEDIUM TYPE: Flop.
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CORRESPONDENCE ADDRE.
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Pred. No. 5.7e-39;
5; Mismatches 16;
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                                                                                                                                                                                                                   Patent No. 5840299
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE:
                                                                                      APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY_AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette -
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TITLE OF INVENTION:
                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applic
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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2300 Richmond-Adelaide Centre
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RESULT 6
US-08-525-539A-77
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INFORMATION FOR SEQ ID |
SEQUENCE CHARACTERIST:
LENGTH: 129 amino (
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 630963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 77,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 25-JAI
ATTORNEY/AGENT INFORM/
NAME: Smith, Willi.
REGISTRATION NUMBER
REFERENCE/DOCKET NUM
TELECOMMUNICATION INFO
TELECOMMUNICAT
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COMPUTER READABLE FOR:
MEDIUM TYPE: Flopp)
COMPUTER: IBM PC CC
OPERATING SYSTEM: |
SOPTWARE: Patentin
CURRENT APPLICATION D.
                                                   ZIP: 94304-1018
COMPUTER READABLE FORMEDIUM TYPE: Floppy
COMPUTER: IBM PC CC
OPERATING SYSTEM: I
SOFTWARE: PRECELLIN
CURRENT APPLICATION DI
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APPLICANT: PETERSON,
TITLE OF INVENTION: |
TITLE OF INVENTION: |
TITLE OF INVENTION: |
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: MORRISON
STREET: 755 Page Mi
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                                                                                                                                                                                                                                                                                          STREET: 755 Page
CITY: Palo Alto
STATE: CA
APPLICATION NUMBER: FILING DATE: 14-SE
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DOS/MS-DOS
lease #1.0, Version #1.30
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S/08/525,539A
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US-08-525-539A-77
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GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 77
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
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Best Local Similarity
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                                                      APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                     TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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CITY: San Francisco
STATE: California
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ATTORNEY/AGENT INFORMATION:
SEQUENCE
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  CHARACTERISTICS:
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                                   415-543-5043
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linear
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; LENGTH: 129 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
PCT-US95-01219-45
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Patent No. 5800
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Best Local Similarity
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                                                                                                        TELEFAX: 415-326-:
INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIS;
LENGTH: 128 amino
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC (
OPERATING SYSTEM:
SOPTWARE: PatentI:
CURRENT APPLICATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                           ATTORNEY/AGENT INFORM NAME: Smith, Willi REGISTRATION NUMBER REFERENCE/DOCKET NU
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CORRESPONDENCE ADDRES
                                                                                                                                                                TELECOMMUNICATION INF
TELEPHONE: 415-320
                                        FEATURE:
                                                       MOLECULE TYPE:
                                                                                                                                        TELEPHONE: 415-326-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Market
CITY: San Francisc
STATE: California
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NAME/KEY: Protein LOCATION: 1.128 OTHER INFORMATION:
                                                                   STRANDEDNESS: sing TOPOLOGY: linear
                                                                                             TYPE: amino acid
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Pred. No. 3.7e-38;
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NAME: Smith, William M. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 14137-77 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400 TYPE: amino acids STRANDEDNESS: single TYPE: amino acids STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein FATURE: NAME/KEY: Protein NAME/KEY: Prot	RESULT 9 US-08-964-690-22 Sequence 22, Application US/08964690 Patent No. 6033667 GENERAL INFORMATION: APPLICANT: CHESNUT, Robert W. APPLICANT: POLLEY, Margaret J. APPLICANT: POLLEY, Mary M. APPLICANT: BALDANHA, JOSE W. APPLICANT: BALDANHA, JOSE W. APPLICANT: BENDIG, Mary M. TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94105 COMPUTER: Eloppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION UNMBER: US/08/964,690 FILING DATE: CLASSIFICATION APPLICATION UNMBER: US/08/964,690 FILING DATE: CLASSIFICATION DATA: APPLICATION UNMBER: US/08/964,690 FILING DATE: 25-FEB-1994 ATTORNEY APPLICATION DATA: APPLICATION NUMBER: US/08/202,047 FILING DATE: 25-FEB-1994	Ouery Match 66.9%; Score 476; DB 1; Length 128; Best Local Similarity 71.4%; Pred. No. 4.1e-38; Matches 95; Conservative 11; Mismatches 21; Indels 6; Gaps 2; Oy 1 OVOLLOSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWMGWISIY-SGNTD 59
RESULT 11 US-08-652-816A-19 Sequence 19, Application /08652816A Patent No. 5872215 GENERAL INFORMATION: APPLICANT: OBCOURD. APPLICANT: MCCafferty JG TITLE OF INVENTION: n hods. NUMBER OF SEQUENCES: CORRESSES: Marshall O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Wer, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United Sta Sof America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy isk COMPUTER: IBM PC cc OPERATING SYSTEM: 1 Lease #1.0, Version #1.25 (EPO)	JECOP199-149-3 Sequence 3, Application (09199149) PRENET NO. 6160099 GENERAL INFORMATION: APPLICANT: Jonak, Zdenk: APPLICANT: Taylor, Alexx ler H. APPLICANT: Tolar, S. Sphen H. APPLICANT: Tolar, Ky, 10. APPLICANT: Tolar, Ky, 10. FILE REFERENCE: P50860 CURRENT APPLICATION NUM: CURRENT FILING DATE: 19: 11-24 NUMBER OF SEQ ID NOS: 3; SOFTWARE: PATENTIN 'cr0 SEQ ID NO 3 LENGTH: 125 TYPE: PRT GORGANISH: Kabat VH subc .up I US-09-199-149-3 QUETY Match Best Local Similarity 1%; Pred. No. 1.1e-37; Marches 96; CONSETVAL: .ASMKVSCNASGYPFTSYDISMYRQAPGQGLEMWGWIN-PGGDTNY 59 DD 1 QVOLLOSATEVK: .ASMKVSCNASGYPFTSYDISMYRQAPGQGLEMWGWIN-PGGDTNY 59 GORGANISH: ASDERVINE: .ASVKVSCKASGYTFTSYAISWYRQAPGQGLEMWGWIN-PGGDTNY 59 GORGANISH: ASDERVINE: .ASVKVSCKASGYTFTSYAISWYRQAPGQGCY	QY 1 QVQLLQSATEVK) :ASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGWISIY-SGNTD 59

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US-08-933-983-21
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Best Local S
Matches 94
                                                                                                                                                                                                  Sequence 21
Patent No.
          GENERAL INFORMATION:

APPLICANT: HAERIS, LINDA
APPLICANT: HARRIS, LINDA
APPLICANT: BAJORATH, JURGEN
APPLICANT: MATSUEDA, GARY
APPLICANT: MOVOTIN, JIRI
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING
TITLE OF INVENTION: FIBRINOLYSIS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
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FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 23-MAY-
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FILING DATE: 23-SEP-1992
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 ADDRESSEE:
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STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
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23-MAY-1996
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RESULT 13
US-08-545-809A-105
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APPLICANT: Honjo, Ta
APPLICANT: Matsuda,
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INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
LENGTH: 139 amino
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FILLING DATE: 19-SE
CLASSIFICATION: 53
PRIOR APPLICATION DATI
APPLICATION NUMBER:
FILLING DATE: 20-SE
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prote
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REGISTRATION NUMBER
REFERENCE/DOCKET NU
TELECOMMUNICATION IN
TELEPHONE: (202) 3
                                         COMPUTER READABLE FOR MEDIUM TYPE: Disk. COMPUTER: IBM COMPUTER: C
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
ADDRESSEE: Fish &
STREET: 225 Frankl
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SOFTWARE:
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SOFTWARE: Patent
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CLASSIFICATION:
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ZIP: 02110-2804
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ARE: FastSEQ
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or Windows Version A:
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GMENTS AND DNA FRAGMENTS CO
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RESULT 14
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TELEFAX: 64,
TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
TYPE: 110ear
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Best Local Similarity 86.7%;
Matches 85; Conservative
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REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPAX: 617-542-8906
TELEFAX: 201-831-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Syn
NUMBER OF SEQUENCES: 73
                                  NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31.088
REFERENCE/DOCKET NUMBER: 32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
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FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/253,877C FILING DATE: 03-UN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TELEPHONE: 201-C-
TELEPHONE: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: American Cyanamid Company STREET: One Cyanamid Plaza CITY: Wayne
                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 07470-8426
                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
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Patent No. 5
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Best Local Similarity
                                                                                                                         TELEFAX: 201-683-4:
INFORMATION FOR SEQ ID )
                                                                                                                                                                                                                               COMPUTER READABLE FORMEDIUM TYPE: Floppy COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PATENTING SYSTEM: SOFTWARE: PATENTING SYSTEM: SOFTWARE: PATENTING DATE: 26-MA)
CLASSIFICATION NUMBER: FILING DATE: 26-MA)
CLASSIFICATION: 53
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STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                         TOPOLOGY: 1i
                                                                               SEQUENCE CHARACTERIST:
LENGTH: 139 amino :
TYPE: amino acid
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NAME: Barnhard, Els
REGISTRATION NUMBER
REFERENCE/DOCKET NUMBER
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ADDRESSEE: America:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsou, Hwen APPLICANT: Weiss, Man
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                                                                                                                                                               TELECOMMUNICATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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STATE: New Jerse
                                                                STRANDEDNESS:
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                                                                                                                                       201-683-42
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                                                                                                                                                                                                                                                                                                                                                                                                                 ive Products Corporation
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 Score 448;
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Result
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Maximum Match 100%
Listing first 45 summaries
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1: pir1:*
2: pir2:*
3: pir3:*
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Match
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Ig heavy chain V r
anti-PR2 erythrocy
Ig heavy chain V r
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RESULT 2 S36260 Ig heavy C/Species C/Accessi R/Griffit EMBO J. 1 A/Title: A/Referen A/Accessi A/	Query M Best Lo Matches Qy Db Qy	RESULT 1 S26919 Ig heavy C;Species C;Date: 2 C;Date: 2 C;Date: 3 H;Tomlins R;Tomlins R;Tomlins A;Title: A;Title: A;Title: A;Accessi A;Accessi A;Accessi A;Accessi A;Accessi A;Status: A;Molecul A;Residue A;Csuperfa C;Keyword F;15-98/E	0 4 6 8 8 8 9 9 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8
RESULT 2 S36260 Ig heavy chain V region (clone C;Species: Homo sapiens (man) C;Pate: 03-Feb-1994 #sequence r C;Accession: S36260 R;Griffiths, A.D.; Malmqvist, M RSBO J. 12, 725-734, 1993 A;Title: Human anti-self antibo A;Reference number: S36256; MUI A;Accession: S36260 A;Status: preliminary; nucleic A;Molecule type: mRNA A;Residues: 1-129 <gri>A;Cross-references: EMBL:218851 C;Superfamily: immunoglobulin V C;Keywords: heterotetramer; immuncglobulin</gri>	Match Local Similarity ues 86; Conservat	RESULT 1 \$26919 Ig heavy chain V region (D. C; Species: Homo sapiens (m. C; Date: 22-Nov-1993 #seque: C; Accession: \$26919 R; Tomlinson, I. M; Walter, J. Mol. Biol. 227, 776-798. A; Title: The reportoire of A; Reference number: \$26885 A; Accession: \$26919 A; Accession: \$26919 A; Accession: \$26919 A; Residues: Deliminary A; Molecule type: DNA A; Residues: 1-98 < TOM> A; Cross-references: EMBL: 212 C; Superfamily: immunoglobuli C; Keywords: heterotetramer; F; 15-98/Domain: immunoglobuli	382 73.3 1 381 73.1 1 380 72.9 1 379 72.7 1 377 72.4 1 377 72.4 1 377 72.4 1 377 72.4 1 377 72.4 1 377 72.4 1 370 72.2 1 370 70.4 1 369 70.8 1 369 70.8 1 369 70.4 1
alpha-CEA4-8A) evision 03-Peb (;; Marks, J.D. dies with high D:93178448; PW acid sequence ; NID:933124; region; immun unoglobulin homology <imm's< td=""><td>87.5%; Score 456; DB 2; imilarity 87.8%; Pred. No. 1.7e-39; Conservative 4; Mismatches 8 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVR </td><td>4) - human (fr :_revision 10-N ; Marks, J.D.; 992 man germline V [UID:93021117; [UID:93021117; an V region; imm in homology <im< td=""><td>2 PH1666 2 A32483 2 S23623 2 PH0871 2 JN0295 2 S31667 1 HVHU35 2 S31667 2 144151 2 144151 2 2144151 2 S24680 2 S26921 2 PH1665 2 S26915 3 S26915 3 S1698 ALIGNMENTS</td></im<></td></imm's<>	87.5%; Score 456; DB 2; imilarity 87.8%; Pred. No. 1.7e-39; Conservative 4; Mismatches 8 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVR	4) - human (fr :_revision 10-N ; Marks, J.D.; 992 man germline V [UID:93021117; [UID:93021117; an V region; imm in homology <im< td=""><td>2 PH1666 2 A32483 2 S23623 2 PH0871 2 JN0295 2 S31667 1 HVHU35 2 S31667 2 144151 2 144151 2 2144151 2 S24680 2 S26921 2 PH1665 2 S26915 3 S26915 3 S1698 ALIGNMENTS</td></im<>	2 PH1666 2 A32483 2 S23623 2 PH0871 2 JN0295 2 S31667 1 HVHU35 2 S31667 2 144151 2 144151 2 2144151 2 S24680 2 S26921 2 PH1665 2 S26915 3 S26915 3 S1698 ALIGNMENTS
- human (fragment) -1994 #text_change 23-Jul-1999 ; Bye, J.M.; Embleton, M.J.; McCafferty, specificity from phage display libraries ID:7679990 not shown PIDN:CAA79303.1; PID:g939903 loglobulin homology	87.5%; Score 456; DB 2; Length 98; imilarity 87.8%; Pred. No. 1.7e-39; O'CONSERVATIVE 4; MISMATCHES 8; Indels 0; Gaps 0; O'COLLOSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGGLEMVGWISAYNGNTHY 60	agment) Ov-1995 #text_change 23-Jul-1999 Llewelyn, M.B.; Winter, G. (H) sequences reveals about fifty groups opMID:1404388 pMID:1404388 pMID:CAA78186.1; PID:g32856 unoglobulin homology	Ig heavy chain V r

Query Match

86.9%;

Score 453;

DB 2;

Length 129;

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C;Accession: S36271
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity
A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
                                                                               submitted to the EMBL Data Library, October 1991

A, Reference number: $24442

A, Reference number: $24442

A, Rocession: $2442

A, Rocession: $2442

A, Rocession: $2442

A, Rocession: $2462

A; Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g135368

A; Cross-references: EMBL:X61647; NID:g37667; PIDN:CAA43828.1; PID:g135368

A; Cross-reference for residues 41-60 results from misplacement of 10 b

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S1965; S24442
C;Accession: S1965; S24442
J. Mol. Biol. 222; 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on A;Reference number: S19663; MUID:92085276; PMID:1748994
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A; Residues: 1-122 < GRI>
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A;Status: prelimina
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A; Residues: 1-124 < MAR>
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Best Local
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                     86.4%;
86.7%;
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Score 450; DB 2;
Pred. No. 9.1e-39;
3; Mismatches 10
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Pred. No. 7.1e-39;
4; Mismatches 8
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1 QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY

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RESULT 6
PL0105
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S21924; S21923
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J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0105.
                                                                                                                                                                                                                                                                                                                                                                                                                           anti-PR2 erythrocyte autoantibody heavy chain precu
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
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A; Residues: 1-131 <FRI>
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                                                                                                         P;49-54/Region: complementarity-determining F;69-84/Region: complementarity-determining F;118-131/Domain: D region <DRG>
                                                                                                                                                              A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as G;Comment: The antibody is one of the cold agglutinins that preferentiall C;Cuperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: autoantibody; hemagglutinin F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology 
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                                                                            F;145-160/Domain:
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Best Local :
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                                                                                               132-144/Domain:
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                                      Query Match
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                                                                            C region <CRG>
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82.7%;
                      82.1%;
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     Score 428; DB Pred. No. 2.1e. 6; Mismatches
       6.
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Pred. No. 6.5e-37;
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e 428; DB 2; LE
1. No. 2.1e-36;
1. No. 2.1e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                       R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21925
R;Friedman, D.F.
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A; Residues: 1-98 < TOM>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26918
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A; Residues: 1-111 <FRI>
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RESULT
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                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
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Pred. No. 1.7e-34;
9; Mismatches 12
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Pred. No. 9.1e-36;
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Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S18553; S26916
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.;
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18553
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$31600

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul

C;Accession: $31600

C;Accession: $31600

R;Cuisinier, A.M. Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted F;34-117/Domain: immunoglobulin homology <IMM>
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J. Mol. Biol. 227, 776-798 and germline V(H) sequences reveals about fifty groups
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26916
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A; Residues: 1-136 < CUI>
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A;Accession: S31600
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A; Residues: 20-117 < TOM>
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AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
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78.6%;
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Pred. No. 2.4e-34;
9; Mismatches 12
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Ig heavy chain V region - human (fragment)
N;Alternate names: anti-cytomegalovirus glycoprotein B antibody
C;Species: Homo sapitens (man)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: S68170
R;Boeldicke, T.; Haase, B.; Boecher, M.; Lindenmaier, W.
Eur. J. Blochem. 234, 397-05, 1995
A;Title: Human monoclonal antibodies to cytomegalovirus. Characterization and z A;Reference number: S68170; MUID:96128166; PMID:8536681
A;Reference number: S68170; MUID:96128166; PMID:8536681
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <BOE>
A;Cross-references: GB:S80750; NID:g1246061; PIDN:AAB35861.1; PID:g1246062
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: $26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388
A;Accession: $26938
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, (C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                       RESULT
S31680
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision
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Matches 76
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76.5%;
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Pred. No. 3.5e-34;
9; Mismatches 14;
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Pred. No. 6.8e-34;
7; Mismatches 15
         10-Nov-1995
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    #text_change
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C; Accession: $31680
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A; Description: Mechanisms that generate human immunoglobulin diversity A; Reference number: $31585
A; Accession: $31680
A; Status: preliminary A; Molecule type: mENA A; Residues: 1-117 <CUI>A; Cross-references: EMBL: 214213; NID: 937795; PIDN: CAA78582.1; PID: 9377 A; Cross-references: EMBL: 214213; NID: 937795; PIDN: CAA78582.1; PID: 9377 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S18551; S23625 R;Accession: S18551; S23625, Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E. R;Shin, E.K.; Mateuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E. EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: A;Reference number: S18551; MUID:92037524; PMID:1935893
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S18551
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A;Residues: 1-117 <SHI>
A;Residues: 1-117 <SHI>
A;Cross-references: EWBL:X62106; NID:g37831; PIDN:CAA44016.1; P
A;Close-references: EWBL:X62106; NID:g37831; PIDN:CAA44016.1; P
A;Olee, T.; Lu, E.M.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.;
J. Exp. Med. 175, 831-842; 1992
A;Title: Genetic analysis of self-associating immunoglobulin G
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; ommunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S18551; S23625
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A; Residues: 1-117 < OLE >
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                                          AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                  OVOLVOSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR
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Pred. No. 8.2e-34;
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Pred. No. 8.2e-34;
7; Mismatches 15
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R.W.; Deftos, M.; Kozin, F.;
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D. A.

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S49530
anti-Sm antibody VH chain (VH/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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521
   SwissProt_41:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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     HV3J—HUMAN
HV1F HUMAN
HV55—MOUSE
HV1H—HUMAN
HV0B—HUMAN
HV1H—HUMAN
HV1H—HUMAN
HV1H—HUMAN
                                                                                                                HV1C_HUMAN
HV52_MOUSE
HV1A_HUMAN
HV00_MOUSE
HV01_MOUSE
HV03_MOUSE
HV04_MOUSE
HV06_MOUSE
HV06_MOUSE
HV07_MOUSE
HV05_MOUSE
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HV07_MOUSE
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P23083 homo sapien
P23083 homo sapien
P01744 homo sapien
P016327 mus musculu
P01742 homo sapien
P01741 mus musculu
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P01751 homo sapien
P01745 mus musculu
P01771 homo sapien
P01745 mus musculu
P01775 homo sapien
P01768 homo sapien
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P01768 mus musculu
P01777 homo sapien
P01768 homo sapien
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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79

QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY

Query Ma Best Loo Matches		HV1B_HUMAL ID P0171B AC P0171B AC P0171B DT 21-JT DT 15-83B DE 19 homo OC Eukas OC Mamma OX (1) T RN MEDL: RA Recha RT "Bvo. RT Proc CC This CC This CC the 1 CC use CC modii: CC entiv	9 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1991 (Rel. 20, Last sequence upda
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Ig heavy chain V-I region V35 precursor.
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GO; GO:0005576; C:extracellular; NAS.
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EMBO J. 7:1047-1051(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Pfam; pR00047; ig; 1.
SMART; SM00406; IGv; 1.
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Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
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Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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GO; GO:0005576; C:extracellular; NAS.
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Mammalia; Eutheria;
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Mammalia; Eutheria;
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SEQUENCE
                 NCBI_TaxID=10090;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region VH558 A1/A4 precursor.
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                                                                                                                                             _TaxID=9606;
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                                                                                                                                                                                                                                                                                                        NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                  QVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY
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1 19
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                                                                                                 Rutishauser U.,
                                                                                                           PubMed=5489771;
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Pred. No. 1e-32;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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H1-H4.";
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"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
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21-JUL-1986
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                      SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence upd
15-SEP-2003 (Rel. 42, Last annotation u
Ig heavy chain V region (Anti-arsonate
Mus musculus (Mouse)
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SMART; SM00406; IGv; I.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
1 112
IG-LIKE.
                                                                                                                                      Pfam; PF00047; ig; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02022; GIMSAA.
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Mammalia; Eutheria;
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GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
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Biochemistry 9:3188-3196(1970)
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HSSP; P01772; 2FB4.
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-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                     InterPro; IPR007110;
InterPro; IPR003006;
InterPro; IPR003596;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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THE IGG1 SUBCLASS. THERE
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Ig_MHC.
Ig_v.
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InterPro; IPR00710; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regin; Signal.
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81245215; PubMed=6789211; Givol D., Zakut R., Effron K., Rechavi G., Ram D., "Diversity of germ-line immunoglobulin VH genes."; Nature 292:426-430(1981).
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Mammalia; Eutheria;
                                                                                                                                                     SEQÜENCE
                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                     HSSP;
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    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLQQSGAELVKAGSSVKMSCKATGYTFSSYELYMVRQAPGQGLEDLGYISSSSAYPNY
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                                                                        QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
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              AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                EVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSLEWIGYIYPYNGGTGY
NOKEKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR
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117
117 AA;
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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117
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Rodentia;
                                                                                                                                                     12972 MW; 428CB44DF25D1BC2 CRC64;
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63.9%;
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Pred. No. 4.4e-31;
                                                                                                 Score 326; DB 1;
Pred. No. 4.5e-31
6; Mismatches 2
                                                                                                                                                                             IG HEAVY CHAIN V REGION 108A. IG-LIKE.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                        Length 117;
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Best Local S
Matches 59
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HV03_1
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NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region 36-65.
antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
1g heavy chain V region 23 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                      HV04 MOUSE
P01748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siekevitz M., Gefter M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                         Baltimore D.;
                                                                                               MEDLINE=81234548;
Bothwell A.L.M., I
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genetic basis of antibody production: idiotype response of the strain A mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshak-Rothstein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=83131846; PubMed=6186498;
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                                                                                                                                             STRAIN=C57BL/6;
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P; P01789; 1MCP
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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120 AA;
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                                                                                                 PubMed=6788376;
Paskind M., Reth M.,
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13307 MW; FF04E4A167B654AF CRC64;
THIS GERMLINE
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Rodentia;
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Pred. No. 4.6e-31
                                    contribution evident in a
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Sciurognathi; Muridae; Murinae;
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BELONGS
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; Murinae; Mus
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21-JUL-1986
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                               HV02_MOUSE
P01746;
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NON TER
SEQUENCE
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
DOMAIN
           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                   EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7. HSSP; P01810; 2FBJ.
                                                                                                                                                                                           "Somatic mutation in genes for the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                             Capra J
                                                                                                                                                                                                                                                 MEDLINE=82152818;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                      heavy chain
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A02030; HVMS
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IGV;
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T.H., Estess P.
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Pred. No. 5.9e
15; Mismatches
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION 23.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                       Tucker P.W.,
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RESULT 11
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Best Local S
Matches 59
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Best Local
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SIGNAL 1
CHAIN 20
DOMAIN 20
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SEQÜENCE 140
                                                                                                                                                                                         DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 1.
Fmmunoclobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 186-1 precursor.
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies: somatic m
Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV09 MOUSE
P01753; P11271
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                                                                                                                                                                                                                                                                                        DOMAIN
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HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V reg
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (nterPro; IPR007110;
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                                                                                                               . Similarity 60.2
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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obulin V region; Hybridoma; Signal.
 AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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                                     QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY
                                                       QVQLLQSATEVKKPGASMKVSCMASGYPPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
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; Ig_MHC.
; Ig_v.
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59.2%;
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                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
                                                                                                             Score 319; DB 1; I
Pred. No. 2.9e-30;
5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contribution evident in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 324; DB 1;
Pred. No. 9.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 93G7.
                                                                                                                                                                                         16191A088CB17F5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imanishi-Kari T., Rajewsky
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                                                                                                                                                 Length 117;
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 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2a variable region.";
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                                                                                                             Indels
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RESULT
HV51_M
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      RRARRAN OCC
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Best Local
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P01750;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence of the se
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lymphocytes is encoded by a
EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
HSSP; P01789; IMCP.
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01-JAN-1988
01-JAN-1988
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84182519; PubMed=6201362,
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e:
lymphocytes is encoded by a large se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
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"Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                              MEDLINE=81234548; PubMed:
Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003596;
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                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6;
                                                                                         Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR007110;
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-JUL-1999 (Rel. 38, Last annotation
heavy chain V region AC38 205.12.
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38, Last annotation updat
region 102 precursor.
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                                                                                                                 PubMed=6788376;
Paskind M., Reth
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Ig_v.
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Pred. No. 8.7e-30;
6; Mismatches 24
                              contribution to the evident in a gamma
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Sciurognathi;
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) expressed at high frequency in
set of antibody structural gen
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Best Local S
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                   Query Match
Best Local 8
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Z01810;

LPTO; IPRO07.

LerPro; IPRO03006.

InterPro; IPRO03596;

IPRO03596;

IPRO03596;

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IPRO03
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG_LIKE; 1.
Temminocolobulin V region; Sign
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RELATED GENES THAT COULD
PIR, A02032; HYMS02.
HSSP; P01810; 2FBJ
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.

MEDLINE=84182519; PubMed=6201362;

MEDLINE=87, Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

Dildrop R., Bovens J., Siekevitz M., Beyressed at high frequency i

"A V region determinant (idiotope) expressed at high frequency i

"A V region determinant (idiotope) expressed at high frequency i
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01-JAN-1988 (Rel. 06, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig heavy chain V region AC38 15.3.
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Mammalia; Eutheria; Rodentia;
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PIR; A02037; MHMS15.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-
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57; Conserv
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IPR003006; Ig_MHC.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                      Score 314;
Pred. No. 1
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Sciurognathi; Muridae; Murinae; Mus
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ore 314; DB 1; 1
ed. No. 1.2e-29;
Mismatches 25;
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CHAIN 20
DOMAIN 20
DOMAIN 50
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P01749;
                                                                                                             DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ig heavy chain V region 3 precursor.
IGH-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                       MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00536; AAA38605.1; -. PIR; A02031; HVMS3. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                        DOMAIN
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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                                                                    Similarity
QVQLQQPGAELVRPGSSVKLSCKASGYTFTSYMMDWVKQRPGQGLEWIGNIYPSDSETHY 79
                          QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
                                                                                                                                                                                                                                                      PS50835; IG_LIKE; 1.
obulin V region; Signal.
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                                                                   60.1%; Score 313; DB 1; Length 117; 59.2%; Pred. No. 1.5e-29;
                                                       15;
                                                                                                                                                                                 IG HEAVY CHAIN V REGION 3.

FRAMEWORK-1.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-2.
                                                                                                                                         BY SIMILARITY.
                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
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Search completed: December 30, 2003, 10:55:49 Job time : 5.25426 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Q96GA6
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Q9UL94
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Q9u194 homo sapien
Q9u192 homo sapien
Q9u192 homo sapien
Q9dga6 homo sapien
Q9dga6 homo sapien
Q9dgy2 schistosoma
Q8wy24 homo sapien
Q9u198 homo sapien
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Q91wt1 mus 1
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Q8k0z4 mus 1
Q8vij1 mus 1
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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Q9UL95;
Q9UL95;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035019; AAD56255.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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125 125
125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
                                                                                                                                                                                              73.9%; Score 385; DB 4; Length 125; ilarity 73.5%; Pred. No. 7.3e-35; Conservative 10; Mismatches 16; Indels
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Matches 72
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InterPro; IPR003006; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SMAAA?
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                              Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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         Submitted (APR-2001) to the EMBL; BC005951; AAH05951.1; HSSP; P01789; 1MCP.
                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                         Strausberg R.;
                                                TISSUE=Prostate;
                                                                        NCBI_TaxID=9606;
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                                                             SEQUENCE FROM N.A.
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E; PS50835; IG_LIKE; 1.
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Similarity 73.5%;
72; Conservative 1
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IPR007110;
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119 AA;
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Primates;
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Ig-like
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Pred. No. 8.9e-35;
0; Mismatches 16;
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Catarrhini; Hominidae;
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Best Local :
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AR035022; AAD56258.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
NON_TER 124 124
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SMART; SM00406; IGv;
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Q9UL92;
01-MAY-2000
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW;
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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Mammalia; Eutheria;
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124 AA;
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EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
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Primates;
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Pred. No. 4
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Pred. No. 8.2e-34;
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Best Local S
Matches 69
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PROSITE;
SEQUENCE
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Eukaryota; Metazoa; (
Mammalia; Eutheria;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LI
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                               Tilson M.D
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SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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EMBL; BC009851; AAH09851.1; -
Interpro; IPR000005; HTHArac.
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Mammalia; Eutheria; Primates;
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01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
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                                                                                                                                  Match
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                                                                                         68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Conserv
                                                                                                           Similarity
QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGDEWMGVINPSGGSARY
                             QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCAR
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                                                                                   69.7%;
nilarity 69.4%;
Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 AA; 67921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                        A.
                                                                                                                                                                        IG_LIKE; 1.; 17497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%;

    Created)
    Last sequence update)
    Last annotation update)

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23,
                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 371; DB ...
Pred. No. 1.7e-32;
                                                                              Score 363; DB 4; L
Pred. No. 2.6e-32;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last
Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55EF536E77AA9BBB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                      Length 159;
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                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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79
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                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
   Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNC66, a Ig-like
down-regulated in colorectal cancer.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF283666; AAL36987.1;
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003556; Ig_v.
                                                                                                                                                                01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                             Q8WY24;
Q8WY24;
                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                      SNC66 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GYZ2
Q9GYZ2;
01-MAR-2001
                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF282622; AAGO1452.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song X.T., Feng Z.Q., Gu
"Amplification, cloning
variable region gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
Monoclonal anti-idiotypic an
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
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                                                                                                                                                                                                                                                                                                                                         l Similarity 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
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                                                                                                                                                                                                                                                                   AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
                                                                                                                                                                                                                                                                                           QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY
                                                                                                                                                                                                                                                                                                            QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY
                                                                                                                                                                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                119
119 AA;
                                                                                                                                                             (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
19; 4.
                                                                                                                                                                                                                                                                                                                                                                             119
.; 13567 MW;
                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                         : Ig-like.
: Ig_MHC.
: Ig_v.
                                                                                                                                                                                                                                                                                                                                                 68.7%;
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g and sequence and monoclonal and
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20,
23,

    Last sequence update)
    Last annotation update)
    antibody NP30 heavy chain

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                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                 Score 358;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                             BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e analysis of the heavy anti-idiotypic antibody
                                                                                                                                                                                                       497
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Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                     DB 5; L
5.7e-32;
nes 17;
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                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                       Length 119;
                                                                   g Q.;
Ig-like
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                                                                   gene
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                                                                   which
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RESULT POPULAR PROPERTY OF THE RESULT 10
Q925S3
ID Q925S
AC Q925S
DT 01-DE
DT 01-DE
DT 01-MA
DE MRP3.
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Best Local S
Matches 65
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Best Local
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Q9UL89;
01-MAY-2000
                                    Q925S3;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF035025; AAI
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Q925S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. Immunopathol. 87:184-192(1998) AF035025; AAD56261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08
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                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
67; Conserv
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                                                                                                                                                                                                                                                                                                            AQKFQGRLTFSRDTSINTAYMVLSSLSTEDSAIYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR
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                                                                                                                                                                                                                          QGRVTITADKSTSTAYMELSSLRSEDTAVYYCA
                                                                                                                                                                                                                                                             QGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 AA;
                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                         PRELIMINARY;
(Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Chordata; 
; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                der Merwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12605 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                              65.3%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                               8
                                         Last annotation update)
                                                            Last
                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 357; DB 4;
Pred. No. 4.7e-31;
4; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                Score 340; DB 4;
Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C8F9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F24D08DFA5A663E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                              sequence
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InterPro; IPRO13490.1; -.

InterPro; IPRO1310; Ig-like.

InterPro; IPRO1306; Ig-MHC.

InterPro; IPRO13596; Ig-v.

Pram; PP00047; ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS05035; IG LIKE; 4.

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Q91WT1;
01-DEC-2001 (
01-DEC-2001 (
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the repair of intestinal
World J. Gastroenterol. 6
[2]
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Cui D., Zeng G.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse)
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of the irradiated mice h
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   l Similarity
62; Conserv
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
[52.1 kDa protein.
   Conservative
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Pred. No. 1.8e
12; Mismatches
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   ed. No. 1.2e-2
Mismatches
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RESULT 13
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                                                                                                                          Q8K0Z4;
Q8K0Z4;
01-OCT-2002
                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SIGNAL
Strausberg
           SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                             NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
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HSSP; P01772; 2FB4.
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Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with an
IgG4 monclonal antibody derived from a hemophilia A patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                           AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCA 97
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                                                                                                                                                                                                                                 AREFOGSVIMTADISTDIAYMELSSLRSDDIAVYYCA 116
                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRPGQGLVWIGWIYPGDGNTKY
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150
150 AA;
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                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      IG_LIKE;
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150
                                                                                                                                                                                                                                                                                                                                                                                      16031 MW;
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67.0%;
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Pred. No. 4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                      563D164AB22802D5 CRC64;
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RESULT 14
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Best Local S
Matches 59
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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QBVIJ1;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2004 (Fragment).
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                                                                                                                                                                                                                                                                                                                        STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
Wloch M.K., Alexander A.L., Pippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 480 AA; 51645 MW;
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                                                                                                                                                                                                                                                                         EMBL; U59154; AAB02916.1;
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InterPro; IPR003006;
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59; Conserv
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SQKFKDKATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR
                                                                         QVQLLQSATEVKKPGASMKVSCMASGYPFTSYDISMVRQAPGQGLEWVGWISAYNGNTHY
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                        AOKFOGRVIMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                  EIQLQQSGTELVKPGASVKISCKASGYSPTGYNMNWVKQSHGKSLEWVGDINPYYGGTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEKFKGKATLTADKSSNTAYMHLSSLTSENSAVYFCAR 117
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123 AA;
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                                                                                                                                                      13806 MW; CC0037A806E9911E CRC64;
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Ig-like.
Ig_cl.
Ig_MHC.
Ig_v.
                                                                                                                63.3%;
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Pred. No. 3.4e-28;
LB; Mismatches 21;
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                                                                                                    Score 330; DB 11;
Pred. No. 8.6e-29;
9; Mismatches 20;
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98
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RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Havyashizaki Y.,
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Best Local S
Matches 60
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Q9D8L4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1810060009Rik protein.
IGH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 4. —
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                                                                                     l Similarity
60; Conservat
                                                                            QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                    AQKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
                                                                                                                                                                                                                                                     63.3%; Score 330; DB 11; Length 473; ilarity 61.2%; Pred. No. 4.3e-28; Conservative 17; Mismatches 21; Indels
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RESULT 14
Q94MR7
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Matches 10; Conserv
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Q94MR7;
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"Cloning and expression of the gene encoding GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase from Clostridium perfringens.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB05955; BAB69460.1; -.
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18 420 POTENTIAL.
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0934G8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01_CNAC-alpha-1,4-Gal-releasing endo-beta-galactosidase.
                                                                                                                                             Youderian P., Walthers D., Salmi D., Magrini V., Hartzell P.L.;
"Genome organization of temperate Myxococcus phage Mx8 ";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF396866; AAK94387.1; -.
SEQUENCE 536 AA; 56864 MM; 08BCA8810380E0BD CRC64;
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Nature 366:748-751(1993).
EMBL; L22579; AAA60931.1; -.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=49964;
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                                                                                                                                                                                                                                                                                                                                                               Viruses
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hes 6; Conservation
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     GGGGAYE--
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(TrEMBLrel.
(TrEMBLrel.
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     -- DVWSGEY 15
                                                                            38.8%;
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19,
21,
                                                 Score 52; DB Pred. No. 78; 2; Mismatches
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Last sequence update)
Last annotation update)
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Pred.
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Pred. No. 60;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB025632; BAB10261.1; InterPro; IPR006153; Na H porter.
Pfam; PF00999; Na H Exchanger; 1.
SEQUENCE 857 AA; 95833 MW; 5EA87F54AC2EEE73 CRC64;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Tabata S.;
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Q89096;
01-NOV-1996
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Virology 221:291-300(1996). 
EMBL; U18341; AAA69465.1; -. 
SEQUENCE 1896 AA; 213552 MW; 70444AODAE289E37 CRC64;
                                                                                                                                                                                                                                                                     SPECIES-Variola virus; STRAIN-Garcia-1966; Shchelkunov S.N., Blinov V.M., Totmenin A.V., R Sandakhchiev L.S., Sandakhchiev L.S., "XhoI-I,P DNA fragments of variola minor virus
                                                                                                                                                                                                                                                                                                                                                  SPECIES-Variola minor virus; STRAIN-GARCIA-1966; Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F., Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M Esposito J.J., Sosnovtsev S.; "Analysis of the complete coding sequence of DNA of alastrim variola minor virus strain Garcia-1966.";
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                                                                                                                                                                                                                                                            Submitted (JAN-1993) to the EMBL/GenBank/DDBJ
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Q85406;
01-NOV-1996
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Shchelkunov S.N., Blinov V.M., Sandakhchiev
"Genes of variola and vaccinia viruses neces
protective mechanisms.";
FEBS Lett. 319:80-83(1993).
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Viruses; deDNA viruses,
Orthopoxvirus.
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MEDLINE=95320969; PubMed=7597802;
Shchelkunov S.N., Totmenin A.V.;
"Two types of deletions in orthop
Virus Genes 9:231-245(1995).
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Massung R.F., Esposito J.J., Liu L., Qi J., Utterback
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Lope
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy
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                                                                               STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
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STRAIN=India-1967;
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Q89230;
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01-NOV-1996 (TrEMBLrel. 0
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                                    Camelpox virus (str. Viruses; dsDNA viruses) Orthopoxvirus.
NCBI_TaxID=203174;
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Orthopoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes.";
Dokl. Akad. Nauk SSSR 321:404-406(1991).
EMBL; X67117; CAA47538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shchelkunov S.N., Marennikova S.S., Totmenin A.V., Blinov V.M., Chizhikov V.E., Gutorov V.V., Safronov P.F., Pozdnyakov S.G., Shilkikov V.E., Gashnikov P.V., Anjaparidze O.G., Sandakhchiev L.S.; "Constructions of clonoteques of the genomic fragments of poxvirus and study of structural and functional organization of host range viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolykhalov A.A., Blinov V.M., Chizhikov V.E., Frolov I.V., Sandakhchiev L.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence analysis of the region of Variola virus H P Q genome fragment.";
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PubMed=11907336;
Gubser C., Smith G.L.;
"The sequence of camelpox virus shows if variola virus, the cause of smallpox.";
J. Gen. Virol. 83:855-872(2002).
SEQUENCE FROM N.A.
STRAIN=Somalia-1977;
MEDILINE=96295428; PubMed=8661439;
Massung R.F., Loparev V.N., Knight J.C.
Chizhikov V.E., Parsons J.M., Safronov Shchelkunov S.N., Esposito J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L., Kerembekova U.Z., Sandybaev M.T., Kutish G.F., Rock D.L. "The genome of camelpox virus.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF438165; AAL73914.1;
SEQUENCE 1869 AA; 210498 MW; 64ABEF98F88237A9 CRC64;
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Submitted (OCT-2000) to the EMBI
EMBL; AY009089; AA6337713.1; -.
SEQUENCE 1869 AA; 210470 MW;
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Q8R3W5;
Q0R3W5;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 5730449118 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
Q9BZQS;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC022030; AAH22030.1; -.
Hypothetical protein.
SEQUENCE 171 AA; 18641 MW; E728BF39A89DDII
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Mammalia; Eutheria;
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Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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STRAIN-Nipponbare;
Spiegel L., de la Bastide M., Nascimento L., Kirchoff K., King L.
Preston R., Vil M.D., Baker J., Bell M., Zutavern T., Santos L.,
Miller B., Kuit K., Rodriguez S., Cunnius D.M., Balija V., Shah
Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;
"Genomic Sequence for Oryza sativa, Nipponbare strain, clone
OSJNBA0089015, from Chromosome 10, complete sequence.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=21218927; PubMed=11318611;

Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins
Connors T.D., Morgenbesser S.D., Su K., Faruque M.U., Pinke
Graham C., Baxevanis A.D., Klinger K.W., Landes G.M., Trent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Shrhartoideae; Oryzeae; Oryza.
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Oryza sativa (Rice)
Eukaryota; Viridiplantae;
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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Carpten J.D.
SEQUENCE FROM N.A.

STRAIN=Nipponbare;

Palmer L.E., Spiegel L., de la Bastide M., Nascimento Palmer L.E., Spiegel L., de la Bastide M., Zut King L., Preston R., Vil M.D., Baker J., Bell M., Zut Santos L., Miller B., Kuit K., Rodriguez S., Cunnius Shah R., Bahret A., Bal H., O'Shaughnessy A., Dedhia
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McCombie W.R.;
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Genomics 73:211-222(2001).
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	5 Q8MSY1	321	35.4	47.5	Φ
Q8inh1 drosophila	5 QBINH1		35.4	47.5	7
N	10 Q8H6Q2		35.4	- 1	σ
Q8ih71 drosophila	5 Q8IH71	178	35.4	47.5	u
9	10 Q9AV49	840	35.8	48	42
Q90wq6 oncorhynchu	13 Q90WQ6	464		48	w
Q90wq7 oncorhynchu	13 Q90WQ7	461		48	N
		139	35.8	48	_
Q9fc56 streptomyc		262		48.5	0
		166		48.5	Ψ
Q8v4q7 monkeypox	12 Q8V4Q7	1879		49	8
Q9p3c8 neurospora	3 Q9P3C8	1340	36.6	49	7
Q9fmh4 arabidopsis	10 Q9FMH4	527	•	49	õ
		509	•	49	U
072759 cowpox viru	12 072759	1933	37.3	50	-
		531		50	w
		360		50	ຮັ
062458 caenorhabdi	0	292	37.3	50	_
Q91859 xenopus	13 Q91859	433	37.7	50.5	٠
Ф	0	800	38.1	51	w
9		554	38.1	51	w
Q8h564 oryza	10 Q8H564	187	38.1	51	7

ALIGNMENTS

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RESULT
Q9CYI5
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischman W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischman W., Gaasterland T., Gissi C., Ving B., Kochiwa H.,

RA Fleischman W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Mordone P., Raing B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Nordone P., Raing B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                EMBL;
                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK017650; BAB30855.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9CYI5
MGD; MGI:1913887; 5730449L18Rik
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DR EMBL; AL627275; CAD02714.1; ...

DR EMBL; AL627275; CAD02714.1; ...

DR EMBL; AL627275; CAD02714.1; ...

DR InterPro; IPR003753; Exonuc VII L.

DR InterPro; IPR003753; Exonuc VII L.

DR InterPro; IPR003753; Exonuc VII L.

DR InterPro; IPR003755; ExNA, anti; 1.

DR Pfam; PF02601; Exonuc VII L; 1.

DR Pfam; PF01336; ExNA, anti; 1.

DR TIGRAMS; TIGR00237; XseA; 1.

KW Hydrolase; Nuclease; Exonuclease; Complete proteome.

SQ SEQUENCE 449 AA; 50720 MW; 511957DEC878F5D2 CRC64;

Query Match

Best Local Similarity 70.0%; Pred. No. 78;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 206 GGGSLEDLWS 215

Search completed: December 30, 2003, 10:55:52

Job time: 2.23314 secs
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EX7L_RICCN
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Best Local (
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subun
(Exonuclease VII large subunit).
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REPEAT
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EMBL; D00295; BAA00209.1; AX
EMBL; D00295; BAA00207.1; AX
EMBL; D00295; BAA00207.1; AX
HSSP; P25963; 1NFI.
                                    the Buropean Bioinformatics Institute. There are no restrictions we have a substitutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                     "Mechanisms of evolution in Rickettsia conorii and R. Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                        Ogata H., Audic S.,
Samson D., Roux V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q92GU6;
28-FEB-2003
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REPEAT
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                                                                                                                                                                                                                                                                                                                STRAIN=Malish
                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia conorii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
                                                                                                                                                                       FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity) CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic (By similarity) SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                                                                                                 SUBUNIT: Heterooligomer similarity).
                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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AE008654; AAL03564.1; ALT_INIT
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                        an email to license@isb-sib.ch).
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PS50297; ANK_REP_REGION;
ical protein; Repeat; ANK
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132
169
202
238
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Cossart P., Weissenbach
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repeat.
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ch J., Claverie
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RESULT 15
EX7L_SALTI
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                                                                                                                                                                                                                                                         STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Ro Burland V., Kodoyianni V., Schwartz D.C., Blattner F. "Comparative genomics of Salmonella enterica serovar and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21534947; PubMed=11677608; MEDLINE-21534947; PubMed=11677608; Thomson N.R., Pickard D., Wain J Parkhill J., Dougan G., James K.D., Holden M.T.G., Sebaihia M., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last ann
Probable exodeoxyribonuclease
(Exonuclease VII large subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003753; Exonuc VI
Interpro; IPR004365; ERNA anti
Pfam; PP02601; Exonuc VII L; 1
Pfam; PP01336; tRNA anti; 1
TIGRFAM8; TIGR00237; xseA; 1
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                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                       (Exonuclease VII large subunit).
XSEA OR STY2753 OR T0345.
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41, Last sequence up
42, Last annotation
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; Exonuclease; Complete proteome.
49886 MW; CAB0B6BB443F476B CRC64;
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Typhi strains Ty2
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Best Local S
Matches 10
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                         CIBA PAEPP STANDARD; PRT; 675 AA. 157051; PRT; 675 AA. 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Parasporal crystal protein cry18Ba (Parasporal CryXVIIIB(a)) (Crystaline parasporal protoxin)
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DNA_BIND
DOMAIN
STRAIN=BP3;
Patel R., Yousten A.A., Rippere "Detection of two new cry genes"
                                                                                                                                                CRY18BA OR CRYXVIIIB(A).
Paenibacillus popilliae (Bacillus
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC;
DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; I48694; I48694.
HSSP; P34707; ISKN.
MGD; MGI:99421; MF6211.
InterPro; IPR004827; TF bZIP.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X78709; CAA55362.1; -. EMBL; AF015881; AAC40108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + +
                                                                                                                       NCBI_TaxID=78057;
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TISSUE SPECIFICITY: Widely expressed.
PTM: COULD BE DEPENDENT ON CKII PHOSPHORYLATION FOR BII
SIMILARITY: Belongs to the bZIP family. CNC subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEVERAL TRANSCRIPTION FACTORS.
SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q61985-2; Sequence=VSP_000580, VSP_000581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GREREDTWSGEGAEALARDL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAYEDVWSGEYPEYYAMDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
387
741 AA;
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414
467
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387
81545 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         583
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Pred. No.
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LEUCINE-ZIPPER (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (P
Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation; Alternative splicing.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing
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     i K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C01E89DD26E7CDEF CRC64;
                                                                                                                                                   popilliae).
Paenibacillaceae;
  Paenibacillus popilliae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION FOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (In isoform Short).
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                                                                                                                                                                                                                                              delta-endotoxin
(76 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                      Paenibacillus
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Best Local S
Matches 8
                                                                                                                                                                          SEQUENCE OF 65-428 FROM N.A.
STRAIN=FP-9 / Isolate HP-438;
MEDLINE=88229622; PubMed=2836548;
Tomley F., Binns M., Campbell J., Boursnel
"Sequence analysis of an 11.2 kilobase, ne
of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-I- SIMILARITY: Contains 8 ANK repeats.
-I- CAUTION: Ref.2 sequence differs from t
in position 204, 219 and 237.
                          modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF169250; AAF89667.1; ...
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V234 FOWPV STANDARD; PRT; 428 AA.
P14356; P14357; Q9J501;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative ankyrin-repeat protein FPV234 (BamHI-ORF12/ORF13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POMPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outer the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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-!- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE CELLS OF P.POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                          between
                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Afonso C.L., Tulman E.R., Lu Z., "The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fowlpox virus (FPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDLINE=20193820; PubMed=10729156;
                                                                               European Bioinformatics Institute.
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                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its constitution in the constitution of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 36.48; Conservative
  non-profit institutions as long as its content and this statement is not removed. Usage by ar requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLGTGYASAWT-SYPDYYITNI 475
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199
675 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 P
204 P
75848 MW;
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Pred. No. le
4; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA stage;
  is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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POLY-LEU.
823B588B4AE81DF5
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                                                                                                                                                                                                                                                                                                                                       Boursnell M.E
                                                                                                                                                                                                          from that shown
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                                                                                                                                                                                                                                                                                                            near-terminal,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.F., Rock D.L.;
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                                                                                                             collaboration
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SALAR BARRARA 
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YKQ9_CAEEL
ID YKQ9_(
     RRRRR OCC OG DET DE LE
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Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
A Houmiel K., Goldman B.S., Vaudin M., Iartchouk O., Epp A., Liu F.,
A Houmiel K., Gordon J., Vaudin M., Iartchouk C., Eppas C., Markelz B.,
A Flanagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
A Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
A Flanagan C., Strub G.,
T' "Genome sequence of the plant pathogen and biotechnology agent
T' "Genome sequence of the plant pathogen and biotechnology agent
T' Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
C --- FUNCTION: Catalyzes the ferrous insertion into protoporphyrin IX.
C --- CATALYTIC ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).
C --- SUNCILARITY: Belongs to the ferrochelatase family.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nester E.W.;
"The genome o
                                                                                                                                                                                                                                                                                                                                             P34304;
01-FEB-1994
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE009308; AAL44581.1; -.
EMBL; AE008306; AAK89636.1; ALT_INIT
PIR; AG3020; AG3020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21608551; PubMed=11743194;
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InterPro; IPR001015; Ferrochelatase.
Pfam; PF00762; Ferrochelatase; 1.
ProDom; PD002792; Ferrochelatase; 1.
TIGRFAMs; TIGR00109; hemH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                       Hypothetical C06E1.9.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks Bonfield J., Burton J., Connell M., Copsey T., Cooper
                                                        MEDLINE=94150718; PubMed=7906398;
                                                                                   STRAIN-Bristol N2;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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PROSITE; PS00534; FERROCHELATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAEEL
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8; Conserva
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(Rel. 41, Last sequence update)
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protein C06E1.9 in chromosome II
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Prieschl E.E., Novethy V., Csonga R., Jaksche D., Elbe-Buerger A., Thumb W., Auer M., Stingl G., Baumruker T.;
"A novel splice variant of the transcription factor Nrf1 interacts with the TNPalpha promoter and stimulates transcription.";
Nucleic Acids Res. 26:2291-2297(1998).
-1- FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3
-1- FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3
SITE OF THE TWP ALPHA PROMOTER AFTER FC GAMMA RIII STIMULATION IS BITHER INACTIVE OR REPRESSES THE TRANSCRIPTIONAL ACTIVATION.
IS EITHER INACTIVE OR REPRESSES THE TRANSCRIPTIONAL ACTIVATION.
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elegans.";
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MEDLINE=95278942; PubMed=7759107;
McKie J., Johnstone K., Mattei M.-G., Scambler
"Cloning and mapping of murine Nfe211.";
Genomics 25:716-719(1995).
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MEDLINE=98248571; PubMed=9580677;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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Pfam; PF01055; Glyco hydro 31; 1.
PROSITE; PS00129; GLYCOSYL HYDROL F31 1; 1.
PROSITE; PS00707; GLYCOSYL HYDROL F31 2; 1.
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SUBCELLULAR LOCATION: CELL WALL ASSOCIATED.
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
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glucohydrolase).
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MEDLINE=20485545; PubMed=11029414;
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T4-like viruses.
NCBI_TaxID=66711;
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28-FEB-2003
28-FEB-2003
28-FEB-2003
SEQUENCE FROM N.A.

MEDILINE=2160850; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin G., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMZ AGRTS
Q8U9F7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
Fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC 33970)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhiz
Rhizobiaceae; Rhizobium/Agrobacterium group; Agroba
                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
Ferrochelatase (EC 4.99.1.1) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fiber protein;
SEQUENCE 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 182:5962-5968(2000).
-I- FUNCTION: VGJ8 IS AT THE TIP OF THE LONG TAIL FIBERS AND AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.
-I- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEIN OMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage AR1.
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                   NCBI_TaxID=176299;
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003 (Rel. 41, Last sequence up
003 (Rel. 41, Last annotation
recognizing protein (Protein
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AA; 26277 MW; 042225B00128AE5B CRC64;
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    Last sequence update)
    Last annotation update)
    4.99.1.1) (Protoheme ferro-lyase) (Heme

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Pred. No. 32;
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(Gp38).
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                                                                                                                                                                                                                                                                                                                        Rhizobiales
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Matches
                      EMBL; X03675; CAA27310.1; -.
EMBL; X56002; CAA39476.1; -.
EMBL; X56003; CAA39477.1; -.
PIR; S24931; MMECOF.
InterPro; IPR000015; Fimb_usher.
Pfam; PF00577; Usher; 1.
PROSITE; PS01151; FIMBRIAL_USHER; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86176742; PubMed=2870470; MEDLINE=86176742; PubMed=2870470; Series D.,
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01-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Regulation and structure of an Escherichia outer membrane protein involved in export of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07,
01-MAY-1991 (Rel. 18,
15-DEC-1998 (Rel. 37,
                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                        -i- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF SUBUNITS ACROSS THE OUTER MEMBRANE.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                               enterotoxigenic Escherichia col
Mol. Microbiol. 5:875-886(1991)
                                                                                                                                                                                                                                                                                                                              "Structure and function of periplasmic chaperone-like proteins involved in the biosynthesis of K88 and K99 fimbriae in enterotoxigenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96020654; PubMed=8577257;
Valent Q.A., Zaal J., de Graaf F.K., On
"Subcellular localization and topology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
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                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91312125; PubMed=1713284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli."
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Graaf F.K.;
                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
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            Transmembrane; Fimbria; Transport; Signal; Plasmid
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   F.R.,
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K88ab fimbrial
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RESULT 6
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Matches 11
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DISULFID
SEQUENCE
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15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibbon R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Tomplete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                      ProDom: PD011569; DUF39; 1.

PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.

Hypothetical protein; Complete proteome.

SEQUENCE 431 AA; 46950 MW; 802FA39757194B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the company of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 179:7135-7155(1997).
-!- SIMILARITY: STRONG, TO M.JANNASCHII MJ1681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTH1684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98037514; PubMed=9371463;
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                                                                                                                                                                                                                                                                                       Pfam; PF01837; DUF39; Pfam; PF00037; fer4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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InterPro; IPR002708; DUF39
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(Rel. 40, Last annotation update)
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(See http://www.isb-sib.ch/announce/
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PROSITE; PS00030; RRM_RNP_1;
RNA-binding; Nuclear protein;
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GO; GO:0005717; C:chromatin; IDA.
GO; GO:0016607; C:nuclear speck; IDA.
GO; GO:0005634; C:nucleus; IDA.
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or send a
                                                             SEQUENCE OF 318-393 FROM N.A. MEDLINE=94008528; PubMed=8404528; Whittaker C.A., Desimone D.W.;
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95344994; PubMed=7619730;
JOOS T.O., Whittaker C.A., Meng F.,
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranžata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pfam; PF00076; rrm; 2.
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                                              Whittaker C.A., 
"Integrin alpha
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15-JUL-1998 (Rel. 36, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
Integrin alpha-5 precursor (Fibronectin
(Integrin alpha-F) (VLA-5).
Xenopus laevis (African clawed frog).
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                 Xenopus embryos.";
Development 117:1239-1249(1993)
                                                                                                                         "Integrin alpha 5 during early development of Xenopus laevis.";
Mech. Dev. 50:187-199(1995).
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   FUNCTION: INTEGRIN ALPHA-5/BETA-1
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to license@isb-sib.ch).
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or send an email to license@isb-sib.ch).
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Pfam; PF00357; integrin A; 1.

PRINTS; PR01185; INTEGRINA.

SMART; SM00191; Int alpha; 5.

PROSITE; P800242; INTEGRIN_ALPHA; 1.
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EMBL; L10191; AAA16249.1;
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HSSP; P06756; 1JV2.
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. TH
SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKE.
DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: Contains 7 FG-GAP repeats.
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INTEGRIN ALPHA-5
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35.4%;

Score 47.5;

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Length 1050;

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RESULT 2
SYC1_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cysteinyl-tRNA synthetase 1 (EC 6.1.1.16) (Cysteine--tRNA ligase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterineae; Mycobacteriaceae; NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSS1 OR CYSS
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CDC 1551 / Oshkost
Fleischmann R.D., Alland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98295987;
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                                                                                                                                                                                                                            EMBL; Z92774; CAB07154.1; -. EMBL; AE007169; AAK48044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
-1- CATALYTIC ACTIVITY: ATP + L-cysteine + tR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical
                          Pfam; PF01406; tRNA-synt le; 1
PRINTS; PR00983; TRNASYNTHCYS.
                                                                       HAMAP; MF_00041; -; 1.
InterPro; IPR002308; Cys_tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                       TubercuList;
                                                                                                                                                                                 TIGR; MT3686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyars
                                                                                                                                                                                                       PIR; B70607; B70607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate + L-cysteinyl-tRNA(Cys).
SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strong, to methionyl-tRNA synthetase.
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tRNA(Cys) = .
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BINDING
CONFLICT
SEQUENCE
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Aminoacyl-tRNA synthetase; Protein k
Complete proteome.
SITE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995
01-FEB-1996
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQD_DRON
Q08473;
                      between
the Euro
                                                                                                                                                                                                                                                                                                                                                       Kelley R.L.; "Initial organization of the Drosophila dorsoventral an RNA-binding protein encoded by the squid gene."; Genes Dev. 7:948-960(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding
                                                                                                                                                                                         +
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                                                                                                                                                                                                                                                                                                       MEDLINE=92112968; PubMed=1730754;
Matunis E.L., Matunis M.J., Dreyf
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93279471;
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                                                                  <del>-</del>
                                                                                                                                                                                                                                                                                          "Characterization of the
                                                                                                                                                                                                                                                                                                                             STRAIN=Canton
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HNRNP 40)
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                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. IT IS POSSIBLE THAT SOME ISOFORMS ARE FOUND ONLY IN ONE OF THESE LOCATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROME
  European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed
                                                                           ISOId=Q08473-3; Sequence=VSP_005877; DISEASE: FEMALES WITH MUTATIONS IN SQD THAT DISPLAY ONLY DORSAL STRUCTURES.
                                                                  SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                       Name=SqdA; Synonyms=HRP40.1;
IsoId=Q08473-2; Sequence=V
                                                                                                                                            Name=SqdS; Synonyms=HRP40.2;
IsoId=Q08473-1; Sequence=Displayed;
                                                                                                                                                                  Event=Alternative splicing; Named : Comment=Additional isoforms seem
                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
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                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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(Rel. 33, Last sequence update)
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                                                                                                                    Sequence=VSP_005876;
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D -> E (IN REF. 2).
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biosynthesis;
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There are no restrictions
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                                     EMBL outstation
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mplete proteome	pro126 FAMILY. STRONG, TO E pr	M N.A. KW20 / ATCC 51907; 0630, PubMed=7542800; 0630, PubMed=7542800; 0630, PubMed=7542800; R.D. Adams M.D., White O., Clayton R.A., Kirkne R.D., Adams M.D., White O., Clayton R.A., Merri Sutton G., Fitzhugh W., Fields C.A., Gocayne J. Shirley R., Liu LI., Glodek A., Kelley J.M., Phillips C.A., Spriggs T., Hedbhom E., Cotton Phillips C.A., Spriggs T., Baudek D.M., Brando R., Hanna M.C., Nguyen D.T., Saudek D.M., Brando R., Hanna M.C., Nguyen D.T., Saudek D.M., Smith H., McDonald L.A., Small K.V., Fraser C.M., Smith H.	220 AA. e update) ion update) teobacteria; Pasteurellale	T
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Query Match Best Local Similarity

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C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_ch
C;Accession: B41732
R;Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.
J. Cell Biol. 116, 257-269, 1992
A;Title: Characterization of the major hnRNP proteins from A;Reference number: A41732; MUID:92112968; PMID:1730754
A;Accession: B41732
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A;Note: sequence extracted from NCBI backbone (NCBIN:132997, NCBIP:133000)
R;Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.
J. Cell Biol. 116, 257-269, 1992
J. Cell Biol. 116, 257-269, 1992
A;Title: Characterization of the major hnRNP proteins from Drosophila mela A;Reference number: A41732; MUID:92112968; PMID:1730754
A;Accession: C41732
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C;Superfamily: unassigned ribonucleoprotein repeat-containing
F;57-123/Domain: ribonucleoprotein repeat homology <RRM1>
F;137-203/Domain: ribonucleoprotein repeat homology <RRM2>
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A;Residues: 1-168,'F',170-321 <MAT>
A;Residues: 1-168,'F',170-321 <MAT>
A;Cross-references: CB:X62637; GB:S76630; NID:g11037; PIDN:CAA44503.1; PID:g11038
A;Note: sequence extracted from NCBI backbone (NCBIN:76630, NCBIP:76631)
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A; Residues: 1-321 < KEL>
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;Residues: 1-345 <MAT>
;Cross-references: GB:X62638; NID:gl1039; PIDN:CAA44504.1;
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3; Mismatches
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C;Accession: T40651
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hamlin,
submitted to the EMBL Data Library, February 1998
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C;Supperfamily: helix-destabilizing protein; ribonucleoprotein repeat
F;57-123/Domain: ribonucleoprotein repeat homology <RRM1>
F;137-203/Domain: ribonucleoprotein repeat homology <RRM2>
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A; Residues: 1-558 < WOO>
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A; Accession: T40651
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Species: Schizosaccharomyces pombe
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Search completed: December 30, Job time: 4.20471 secs
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A; Introns: 37/3;
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Pred. No. 4
                                                                                                                                                       Score 47.5;
Pred. No. 84;
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C:Accession: E64169

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C;Accession: E64169

R;Eleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, I.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fraser, C.M.; Smith, H.O.; Wenter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: E64169

A;Accession: E64169
hypothetical protein CAC0334 [imported] - Clostridium acetobutylicum C;Speciles: Clostridium acetobutylicum C;Speciles: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: H96940 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
H87389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaev, White, O.; Salsey, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87389
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A; Residues: 1-509 < STO>
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C;Species: Caulobacter crescentus
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A; Residues: 1-220 <T
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                                                                                                                  H96940
                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CC1132
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9; Conserv
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1; Mismatches
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                             Pred.
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    Q.; Gibson,
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    Lee,
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C;Superf
                                                                                                                                                                                                                                                                                      RNA-binding protein (alternatively spliced) SqdB - fruit fly (Dr C;Species: Drosophila melanogaster C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change C;Accession: B47369
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A;Gene: CAC
    A; Gene: FlyBase: sqd
A; Cross-references:
                                                                      A;Cross-references: GB:S62100; NID:g385453; PIDN:AAB26989.1; A;Note: sequence extracted from NCBI backbone (NCBIN:132997,
                                                                                                             A; Molecule type: nucleic acid
A; Residues: 1-308 < KEL>
                                                                                                                                                                           A;Accession: B47369
                                                                                                                                                                                               A;Title: Initial organization of the Drosophila dorsoventral axis depends A;Reference number: A47369; MUID:93279471; PMID:7684991
                                                                                                                                                                                                                                               R; Kelley, R.L. Genes Dev. 7,
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A; Residues: 1-166 < KI
                                               C; Genetics:
                                                                  A; Note: sequence extracted
                                                                                                                                                        A;Status: preliminary
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Best Local :
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Best Local S
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    FlyBase:FBgn0003498
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PID: 9385455 NCBIN: 132999,

NCBIP: 133001)

(Drosophila melanogaster)

24-Sep-1999

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.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H96940
                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cysS protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jull-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70607
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A;Cross-references: GB:Z92774; GB:AL123456;
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Pred. No.
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Pred. No. 16;
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ATCC824
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                                                                                                                                                Length 469
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                                                                                                                                                                                                                                                                                                            PIDN:CAB07154.1; PID:g1877311
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Hamlin, N.; Ho
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Holroyd, S.
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44111
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A;Reference number: S44105
A;Accession: S44111
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S44111
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Search completed: December 30, 2003, 11:03:18 Job time : 12.078 secs
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A;Molecule type: DNA
A;Residues: 1-120 <HAW>
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C;Specition: S19666
C;Accession: S19666
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bo
J. Mol. Biol. 222, 581-597, 1991
J. Mol. By-passing immunization.
anti-Ss-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jar
C;Accession: PG4281
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragment
A;Reference number: PG4279; MUID:97236289; PMID:9125110
A;Accession: PG4281
A;Molecule type: protein
A;Residues: 1-123 <SUZ>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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PC4281
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A; Residues: 1-121 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
C;Accession: S19666
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Pred. No. 1.4e-36;
5; Mismatches 13
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Pred. No. 2.6e-36;
5; Mismatches 17
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R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.

Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23624

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 CDLE
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                                                                                         A;Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain; immunoglobulin homology <IMM>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                   A;Status: preliminary; nucleic acid
A;Molecule type: mRNA
A;Residues: 1-114 <RAA>
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Best Local
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72.0%;
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Pred. No. 7.3
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Pred. No. 3.3e-36;
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31105
A;Cross-references: GB:W34026
C;Genetics:
A;Gene: GDB:IGH@. Tourn...
                                                                                                                                R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
                                                                                                                                                                                                                                            Ig heavy chain V region (M49) - human (Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998 C;Accession: F36005
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-118 < RAA>
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                                                                    A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
                                                                                                              A;Status: preliminary
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75.4%;
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Pred. No. 5.7e-39;
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                    Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul
C;Accession: S31701
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity A;Reference number: S31585
A;Accession: S31701
A;Status: preliminary
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S31701
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A;Cross-references: EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C;Accession: S31116

C;Accession: S31116

C;Accession: S31116

Ext. J. Immunol. 22, 247-251, 1992

A;Reference number: S31104; MUID:92111633; PMID:1730252

A;Accession: S31116
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A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
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C;Species: Homo s
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Pred. No. 9.9e-37;
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immunoglobulin diversity operate

from the

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A;Molecule Type: mRNA
A;Residues: 1-145 <FEL>
A;Residues: 1-145 <FEL>
A;Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region - human (fragment)
C;Species: Homo sepiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S11239
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F;15-98/Domain: immunoglobulin homology <11</pre>
                                                                                                                                                                         Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Datcession: S31595 C;Accession: S31595 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-128 <CUI>
A;Cross-references: EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID:g31008
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A; Accession: S31595
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77.8%; Pred. No. 1.6e-40;
ive 12; Mismatches 11
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; Pred. No. 2.1e-40;
11; Mismatches 14
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Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H) 3 genes and A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31104
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C.Date: 22-Nov-1993 #Bequence_revision 26-May-1995 #text_change 23-Jul-1999
C.Accession: S31104
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone alpha-THY-32) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 0.3-Feb-1994 #sequence_revision 0.3-Feb-1994 #text_change 2.3-Jul-1999
C;Accession: S36273
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, CEMBO J: 12, 725-734, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA A;Residues: 1-121 <RAA> A;Residues: 1-121 <RAA> A;Residues: 1-121 <RAA A;Residues: 1-121 <RAB: RESIDUES:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A;Cross-references: EMBL:Z18834; NID:g33116; C;Superfamily: immunoglobulin V region; immun C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                             A;Title: Human anti-self antibodies with high specificity A;Reference number: S36256; MUID:93178448; PMID:7679990 A;Accession: S36273
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                                                                                           A; Molecule type: mRNA
A; Residues: 1-120 <GRI>
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Matches 95
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Pred. No. 4.3e-40;
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2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 30, 2003, 10:47:09 ; Search time 12.078 Seconds (without alignments) 1003.251 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283308 seqs, 96168682 residues
    QVQLVQSGGGLVQPGKSLRL.....RRGVAAFDIWGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                  Length
   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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$48797
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$26790
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$31104
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$19666
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$31120
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$31118
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Ig heavy chain V r
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448	448.5	448.5	449	449	449.5	450.5	450.5	451.5	452	452.5	452.5	452.5	453	453.5
67.4	67.4	67.4	67.5	67.5	67.6	67.7	67.7	67.9	68.0	68.0	68.0	68.0	68.1	68.2
114	132	120	139	112	119	135	119	140	136	160	140	123	124	139
N	N	N	N	N	N	N	N	2	N	N	N	N	N	2
S46390	S31603	S36278	S31674	PH1654	C36005	S31598	S31107	S31588	S31587	S05271	S31686	S31114	S20782	137781
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ALIGNMENTS

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RESULT 1
$30532
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-
C;Accession: $30532
C;Acriette, X.
                                                                                                                   Ig heavy chain - human
(;Species: Homo Bapiens (man)
(;Species: Homo Bapiens (man)
(;Date: 02-Decr1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
(;Accession: S31118
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.W.
Bur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse ta;Title: Restricted utilization of germ-line V(H)3 genes and short diverse ta;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31118
A;Cross-references: EMBL:X62969
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                              A;Status: preliminary; nucleic
A;Molecule type: mRNA
A;Residues: 1-121 <RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:218318
C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MAR>
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A; Reference number: $30520
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78.9%;
                                                                                                       acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 123;
                                                                                                         translation
                                                                                                                                                                                                     M.J.D.; Vossen, J.M.; Schuurmar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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NUMBER OF SEQUENCES:

CORRESONDENCE ADDRESS:

CORRESONDENCE ADDRESS:

CORRESONDENCE ADDRESS:

CORRESONDENCE ADDRESS:

CORREST HAYME CYMANAID COMPANY

ADDRESS SE AMERICAN CYMANAID COMPANY

ASSETT HAYME CYMANAID COMPANY

COMPANY

ASSETT HAYME CANAID COMPANY

APPLICATION NUMBER: U.S./08/253,877C

FILING DATE: 03-JUN-1994

CORRATING SYSTEM: PCCDOS/MS-DOS

SOFTMANE APPLICATION NUMBER: 31,088

CORREST APPLICATION NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORREST APPLICATION NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORREST APPLICAN: 201-213-236

FILING DATE: 03-JUN-1994

CORREST APPLICAN: 201-213-236

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICANT NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICANT NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICANT NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 32,368

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICANT NUMBER: 33,468

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 33,468

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 33,688

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 33,688

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 33,688

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA:

APPLICATION NUMBER: 33,688

FILING DATE: 03-JUN-1994

CORRATION FOR SECOND NOTA: 03-JUN-1994

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RESULT 14
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US-08-525-539A-77
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TETLEPAY: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DO COUT-
APPLICANT: CERIANI
APPLICANT: PETERSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/08525539A Patent No. 6309636
                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 1...
TEV: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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45, Application PC/TUS9501219
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                                                                                                                                                YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR-----APGYGSGGGC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DO COUTO, FERNANDO J.R. CERIANI, ROBERTO L. PETERSON, JERRY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                            65.1%; Score 428.5; DB 64.0%; Pred. No. 1e-39; ative 10; Mismatches
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Sequence 19, Patent No. 5

Application US/08253877C 5773001

GENERAL INFORMATION:

APPLICANT:

Hamann,

Philip R.

APPLICANT: APPLICANT: APPLICANT:

Hinman, Lois
Hollander, Irwin
Holcomb, Ryan
Hallett, William
Tsou, Hwei-Ru
Weiss, Martin J.

INVENTION:

Conjugates of Methyltrithio Antitumor

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RESULT 15
US-08-253-877C-19
                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: 1i
; MOLECULE TYPE:
PCT-US95-01219-45
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/180
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: I
FILING DATE: 25-JAN-:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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                                                                                                                                                  61 YAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCAR---
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                                                                                                                                                                                                                                                                                                                         Similarity
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Leger, Olivier J.
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TELEPHONE:

: 650-855-0555 650-845-4166

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RESULT 11
US-08-264-093-3
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Best Local Similarity
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEPHONE: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Applic
Patent No. 5639863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 incl
COMPUTER: IEM PC COmpatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: SYNON
CLONE: 3551457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                 TYPE: amino acid STRANDEDNESS: not
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                    M5H 2J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 SQNFQGRITITRDTSASTAYMELSSLRSEDTAVYYCAR-----VWAGEFTSFDYWGQGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 QVQLVQSGAEVKKPGASVKVSCKTSGYIITSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNDNSGNAGF 60
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                                                     121 amino acide
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linear
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               not applicable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO CELL CYCLE-INDEPENDENT GLIOMA SURFACE ANTIGEN
26
                                                                                                                                                                                                                                                                                             US/08/264,093
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                                                                                                                                                                                                                                                                                                                                                                                     3.5 inch, 1.4 Mb storage
                                                                                                                                                                  NOVOP/106A/7551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 431; DB 3; Length 236; Pred. No. 1.1e-39;
                                                                                                                                                                                                                                        5639863 applicable
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                                                                                                                                                                                                                   TELEPAX: 415-5-1 NO: 45:
INPORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
**PANGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Approx No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.3%; Score 429.5; DB 1
Best Local Similarity 66.4%; Pred. No. 7.2e-40;
Matches 81; Conservative 17; Mismatches 19
                                                                      Best Local Similarity 64.0 Matches 87; Conservative
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/561,521

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223

REFERENCE JOCKET NUMBER: 1370-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Bendig
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Market & CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                   1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMCWMNP-NSGNAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFQGRVSMTTDTSTSTAYMEVRSLRSDDTAVYYCARVGVWDLL----NYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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                                                                                                                                                                                              Bingle
                                                                                     64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/186,269A
                                                                        10;
                                                                      Score 428.5; DB
Pred. No. 1e-39;
LO; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
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                                                                                                          DB 2;
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                                                                          Indels
                                                                                                        Length 129;
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                                                                      Gape
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; OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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Best Local :
                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NUMBE: CHIPTON
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHESNUT, APPLICANT: POLLEY, NAPPLICANT: PAULSON,
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 128 amino
TYPE: amino acid
STRANDEDNESS: sin
                                                                                                         APPLICATION NUMBER: US/08/964,690 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CTTY: San Francisco
       REGISTRATION
                                                                                                                                                                                                                                                                  ZIP: 94105
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 YRGDYFDYWGOGTLV 124
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                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                                   PAULSON, James C.
JONES, S. Tarran
SALDANHA, Jose W.
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                     BENDIG, Mary M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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William M.
NUMBER: 30,223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Margaret J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert W.
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                                                                      US/08/202,047
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASCSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
RUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                       ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                       ZIP: 94304
                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 YRGDYFDYWGQGTLV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                         Palo Alto
: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 435; DB 3; Similarity 64.4%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP------ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09049672A
                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                          USA
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 PF-0497
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                                                                                                                                                                                                                                      APPLICANT: Kaplan, Kut.,
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
TITLE OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-477-989B-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bazin, He
APPLICANT: Latinne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 201-994-1744 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/11:
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Ellict M.
             COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOTTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                    STREET: 6 CCC
STREET: Noseland
CTATE: New Jersey
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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APPLICATION NUMBER:
FILING DATE: 29-MAR-
                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Human Amu 5-3 heavy chain variable region
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                                                                                                                            07068
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                                                                                                                                                                                      6 Becker Farm Road
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                                                                                                                                                                                                          Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.5%; Score 437.5; DB 69.7%; Pred. No. 9.7e-41
US/08/477,989B
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GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: DOLLEY, Margaret J.
APPLICANT: JONES, S. Tarran
APPLICANT: BENDIG, Mary M.
APPLICANT: BENDIG, Mary M.
ITILE OF INVENTION: Antibodies to P-Selectin and Their U.
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
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US-08-202-047-22
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Best Local S
Matches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FORDS/MS-DOS
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
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    NAME/KEY: Human Amu 5-3 heavy chain variable
    NAME/KEY: region.
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FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: 08/4
APPLICATION NUMBER: 08/4
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/1
FILING DATE: 09-SEP-1993
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o. 5800815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGRTEYIV---VAEGFDYWGQGT
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                                                                                                                                                                                                                                                                                                                      BENDIG, Mary M.
VENTION: Antibodies to P-Selectin and Their Uses
                                                                                                                                                                                            USA
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RESULT 5
US-08-477-877B-94
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FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latine, Dominique
APPLICANT: Latine, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
               STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                   STREET:
                                                                                                                                                                       ADDRESSEE:
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OPERATING SYSTEM:
                                                                                                                                   CITY: Roseland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTPTSYYMHWVRQAPGQGLEWMGWINPNSGNTNY 60
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                                                                                                                                                 E: Carella, Byrne, Bain, Gilfillan, E: Cecchi, Stewart & Olstein 6 Becker Farm Road
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YSTEM: PC-DOS/MS-DOS
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69.7%;
MS-DOS
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Pred. No. 3.3e-41;
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US-08-477-877B-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 94, Application US/08472281A Patent No. 5817311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olbtein, Elliot M.
REGISTRATION NUMBER: 24,0
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                              ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi, Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland
             APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
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                                                                                                                                                                              STATE: New Jersey COUNTRY: U.S.A.
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 61750-146
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT 120
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05-MAR-1993
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                                                                                                                            inch diskette
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; Pred. No. 9.7e-41;
13; Mismatches 21
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US-09-025-769B-59
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Matches
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APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5
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APPLICANT: Knappi
APPLICANT: Pack,
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000
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CITY: New York
                                                                                                                                                                                / Match 68.5%;
Local Similarity 71.5%;
nes 88; Conservative
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                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                             OVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
                                   AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR-----WGGDGFYAMDYWGQG 113
                                                     AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPY-YDSWGQG 119
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TLV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                Score 451; DB 4; Length 120; 
Pred. No. 3.1e-42; 
9; Mismatches 18; Indels
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Patent No. 6096878
                                              GENERAL INFORMATION:
APPLICANT: Knappik
APPLICANT: Pack, P
APPLICANT: 11ag, V
APPLICANT: Ge, Lim
                                                                                                                                  Sequence 22, Application US/09025769B Patent No. 6300064
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GENERAL INFORMATION:
Taguku
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INFORMATION FOR SEQ ID NO:
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ATTORNEY AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Funihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TYPE: amino acid
TOPOLOGY: 1:--
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FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                 APPLICANT:
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluekthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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Pack, Peter
Ilag, Vic
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Pred. No. 5e-42;
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Maximum DB seq length: 200000000
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is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/AB_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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US-09-025-769B-59
US-08-545-809A-96
US-08-477-877B-94
US-08-477-281A-94
US-08-477-989B-94
US-08-477-989B-94
US-08-603-672A-13
US-08-561-521-16
US-08-450-803-38
US-08-603-024-99-14
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100000000000000000000000000000000000000	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	

ALIGNMENTS

TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: protein US-09-025-769B-36 US-09-025-769B-36 Sequence 36, Application US/09025769B Patent No. 6300064 APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION: TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: APPLICANT: Knappik, Ach APPLICANT: Pack, Peter APPLICANT: Ilag, Vic COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version APPLICANT: Ge, Liming APPLICANT: Moroney, Simon APPLICANT: Plueskthun, Andreas TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373 CORRESPONDENCE ADDRESS: ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CURRENT APPLICATION DATA: STREET: 1251 Ave CITY: New York STATE: New York TELEPHONE: COUNTRY: LENGTH: 10021 i: 120 amino acids amino acid (212)596-9090 USA Knappik, Achim (212)596-9000 36: #1.30 (EPO)

Query Match
Best Local Similarity 71.9
Matches 88; Conservative

68.5%; 71.5%;

Score 451; DB 4; Pred. No. 3.1e-42; 9; Mismatches 18

Length 120; Indels

8;

Gaps

<u>ب</u>

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APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Francine
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: MUMBER: US/10/041,860
CUURRENT APPLICATION NUMBER: US/10/041,860
CUURRENT APPLICATION N
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Yang, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
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                                                                                                                                                                                                                                                 Match 71.9%; Score 473; DB 12; Length 126; Local Similarity 72.8%; Pred. No. 5e-41;
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QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWMNPNNGNTGY
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Pred. No. 5e-41;
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RESULT 15

US-10-041-860-38

Sequence 38, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Meber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDG
FILE REFERENCE: ADSENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 349
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Best Local Similarity
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYDINWVRQATGQGLEWMGWMNPNNGNTGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.9%; Score 473; DB 12; 72.8%; Pred. No. 5e-41;
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                                                                                                                                        PDGFD
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APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
IITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THERROF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FF8USCE for Windows Version 4.0
SEQ ID NO 201
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-201
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US-10-041-860-201
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         GENERAL INFORMATION: JOSE R.F.
APPLICANT: CORVAIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
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Best Local Similarity
Matches 93; Conserv
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APPLICANT:
REFERENCE: ABGENIX.051A
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Yang, Xiao-Dong
Chen, Francine
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Pred. No. 3.9e-41;
8; Mismatches 18;
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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 288
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-288
                                                                                                                                                                                                                                                                               APPLICANT: CORVALION:
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Meber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PROBLEM OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 126
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Best Local Similarity 74.4%;
Matches 93; Conservative
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                                                                                                                                                                              Matches
                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: homo sapiens
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                          118 QGTLV 122
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                                                        61 AQKPQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR---DIVVVVTATDYYYGMDVWG
                                                                                   61 AOKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYY---DSWG
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Similarity 72.8%;
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QGTTV 122
                                                                                                                                                                              Conservative
                                                                                                                                                                            ; Score 473; DB 1; Pred. No. 5e-41; 11; Mismatches
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Pred. No. 3.9e-41;
8; Mismatches 18
                                                                                                                                                                                                           DB 12;
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RESULT 12 US-10-041-860-204

Sequence 204,

Application US/10041860

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US-10-041-860-202
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TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 126
TYPE: DATE:
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEO ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 202
LENGTH: 126
                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
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                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: homo sapiens
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Local Similarity 72.8%;
                                                                                                                                                                                                                                           Match 72.2%;
Local Similarity 72.8%;
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                                                                                                                                                                                                                            91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang, Xiao-Dong
Chen, Francine
                                   OGTLV 122
                                                                        AQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCAR---DIVVVVAATNYYNGMDVWG 117
                                                                                             AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYY---DSWG 117
                                                                                                                                                                   QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
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                                                                                                                                                QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDINWVRQATGQGLEWMGWMNPNSGNTGY 60
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OCTIV 122
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                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                         Score 475; DB 12;
Pred. No. 3.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 475; DB 12;
Pred. No. 3.1e-41;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                           Length 126;
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APPLICANT: Gazit, Gadi
APPLICANT: Meber, Richard
APPLICANT: Meber, Richard
APPLICANT: Bezabeh, Binyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO P
ITILE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 126
TYPE: PAT
ORGANISM: homo sapiens
US-10-041-860-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 239
LENGTH: 126
TYPE: PRT
RCANISM: homo sapiens
US-10-041-860-239
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US-10-041-860-19
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US-10-041-860-239
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Query Match 72. Best Local Similarity 74. Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COTVAlan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
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Yang, Xiao-Dong
Chen, Francine
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Chen, Francine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.2%; Score 475; DB 12; 72.8%; Pred. No. 3.1e-41; ative 11; Mismatches 17;
                    72.0%;
   . 8
                  Score 474; DB 12;
Pred. No. 3.9e-41;
   Mismatches
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                                    Length 126;
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118 QGTTV 122

118

QGTLV 122

RESULT 2

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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Yeng, Xiao-Dong
APPLICANT: Yeng, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.OSLA
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 199
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
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; TYPE: PRT; ORGANISM: homo sapiens US-10-041-860-236
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                                                             FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 236, Application US/10041860 Publication No. US20030157109A1
                                                                                                                                                                                                                                                                                  APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
                                                                                                                                                                                                                    APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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APPLICANT:

Feng, Xiao Yang, Xiao-Dong Chen, Francine Gazit, Gadi Weber, Richard

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US-10-041-860-37
; Sequence 37, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO P
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX. OSIA
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 126
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Best Local Similarity 74.4%;
Matches 93; Conservative 10
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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Pred. No. 1.5e-41;
0; Mismatches 16;
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Minimum DB
Maximum DB
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Maximum Match 100%
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USONEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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927.994 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 5 5 5 5 6 6 7 7 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 8 8 8 7 7 7 7 8 8 7 7 7 8 7 7 7 8 7 7 7 7 8 7 7 7 7 8 7 8 7 7 8 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 8 7 8 7 8 7 8 7 8 7 8 8 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 8 7 8 7 8 7 8 7 8 8 7 8 7 8 8 7 8 8 7 8	Score
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Sequence 21, Appl Sequence 199, App Sequence 236, App Sequence 234, App Sequence 37, Appl Sequence 202, Appl Sequence 203, Appl Sequence 19, Appl Sequence 201, Appl Sequence 201, Appl Sequence 204, Appl Sequence 204, Appl Sequence 204, Appl Sequence 349, Appl Sequence 349, Appl Sequence 349, Appl	Description

Sequence 930,	11 US-09-880-748-930			447.5	5
Sequence	US-09			449	44
Sequence	US-10-041-860-			449	43
Sequence	US-10-041-			449	2
Sequence 348	US-10-041-	98	68.2	449	41
Sequence	12 US-10-041-860-344			449	6
	US-10-041-860-			449	39
	US-10-041-			449	38
Sequence	US-10-041-860-			449	37
Sequence 290	US-10-041-		٠	449	36
	US-10-041-860			449	35
æ	US-09-880-			453.5	34
Sequence 238,	US-10-041-860-			460	ü
	US-10-041-860-3			462.5	32
	12 US-10-041-860-237	125		462.5	31
	US-10-041-		70.3	462.5	30
	US-10-041-		70.3	462.5	29
Seguence 360	US-10-041-		70.6	464.5	28
	US-10-041		70.6	464.5	27
	US-10-041-860-2		70.6	464.5	26
	12 US-10-041-860-44		70.6	464.5	25
Sequence 948	11 US-09-880-748-948		70.7	465	24
	11 US-09-880-748-927		70.7	465	23
	15 US-10-269-805-61		70.8	466	22
w	11 US-09-925-299-1050		71.1	468	21
\mathbf{r}	ď		71.1	468	20
Sequence 47,	15 US-10-269-805-47		٠	469	19
Sequence 343	SU			472.5	18
	-10-041-860-2	125 1	71.8	472.5	17
	US-10-041		71.8	472.5	16

ALIGNMENTS

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APPLICANT: COTVAIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
FTITLE OF INVENTION: ANTIBODIES DIRECTED TO PDG
FTITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                                                      Query Match 72.6%; Score 478; DB 12; Best Local Similarity 74.4%; Pred. No. 1.5e-41; Matches 93; Conservative 10; Mismatches 16;
1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                             QVQLVQSGABVKKPGASVKVSCKASGYTFTSYDINMVRQATGQGLEMMGMMNPNSGNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDGFD
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Search completed: December 30, 2003, 10:54:34 Job time: 40.3295 secs
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                                                                                                                                                                                                                                                             Query Match 68.2%; Score 449; DB 16; Length 117; Best Local Similarity 84.7%; Pred. No. 1.1e-35; Matches 83; Conservative 7; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                   117 AA;
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Best Local (
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                 Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other
                                                                                                                                                                                     Hagai Y, I
Plaksin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Fv molecule hypervariable region related peptide #45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-2001; 2001WO-US49440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200259264-A2
                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000US-0751181.
                                                                                                                                 WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                         (BIOT-) BIO-TECHNOLOGY GEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                                                                        Lazarovits J,
, Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 449; DB 23;
Pred. No. 8.9e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC molecule, a construct or fragments or a construct of a fragment with CC enhanced binding characteristics which selectively and/or specifically CC enhanced binding characteristics which selectively and/or specifically CC binds to a target cell in favour of other cells, where binding is CC primarily determined by a first hypervariable region and Fv is a single CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in CC association with or attached, coupled, combined, linked or fused to a CC pharmaceutical agent, is useful in the manufacture of a medicament, where CC the medicament has activity against a diseased cell, preferably a cancer CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an CC composition for use in inhibiting the growth of a diseased or cancer CC cell. This sequence represents a human Fv molecule hypervariable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                         Primer; cosmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunoglobulin variable heavy chain #8
                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR66302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66302 standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 168-169; 232pp; English
Protein sequences (AAR66295-51) are novel human chain sequences encoded by novel isolated genes. (AAQ78939-79002) were isolated and cloned from a
                                                        Claim 17; Page 41-42; 130pp; Japanese.
                                                                                   DNA fragment comprising human immunoglobulin Vh production of human immunoglobulin in mammalian
                                                                                                                              N-PSDB; AAQ78946.
                                                                                                                                             WPI; 1995-006791/01.
                                                                                                                                                                        Honjo T,
                                                                                                                                                                                                                                                           10-MAY-1993;
                                                                                                                                                                                                                                                                                      24-NOV-1994.
                                                                                                                                                                                                                                                                                                                  WO9426895-A1.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO INC
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                                                                                                                                                                                                                                                                                                                                                                       PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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(first entry)
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84.7%;
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Pred. No. 8.9e-36;
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  genes.
from a
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                                                                                       genes
                immunoglobulin heavy
The genes
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RESULT 12
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Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the human antibody heavy variable region synthetic sequence VHIB, used in a human derived antibody gene library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ge L,
                                                                                                                                                                                                                                                                                                                                                                                                   Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A; scFv; A3-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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  WPI; 2000-053102/04
                                                                                                                                                      1998; AM-1998;
                                                                                                                                                                                                        07-MAY-1999;
                                                                                                                                                                                                                                                         18-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FVIII antibody A3-C1 scFv heavy chain protein DP-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY50958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY50958 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 5B; 436pp; English
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                                                                                                                                                                                                                                                                                                        WO9958680-A2
                                                                                                     (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPY-YDSWGQG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ilag V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWNNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                   ű,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR-----WGGDGFYAMDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                 Van Den
                                                                                                                                                      98EP-0201543
                                                                                                                                                                                                     99WO-NL00285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0113021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-EP03647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knappik A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.5%;
                                                   Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moroney S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 451; DB 18;
Pred. No. 7.2e-36;
9; Mismatches 18
                                                   Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pack P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                       This invention describes
                                                                                                                                          Example 8; Fig
                                                                                                                                            9A; 61pp; English.
                                                                                                                      a novel polynucleotide (I) (and complements and
                                                                                                          sequence
                                                                                                                                                                                       the
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hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein DP-15 which is used in the method of the invention.

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                                                                                                     Query Match
Best Local S
                                                                                            Matches
                                                                                                                                         Sequence
61
                      19
                                                                                            83;
                                                                                                        Similarity
            AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR 98
                                                            OVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR 98
                                             QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNPNSGNTGY
                                                                                                                                          98 AA;
                                                                                          Conservative
                                                                                                       68.2%;
                                                                                                       Score 449; DB 21;
Pred. No. 8.9e-36;
                                                                                             Mismatches
                                                                                             8
                                                                                                                 Length 98;
                                                                                             Indels
                                                                                            0
                                                                                          Gaps
                                              60
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0

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RESULT 13
ABG91861
ID ABG91861
AC ABG91
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                                                                                                                                                                                        Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardinal contents of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-674776/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lazarovits J,
Szanthon E, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-2000; 2000US-258948P.
29-DEC-2000; 2000US-0751181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-2001; 2001WO-US49442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2002
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                                                                                                                                          diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200253700-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                          and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J, Hagai Y,
Richter T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plaksin D, Vogel T, Amit B, Kooperman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nimrod A,
Peretz T,
                                                                                                                                                                                                            or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mar-Haim
Levanon
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Disclosure;

Page 246; 310pp; English

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RESULT 10
ABB57555
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and neutralises a matrix metalloprocease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has heparcotropic, cytostatic, nephrotropic and cardiant cardianty. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is elevated. The sequences shown in ABRO1502-ABRO1545 represent the heavy chain regions of a human anti-TIMP-1 antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                    neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcolegsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; crave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates antibody, which binds and neutralises a matu
                                                                                                                                                                                                                                                                                                                                                                                                                        Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-DR-specific protein MS-GPC3 VH sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB57555 standard; Peptide; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-2002
                                12-MAY-2000; 2000EP-0110063.
06-OCT-2000; 2000US-238762P
                                                                                                                                                                  WO200187338-A1
                                                                                                                                                                                                                    Homo sapiens.
                                                                                      14-MAY-2001; 2001WO-US15626.
(GPCB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
GPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP----YYDSW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOGTLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
BIOTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ξ.
                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.7%; Score 452; DB 24; 70.6%; Pred. No. 1.2e-35; tive 11; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a novel purified preparation of a human to a tissue inhibitor of metalloprotease-1
                                                                                                                                                                                                                                                        Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metalloprotease-1 (TIMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                            cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sequence

116 AA;

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The present invention describes a composition (I), comprising a compositide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the suppressor of immune response, and the IC50 for the suppression of immune response is 1 microM or less. (I) has cantidabetic, antiarthritic, neuroprotective, antinflammatory, cantithrematic, antiarthritic, neuroprotective, antinflammatory. Can be used as a suppressor of immune response. (I) has cantidabetic, antipsoriatic, immunosuppressive, dermatological, antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and can be used as a suppressor of immune response. (I) is useful for suppressing activation or proliferation of a cell of the immune system, appressing the secretion by a cell, the interaction of a cell of the immune system, can be used as a suppressor of immunosuppressing a patient and for can be used as a suppressor cell, immunosuppressing a patient and for cell mune system with another cell, immunosuppressing a patient and for cell immune system or cell immunosuppressing a patient and for cell immunological mechanisms are needed to cause or lead to the killing. (I) optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, multiple sclerosis, grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus crythematogus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris, cell haby2469 to ABB27474 and ABB57457 to ABB57590 represent sequence used in the exemplification of the present invention.
Composition for suppressing immune response, treating diseases immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed on a cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-075289/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 15; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORP-) MORPHOSYS
                                                     exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tesar M, Thomassen-Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binds antigen
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ð ₽ Ś 밁 Ś Query Match Best Local S Matches 86 121 61 61 96; ب _ Similarity LV 122 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCARLSTRM---Conservative 68.5%; 70.5%; 10; Score 451; DB 23; Pred. No. 6.9e-36; 0; Mismatches 16; Length 116; Indels 10; Gaps 120 60 60

RESULT 11
AAW27551
ID AAW27551
XX AAW27
XX AAW27
XX AAW27
XX LAW27
Human; antibody; preparation; library; VH1B; variable region; heavy chain; consensus. Human Ab heavy chain variable region VH1B consensus 23-JAN-1998 AAW27551 standard; Protein; (first entry)

믕

LV 112

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ર્
RRESULT 8
AAB674619
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX Huma
XX Huma
XX Huma
XX Homc
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 85
                                                                      Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for treatment of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing, miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_3.
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       Claim
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                                                                                                                                                                                                                                                                                                           Kretzschmar T,
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       23pp; English
                                                                                                                                                                                                                                                                                                           Tesar M,
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Pred. No. 9.1e-36;
6; Mismatches 19
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human anti-TIMP-1 antibody heavy chain #12.
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                                                                 hypertrophy or lung cancer
                                                                                       New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                2003-129114/12.
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                                                                                                                                                                                                                                                                                                        Knorr AM, Schauer M,
                                                                                                                                                                                                                                                                                                                                                                      BAYER CORP.
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                                                                                                                                                                                                                                                                                                        Hirth-dietrich C,
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Claim 20;

Page 155-156; 228pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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WPI; 2001-112438/12.
N-PSDB; AAF29048.
                                                                                                                                                                                                                                                  Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                           WO200100678-A1
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                                            Watkins BA,
                                                                                                                                  23-JUN-2000; 2000WO-US17327
                                                                                                                                                               04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AA;
                                                                        DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                monoclonal
                                            Reitz
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72.2%;
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Pred. No. 7.1e-37
                                                                                                                                                                                                                                                                                                SEQ
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                                                                                                                                                                                                                                                                                                ID NO: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                 16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences for variable regions of human monoclonal antibodies which are immunored with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                             BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 51-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                                                                                                                                                                                          Human BLyS binding
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                                                                                        (CAMB-)
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                                              2002-114799/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMVPNSGNAGF
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                                                                                                  HUMAN GENOME
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                                                                  Barash SC,
                                                                                                                      ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                        ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                           SCFV SEQ ID
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                                                                                                   SCI
                                                                   Choi GH,
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                                                                   Vaughan
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RESULT 4
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ABP44916
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2000; 2000US-212210P
17-OCT-2000; 2000US-240B16P
16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P
25-MAY-2001; 2001US-293499P
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                             Claim
                                                                                  Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2001; 2001WO-US19110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           common variable
                                                                                                                                                                       WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                       (CAMB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLyS binding scFv SEQ ID
                             1; Page 1508-1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                               Barash
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Pred. No. 2e-37;
0; Mismatches
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                          English
                                                                                                                                                                                                                            Vaughan
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                                                                                     j polypeptides, useful for 
immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
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                                                                                                                                                                                 25-MAY-2001;
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                                                                                       HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
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                               SC,
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Pred. No. 7.1e-37
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                                  Hilbert
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Matches 122
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This invention describes a novel polymucleotide (I) (and complements and hybridizable polymucleotides) comprising a contiguous nucleotide sequency coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the
                                                                                                                                                                                                                                                                            New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
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hemophilia A; scfv;
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A3-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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Pred. No. 8.6e-56;
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RESULT 3
AAB53510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein B38 which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB53510 standard; Protein; 146
            AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, an
                                                                                                                               Colon cancer associated gene sequences, antigens, useful for the treatment, prevdisorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cyrostatic; cardioactive; neuroprotective; vulne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon cancer antigen protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-2001
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                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              reproductive disorder; gastrointestinal disc
infectious disease; cardiovascular disorder.
                                                                                                    Claim 11; Page 1631; 2104pp; English.
                                                                                                                                                                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                      WO200055351-A1
                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                          2000-587534/55.
DB; AAC98267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLLQYAADVKKPGASVKVSCYASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKFKGRLTLTRDTSTSTAYMELRNLESEDTAVYYCARCDTTLLIWFGPAPYNDSWGQGT
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                                                                                                                                                                                                                                     Ruben SM
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96.7%;
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                                                                                                                                                                                                                                                                  SCI INC
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Pred. No. 3.4e-53;
0; Mismatches 4
                                                                                                                                               prevention,
                                                                                                                                                              referred
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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461.5
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                           is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                      100.0
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658
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493.415 Million cell updates/sec
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Listing first 45 summaries
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                                                                                                                                                                                                            Length DB
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AAY50966
AAY50959
AAB43910
ABP44937
ABP44937
AAB62747
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AAB67619
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Human FVIII antibo
Human FVIII antibo
Human colon cancer
Human BLyS binding
Human HIV-1 monocl
Human HIVS binding
Human BLyS binding
Human BLyS binding
Human BLyS binding
Human BLyS binding
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15			12	11	10
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251	250	248	123	250	249	238	251	221	251	476	251	470	251	248	248	241	228	248	146	249	251	241	251	199	247	120	120	251	251	117	98	98	98	120	116
23	23	23	19	23	23	23	23	24	23	20	23	23	23	23	23	23	24	23	18	23	23	23	23	20	23	24	24	23	23	16	23	23	21	18	23
ABP45867	ABP45711	ABP45866	AAW79228	ABP45549	ABP44908	ABP45896	ABP45861	ABR01537	ABP45551	AAW88464	ABP45727	AAU74296	ABP45858	ABP45860	ABP44882	ABP45937	ABR01526	ABP45461	AAW22841	ABP45624	ABP45859	ABP46020	ABP45575	AAY34302	ABP45718	ABJ18719	ABJ18673	ABP44919	ABP45378	AAR66302 ·	ABG78170	ABG91861	AAY50958	2755	ABB57555
Human BLyS binding	Human BLyS binding	Human BLyS binding	chair	BLyS	BLyS	BLyS	Human BLyS binding	- 1			Human BLyS binding				BLyS	BLyS	anti-	BLyS		BLyS			Human BLyS binding	IgM antibody CEM 1	Human BLyS binding		Antibody library r	š	BLyS	Human immunoglobul	Human Fv molecule	Human antibody fra		~	

ALIGNMENTS

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RESULT 1
AAX50966
ID AAY5
XX AAY5
AC AAY5
XX Huma
XX Huma
XX Huma
XX Homo
XX H
New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for
                                                                                                                                              WPI; 2000-053102/04.
N-PSDB; AAZ43863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; heavy chain; antibody; factor VIII; hemostatic; variable region;
hemophilia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human FVIII antibody heavy chain variable region B38 protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY50966;
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                                                                                                                                                                                                                                                                                   Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
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Q9D8L4
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                          Q9D8L4 PRELIMINARY; PRT; 473 AA.

Q9D8L4;

Q9D8L4;

Q9D8L4;

Q1-JUN-2001 (TrEMBLrel. 17, Created)

Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q1-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q1-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q2-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q3-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q4-JUN-2003 (TrEMBLrel. 23, Last annotation update)

Q5-JUN-2003 (TrEMBLrel. 17, Last sequence update)

Q6-JUN-2003 (TrEMBLrel. 17, Last sequence update)

Q7-JUN-2001 (TrEMBLrel. 17, Created)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Q8-JUN-2003 (TrEMBLrel. 17
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; I
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Q99LC4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Pancreas;
MEDLINE-2108560; PubMedell217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M
Arakawa T., Hara A., Fukunishi Y., Konno H.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., K
Saito T., Okazaki Y., Gojobori T., Bono H., K
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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55.1%; Pred. No. 2.6e-30;
tive 18; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Yoshino M., Itoh M., Ishii
Konno H., Adachi J., Fukuda
sawa H., Kondo S., Yamanaka
Bono H., Kasukawa T., Saito
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Matches 72
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SMART; SM00406; iGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 473 AA; 51699 MW;
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Nature 409:685-690(2001).
EMBL; AK007918; BAB25349:1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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133
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ilarity 59.0%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 358.5; DB 11;
Pred. No. 3.1e-30;
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Search completed: December 30, 2003, 11:01:07 Job time : 29.7319 secs

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RESULT 12
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SEQUENCE
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Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker Bohlen H., Diehl V., Wolf J.;
Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated w somatic mutations within the untranslated regions of rearranged class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv;
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72; Conserv
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157
157 AA;
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(TrEMBLrel. 10, Last sequence up
(TrEMBLrel. 23, Last annotation
precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.9%; Score 367.5; DB 4; 59.0%; Pred. No. 8.7e-32; ... Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 68
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NON TER
SEQUENCE
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF307936; AAL09420.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0920E8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkin J.D., Iape A., Jenning "Definition of the Idiotope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                             1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMVPNSGNAGF
                                                                                                                                                                                                                                                                            68;
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NOKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCA-----VIYYGNSPAWFAYWGQG
                                          AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP-YYDSWGQG
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120 AA;
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13204 MW; DC4834AB1DE56F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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55.9%; Pred. No. 1.5
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                                                                                                                                                                                                                                                                         54.8%; Score 360.5; DB 1
55.3%; Pred. No. 3.6e-31;
tive 25; Mismatches 23
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diotope of Pterin-Mimicking
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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; Murinae; Mus
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Best Local S
Matches 76
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Q9UL89;
01-MAY-2000
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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EMBL;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TYEMBLrel. 13, Created)
01-WAY-2000 (TYEMBLrel. 13, Last sequence update)
01-WAY-2000 (TYEMBLrel. 23, Last annotation update)
01-WAR-2003 (TYEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
SEQUENCE FROM N.A.
Song X.T., Feng Z.Q., Gu
"Amplification, cloning
variable region gene of
                                                                                                                                 Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                           Q9GYZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
Monoclonal anti-idiotypic ar
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                                                                                                             NCBI_TaxID=6182;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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1; SM00406; IGv; 1.
ITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                 Guan X.H.;
    and sequence analysis of the heavy monoclonal anti-idiotypic antibody

    Last sequence update)
    Last annotation update)
    antibody NP30 heavy chain

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Schistosoma
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/ NP30 c
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Best Loc
Matches
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Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBar EMBL; BC009851; AAH09851.1; -.
Interpro; IPR000005; HTHArac.
Interpro; IPR007110; Ig-1ike.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003596; Ig_w.

Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS00041; HTH ARAC FAMILY_1; 1.
PROSITE; PS000404; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; 55EF536E
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q96GA6;
01-DEC-2001 ('
01-DEC-2001 ('
01-MAR-2003 ('
Hypothetical |
Homo sapiens
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Submitted (JUN-2000) t
EMBL; AF282622; AAG014
HSSP; P01772; 2FB4.
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Mammalia; Eutheria;
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                                                                                                                                                                                      Local
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                     AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                               QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%;
57.0%;
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                                                                                                                                                                                      56.8%; Score 373.5; DB 59.8%; Pred. No. 1e-31;
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Pred.
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Catarrhini;
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                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB
                                                                                                                                                                       26;
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      DDAFDIWGQGT
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                                                                                                                                                                                                                           RESULT
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Best Local S
Matches 83
                                                                                                                                              O9BRVO
O9BRVO;
O1-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Homo sapiens putative microfibrillar protein with Ig-like (marna (Matrix Cell Adhesion Molecule-3, Mat-CAM 3) ";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAK82649.1; -.
InterPro; IPR003106; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
InterPro; IPR003596; Ig-MHC.
INTERPRO047; Ig-1.
SMART; SM00406; IG-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0960S0; PRELIMINARY; PRT; 159 AA.
0960S0; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLE 23, Last annotation update)
 Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
                                                                                   NCBI_TaxID=9606;
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative matrix cell adhesion molecule-3.
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tilson M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                 TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                 SQKFQGRLTMTRDTSTSTVYMDLSSLRSDDTAVYFCAR---EMEITFGGAVSKGFYYYGM
                                                                                                                                                                                                                                                                                                                              AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAP-----YY--
                                                                                                                                                                                                                                                                                                                                                                 QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                    PRELIMINARY;
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Primates;
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17,
23,
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Last annotation update)
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                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 409;
Pred. No.
                                                                                                                                                                                                    PRT;
                                                                                                 Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                              Vertebrata; Euteleostomi;
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                                                                                                  Hominidae;
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RESULT 7
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Best Local S
Matches 77
                                                                                  Matches
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Best Local
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q925S3;
Q925S3;
01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

SEQUENCE 147 AA; 16274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanism of exogenous nucleic acids and the repair of intestinal epithelium after World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                             the same strain.";
Int. J. Radiat. Biol. Relat. S
EMBL; AF240166; AAK43731.1; -.
                                                                                                                                                                                                                                                                                                                                                                          "Cloning of mouse genes
of the irradiated mice !
                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of mouse genes related
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11819679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c;
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InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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QVKLHQSGPEVVKPGASVKLSCKASGYIPTSYDIDMVRQTPEQGLEWIGWIFPGEGSTEY
                                           QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSWGQGTLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCQNDYYYY-----YM
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(TrEMBLrel. )
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Ig_MHC.
Ig_v.
                                                                                                      58.0%;
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by treatment with
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19,
23,
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Last annotation updat
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Pred. No. 4.8e-34;
13; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                Score 381.5; DB 11;
Pred. No. 2.5e-33;
4; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                     Stud. Phys. Chem.
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                                                                                                                         DB 11; Length 147;
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                                                                                                                                                                                                                                                                                                                                        Med.
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Best Local Similarity
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01-MAY-2000
01-MAY-2000
01-MAR-2003
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                    OJUMAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies
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                                                                                                                                                                                                                   Q9UL92
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                     (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEMMGMMNPNSGNAGF
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                                                                                                                                                                                                                                                                                                                                                                                        LV 122
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125 AA;
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nilarity 65.6%;
Conservative 19
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Pred. No. 1.3e-37;
5; Mismatches 26;
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Catarrhini; Hominidae;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                              on update)
o variable
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QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF

QEQLEQSGAEVTKPGASVKVSCKASGYTFIAYDINWVRQAPGQGLEWMGWMNPQTGNTEF

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Best Local S
Matches 82
                                                                         Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong T. Identification and characterization of SNC66, a l down-regulated in colorectal cancer."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ data EMBL, AF283666; AAL36987.1; -.

InterPro; IPR0031010; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CF
                 Query Match
Best Local 9
Matches
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Q8WY24;
Q1-MAR-2002
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NON TER
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P01772; 2FB4
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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IPR003596; Ig_v.
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124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
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                   62.4%;
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20,
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    13;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 416; DB 4;
Pred. No. 3.9e-37;
.6; Mismatches 20
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Score 410.5; DB
Pred. No. 8e-36;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1BAAACBD96ACD2A2 CRC64;
                                                                                    F24D08DFA5A663E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497
                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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    28;
                                                                                                                                                                                                                                                                             databases
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Ig-like
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                                         Length
    Indels
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                                                                                                                                                                                                                                                                                                                    gene which
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    Gaps
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Run
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                                                                                                                                                                                                                                                                                               Minimum
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
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2:
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria
    US-09-674-752-40
658
1 QVQLLQSAADVKKPO
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                                                                                                                                                                                                                                                                                                                                          830525 seqs, 258052604 residues
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Listing first 45 summaries
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sp_plant:*
sp_vrodent:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     model
                                                                                                                                                                                                                                                                                                                                                                                                        LLIWFGPAPYYDSWGQGTLV 122
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	0	U	4	u	2	.	Result
356.5	358.5	359	360.5	361.5	367.5	373.5	374.5	381	381.5	394	409	410.5	416	420.5	428.5	Score
54.2	54.5	54.6	54.8	54.9	55.9	56.8	56.9	57.9	58.0	59.9	62.2	62.4	63.2	63.9	65.1	Query Match
481	473	463	120	489	157	614	119	116	147	500	159	497	124	125	119	Length DB
11	11	11	11	11	4	4	ഗ	4	11	4.	4.	₽	4.	4	4.	BB
Q91WT1	Q9D8L4	Q99LC4	Q920E8	Q8VCX4	095978	Q96GA6	Q9GYZ2	Q9UL89	Q925S3	Q9BRV0	Q96QS0	Q8WY24	Q9UL92	S6TN6Ö	Q9UL94	ID
Q91wt1 mus musculu	Q9d8l4 mus musculu	Q991c4 mus musculu	Q920e8 mus musculu	Q8vcx4 mus musculu	095978 homo sapien	Q96ga6 homo sapien	Q9gyz2 schistosoma	Q9ul89 homo sapien	Q925s3 mus musculu	Q9brv0 homo sapien	Q96q80 homo sapien	Q8wy24 homo sapien	Q9u192 homo sapien	Q9ul95 homo sapien	Q9u194 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
337	338.5	339	339	339	339	339	339.5	340.5	340.5	341	341	341	342	343	343	343	343.5	344	344	345.5	346	347.5	348.5	349.5	351	351	351.5	356
51.2	51.4	51.5	51.5	51.5	51.5	51.5	51.6	51.7	51.7	51.8	51.8	51.8	52.0	52.1	52.1	52.1	52.2	52.3	52.3	52.5	52.6	52.8	53.0	53.1	53.3	53.3	53.4	54.1
118	142	496	473	145	145	137	168	144	140	278	143	143	488	145	143	143	480	145	145	117	143	146	117	150	613	241	146	145
11	11	4.	11	11	11	11	11	11	11	11	H	11	11	11	11	11	11	11	11	11	11	11	11	4.	1	11	11	11
Q9Z1C4	Q924Q1	Q96DK0	Q99L25	Q924R4	Q924R3	Q924R6	Q8VDC9	Q924P5	Q924R2	Q921K1	Q924P9	Q924Q0	Q91WR1	Q924Q9	Q924R0	Q91V67	Q8K0Z4	Q924R1	Q924Q6	Q9QXE9	Q924Q5	Q924Q8	Q9QXF0	Q9Y298	QBVCX7	Q921A6	Q924R8	Q924Q7
Q9z1c4 mus musculu		Q96dk0 homo sapien	-	Bnw	mu8	Bru	Bru	mue	978	Bnw	Bum	Bnm	Bum	mus :	8 nw	Bum	ans	สนธ	anu					Q9y298 homo sapien	Q8vcx7 mus musculu	Bnm		Bnm

ALIGNMENTS

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RESULT 1
Q9UL94
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Best Local Similarity
Matches 80; Conserv
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InterPro; IPR003006; Ig_MGC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
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NON_TER
SEQUENCE
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Q9UL94;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035020; AAD56256.1; -. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
119 AA;
                                                                                                                    Conservative
                                                                                                                                                                                                                                 119
13205 MW; 13E64F5345F4A16E CRC64;
                                                                                                                                               65.1%;
                                                                                                                    16;
                                                                                                                Score 428.5; DB 4; Length 119;
Pred. No. 1.6e-38;
L6; Mismatches 19; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalis N.N., Berney S.M.,
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                                                                                                                        7;
                                                                                                                        Gaps
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RESULT 15
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Best Local S
Matches 61
                                                                                                                      EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
HSSP; P01810; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
Dfam: DF00047; ig. 1
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV11 MOUSE
P01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Heavy chain variable region contribution to the NPb family antibodies: somatic mutation evident in a gamma 2a variable Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NPB ANTIBODIES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA ES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
13135 MW;
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Pred. No. 2.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable region.";
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Best Local S
Matches 65
                                                                                                    CHAIN
DOMAIN
DISULFID
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80
                 61
                                  20
                                                  65;
                                                                            Similarity
               AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY
                                                  QVQLLQSAADVKXPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR-----YRLGRYFDYWGQGT
                                                                                                    137
137 AA;
                                                                   Conservative
                                                                                                                      20
20
55
55
69
118
118
41
                                                                                                                      137
49
68
68
117
117
122
137
                                                                                                      15200
                                                                           54.2%;
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                                                                  ; Score 333; DB 1;
; Pred. No. 7.8e-29;
17; Mismatches 30
                                                                                                                                             IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                       JH2 SEGMENT.
BY SIMILARITY.
                                                                                                     ADD5881BF44B8EC9
                                                                                                                                       SEGMENT.
                                                                     30;
                                                                                     Length 137;
                                                                                                     CRC64;
                                                                     Indels
                                                                     8
                                                                    Gaps
131
                  120
                                   79
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Search completed: December 30, 2003, 10:55:53 Job time: 7.54102 secs

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RESULT 12
HV52_MOUSE
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Matches 62
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O1-JAN 1988 (Rel. 06, Createu,
O1-JAN 1988 (Rel. 06, Last sequence update)
O1-JUL-1999 (Rel. 38, Last annotation update)
To heavy chain V region VH558 A1/A4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unrearranged VH gene segments."; Cell 40:271-281(1985).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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"Developmentally controlled and tissue-specific expression
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SMART; SM00406; IGv;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                          1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                           62;
                                                                                                      Similarity
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PS50835; IG LIKE; 1.
obulin V region; Signal.
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            AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR
NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117
                                            QVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                     Score 341; DB 1
Pred. No. 9e-30;
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BY SIMILARIT
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RESULT

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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
PROSITE; PS50835; IG LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 15.3.
Mus musculus (Mouse)
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P01745;
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Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequents of the control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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InterPro; IPR003006;
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                                                           Zakut R., Cohen J., Givol D.; "Cloning and sequence of the CDNA corresponding region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                      REVISIONS.
                                                                                                                                              MEDLINE=81053741; PubMed=6253904;
                                                                                                                                                                      SEQUENCE FROM N.A.
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Cohen J.,
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Pred. No. 1.5e
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HV48_MOUSE
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Interpro; IPROUSS.,
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Glycoprotein.
Immunoglobulin V region; Glycoprotein.
I 16
IG-LIKE.
PROSITE; PS50835; IG LIKE; 1.
IMMUNOGLOBULING REGIONAL RE
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P03980;
23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 heavy chain V region TEPC 1017 prec
    SIGNAL
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Biochemistry 21:5415-5424(1982)
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS 1
PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta in an IgD-secreting plasmacytoma."
Proc. Natl. Acad. Sci. U.S.A. 81:4164-41
PIR; AC2033; HYMST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilliam A.C., Shen A., Tucker P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84248078; PubMed=6429663; Gilliam A.C., Shen A., Richards J.E.,
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain
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HSSP; P01789; 1MCP.
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Pred. No. 2.3e-30;
    IG HEAVY CHAIN V REGION FRAMEWORK-1.
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Matches 69
                                                                           -!- SIMILARITY: Contains 1 immunoglobulin-like dot PIR; A02022; GLMSAA.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";
J. Immunol. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
15-SEP-2003 (Rel. 42, Last annotation updat
1g heavy chain V region (Anti-arsonate anti
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammala; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OOAH
                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                      STRAIN=A/J;
MEDLINE=79195438; PubMed=109536;
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52.3%; Score 344; DB 1;
55.7%; Pred. No. 4.2e-30;
tive 23; Mismatches 23
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COMPLEMENTARITY-DETERMINING-3

FRAMEWORK-4.

BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2.
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 205.12.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQÜENCE
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 121
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                                                                                                                             QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYD-----YYG-SSYFDYWGQGT
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 LV 122
                                     NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR---
                                                        AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                                                                          EVOLOOSGPELVKPGASVKISCKASGYTFTDYYMWWVKQSHGKSLEWIGDINPNNGGTSY
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nilarity 57.5%;
Conservative 2
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139
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
                                                                                                                                                                                                                                                                                    V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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Pred. No. 2.7e-31;
0; Mismatches 25
                                                                                                                                                                                            Score 352; DB 1; Length 118; Pred. No. 6e-31;
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                                                                                                                                                                                                                                                    94F7BEE4C762A018 CRC64;
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                                                                                                                                                                               Mismatches
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                                       ----GYGYDP-FDVWGTGT
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                                                                                                                                                                             Gaps
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RESULT 9
HV12 MOUSE
ID HV12 MOUSE STANDARD; PRT; 117 AA.

AC P01756;
BT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 42, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 19 heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOTTT SERVED BE SERVED BY 
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Best Local S
Matches 68
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P01757;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequing seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rearrangements in heavy chain V-region gene segments ";
Nature 283:35-40(1980).

-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS
BIND DEXTRAN DIFFER PROM THAT SHOWN AT 1-7 POSITIONS,
WHICH OCCUR IN THE D AND J SEGMENTS.

-i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A26242; MHMSJJ.
18SP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rkUSITE; PS50835; IG LIKE; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MußI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=80078170; PubMed=6765983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
SEQUENCE, AND CARBOHYDRATE-LINKAGE MEDLINE=83075344; PubMed=6816276;
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InterPro; IPR003006; Ig_MHC.
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55.7%;
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Pred. No. 1.8e-30;
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BY SIMILARITY
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Sciurognathi; Muridae;
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HYDROULT HYDROUTH ACCOUNTS ACC
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Best Local S
Matches 69
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InterPro; IPKvv...
InterPro; IPKvv...
InterPro; IGV; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
IG-LIKE
IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                      ownatic mutation in genes for the immunoglobulin heavy chain.". Science 216:300-31
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P01746;
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 93G7 precursor.
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Siekevitz M., Gefter M.L., Brodeur P.,
       EMBL; J00493; AAA38128.1; PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=82152818; PubMed=6801765; Sims J., Rabbitts T.H., Estess P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The
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                                                                                                                                                                                                                                                                                                                                                                                     Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
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MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Rodentia;
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Pred. No. 3e-3
22; Mismatches
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slaughter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
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thi; Muridae; Murinae; Mus
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Best Local S
Matches 68
                                                                      EMBL; J00529; AAA38170.1; -.
PIR; A90809; MHMS18.
PDB; 1A6U; 27-MAY-98.
PDB; 1A6W; 15-JUL-98.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
   InterPro;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
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entities requires a license agreement (See http://www.isb-
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region B1-8/186-2 precursor.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybr
                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                  antibodies: somatic mu
Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                           "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V regi
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                     Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110;
                                                                                                                                                                                                                                                                                      MAKING ANTIBODIES TO THE HAPTEN (
                                                                                                                                                                                                                                                                              (NPB ANTIBODIES).
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Ig_MHC.
Ig_v.
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Pred. No. 5.
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(See http://www.isb-sib.
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61

98

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RESULT 2
HV1B_HUMAN
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PIR; AA2024; HVHUHG.

HSSP; P01772; 2F84

G0; G0:0005575; C:extracellular; NAS.

G0; G0:0005575; F:antigen binding activity; NAS.

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MGC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1

SNART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Signal.

SIGNAL

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Best Local (
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P01744;
21-JUL-1986
16-OCT-2001
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
ra heavy chain V-I region HG3 precursor.
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P01743;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.T. MEDLINE=83144028; PubMed=6298778; Rechavi G., Ram D., Glazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., Zakut R., Givol Rechavi G., Ram D., Giazer L., 
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                                                                             HUMAN
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                                                                                                                                                                                                                                                                                                                                           QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF
                                                                                                                                                                                                                                   AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
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117 AA;
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(Rel. 01, Created) (Rel. 40, Last seq
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74.5%;
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Pred. No. 4.9e-35;
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O3_MOUSE STANDARD; PRT; 120
HV03_MOUSE STANDARD; PRT; 120
P01747;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation up
15 heavy chain V region 36-65.
Mus musculus (Mouse).

update)

update)

120

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

HV03

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Best Local :
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
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--- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenten J.H., Molgaard H.V., Houghton
Bell L.O., Gould H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Homo sapiens
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SMART; SM00406; IGv;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennich H.H., Johansson (In) Bach M.K. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-147.
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Ig heavy chain V-I region ND precursor (Fragm
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                                                                                                           -DSWGQGTLV 122
                                                                                                                                                     AQXFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYY-----
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Primates;
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Maximum DB
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Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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imilarity ; Conserva	8; -; HVH 2; EVH 52; 2F 823; 955; 955; 97003 970	E FROM N.A. =88296408; PubMe F., Lee K.H., N Pukuhara S., H sed localization hain locus."; 7:1047-1051(198 ILARITY: Contain ISSPROT entry in the Swiss Inst opean Bioinforma non-profit in d and this state ar equires a lic an email to lic.	N STAND 91 (Rel. 20 91 (Rel. 20 03 (Rel. 42 Chain V-I r ene (Human) ; Metazoa; Eutheria; D=9606;	44444 1222 1222 1222 1222 1222 1222 122
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20783
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20784
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A;Molecule type: DNA
A;Residues: 1-121 <MOR>
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A;Note: the difference for residues 41-60 results from misplacement of 10 bases in the C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:18 Job time : 11.6946 secs
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Best Local S
Matches 82
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                                                                                                                                                                                                         61 AQKLQGRATMTRDTSTSTVYMDLSGLRSEDTALYYCARGSDT----SPASTIDYWGQGT 115
                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVTVSCKASGYTFTSYFMHWVRQAPGQGLEWMGMINPHGGSTTF
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C;Species: Homo sapiens (man)
C;Ante: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_chan.
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46393
A;Status: preliminary
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Emble on, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from hage display libraries A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36260
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A; Residues: 1-129 <GRI>
A; Cross-references: EMBL: Z18851; NID:g33124; PIDN:CAA79303.1; P D:g939903
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-129 < FIG>
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Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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Pred. No. 4.7e-34;
2; Mismatches 19
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J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;KippB, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: A33548
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: A3548; PH0956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P;36-50/Region: framework 2
P;51-67/Region: complementarity-determining
P;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
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A; Residues: 1-129 < MAR>
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C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C;Accession: S19665; S24442
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                                        submitted to the EMBL Data Library, A;Reference number: S24442 A;Accession: S24442
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-124 < MAR>
                                                                                                                                                                                                A;Title: By-passing immunization. Human antibodies from A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19665
                                                                                                                                                                                                                                                                R;Marks, J.D.; Hoogenboom, H.R.;
J. Mol. Biol. 222, 581-597, 1991
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      A;Molecule type: mRNA
A;Residues: 1-40,'GLSGWDGSALTMVTQSILDK',61-118,'T',120-124 <JON>
                                                                                                               R;Jones,
                                                                                                                                 A; Cross-references: EMBL: X61647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 64.1%; Score 421.5;
Similarity 67.2%; Pred. No. 2.70
84; Conservative 12; Mismatches
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                                                                                            October 1991
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120 117 60

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C;Accession: S36265
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Emble
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Emble
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from
A;Title: Timber: S36256; MUID:93178448; PMID:7679990
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                                                                                                                                                                                                                                                                                                                                                                                                                                      S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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A;Residues: 1-110 <HIL>
A;Residues: 1-10 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1670
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A; Residues: 1-118 <GRI>
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;Species: Homo sapiens (man)
;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
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Best Local :
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Best Local S
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AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT
                                                       QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY
                                                                              QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVPQATGQGLEWMGWMNPNSGNAGF
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73.7%;
                                                                                                                                             67.0%; Score 441; DB 2; 70.5%; Pred. No. 3.4e-35;
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Pred. No. 2.6e-35;
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries A;Reference number: 336256; MUID:93178448; PMID:7679990
A;Accession: S36271
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S36271
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36271
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A;Residues: 1-123 «KIP»
G;Superfamily: immunoglobulin V region; imm
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology «IV
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A;Title: Developmentally restricted immunoglobulin heavy A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; randonus; preliminary; nucleic acid sequence not shown; nucleic acid sequence nucleic acid sequence nucleic acid sequence
                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not A;Molecule type: mRNA A;Residues: 1-122 <GRI>
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
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                                                                      1 QVQLLQSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGQGLEWMGWMNPNSGNAGF 60
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNY
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                                                                                                                                                 Score 431.5; DB 2
Pred. No. 2.9e-34;
.3; Mismatches 24
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Pred. No. 9.6e-35;
4; Mismatches 19
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AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCA

119

AQKFKGRLTLTRDTSTSTAYMELRRLESEDTAVYYCARCDTTLLIWFGPAPYYDSWGQGT 120

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Ig heavy chain V region (DP-15) - human (fragment)
C.Species: Homo sapiens (man)
C.Japecies: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: S26918
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty growth of the sequence number: S26885; MUID:93021117; PMID:1404388
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
A;Cession: S26918
A;Cession: S26918
A;Cession: S26918
A;Cross-references: EMBL:Z12317; NID:932857; PIDN:CAA78187.1; PID:932858
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S31596
R;Culstnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
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$31596
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
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A; Accession: S31596
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Matches 87
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; Pred. No. 3.4e-36;
12; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                               Best Loc
Matches
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anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human C;Species: Homo sapiens (man) C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #tex C;Accession: S49530 R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
                                                                                 A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Retatus: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Regidues: 1-135 <MAH>
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
C;Accession: S23623
R;Olee, T; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Ct. J. Exp. Med. 175, 831-842, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S48797
A; Accession: S49530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1994 A;Description: Molecular characterization of natural human anti-Sm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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               Query Match
Best Local Similarity
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84.7%;
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                    67.3%;
  15;
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Pred. No. 4.9e-36;
Score 443; DB 2;
Pred. No. 3.2e-35;
5; Mismatches 17
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  12;
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Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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658
1 QVQLLQSAADVKKPG:
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Match
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Gapop 10.0 , Gapext 0.5
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              QVQLLQSAADVKKPGASVKV.....LLIWFGPAPYYDSWGQGTLV 122
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Copyright (c) 1993 - 2003 Compugen Ltd
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$23623
$H1670
$36265
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Ig heavy chain v r
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RESULT 2 S34014 Ig heavy chain V region - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: S34014; S30535 R; Mariette, X; Tsapis, A; Bro Eur. J. Immunol. 23, 846-851, 1 A; Title: Nucleotidic sequence a A; Reference number: S34001; MUI A; Accession: S34014 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-127 <mar> A; Cross-references: EMBL: Z18321 C; Superfamily: immunoglobulin V</mar>	P;34-117/Domain: Query Match Best Local Sim Matches 91; Qy 1 QV Qy 61 AQ Qy 61 AQ Qy 61 AQ Qy 121 LV Db 130 MV	RESULT 1 S31600 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens of the control of the co	30 400 31 399 32 398 33 398 34 397.5 36 397.5 37 395.5 39 393.5 40 393.5 41 393.5 42 393.5 43 393.5 43 393.5 43 393.9
evision 10-Nov-1995 uet, J.C. 993 nellysis of the varia p:93209281; PMID:768 p:93209281; PMID:768	.n: immunoglobulin homology <imm> 72.5%; Score 477; DB 2; Length 136; imilarity 74.6%; Pred. No. 1.4e-38; COnservative 9; Mismatches 12; Indels 10; Gaps OVOLLOSAADVKKPGASVKVSCTASGYIFTSYDINWVRQATGOGLEWMGWMNPNSGNAGF [: : : : : : : : : : : : :</imm>	(fragment) evision 10-Nov-1995 Boubli, L.; Fouger ary, June 1992 generate human immun NID:g30994; PIDN:C region; immunoglobu unoglobulin	60.8 120 2 PH0962 60.6 126 2 I44151 60.5 110 2 PH1669 60.4 125 2 S68170 60.3 128 2 PH0952 60.3 132 2 PH0954 60.1 131 2 S26792 60.0 98 2 S26920 59.9 118 2 PH1666 59.8 133 2 C33548 59.8 627 2 S14683 59.7 117 2 S18553 59.7 122 2 PH0958 59.6 117 1 HVHU35 59.6 136 2 PH0960
#text_change 16-Aug-1996 ble domains of four human monoclonal 1398	Length 136; Indels 10; Gaps 2; ATGOGLEWMGWANPNSGNAGF 60 ATGOGLEWMGWANPNSGNTGY 79 ATGOGLEWMGWANPNSGNTGY 79 CDTTLLIWFGPAPYDSWGGGT 120	#text_change 23-Jul-1999 eau, M.; Tonnelle, C. oglobulin diversity operate from the AA78534.1; PID:g30995 lin homology	Ig heavy chain V r Ig heavy chain V-1 Ig mu chain precur Ig heavy chain V r

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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTMARE: WordPerfect (Version 5.0)
CURRENT APPLICATION NUMBER: US/08/526,136
FILING DATE: WordPerfect (Version 5.0)
CURSENT APPLICATION NUMBER: US/08/214,036
FILING DATE: WordPerfect (Version 5.0)
CURSENT APPLICATION NUMBER: 07/84,465
FILING DATE: September 23, 1992
APPLICATION NUMBER: 07/84,465
FILING DATE: September 23, 1991
APPLICATION NUMBER: 07/86,4099001
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
TELEPX: 200154
INFORMATION FOR SEG ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
INFORMATION FOR SEG ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
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LENGTH: 466
INFORMATION FOR SEG ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
INFORMATION FOR SEG ID NO: 44: DB 3: Length 466;
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US-09-252-991A-19413
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US-09-343-011B-1
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                RESULT 13
US-09-157-370-1
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US-09-343-0118-1
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; Sequence 1, Application US/09157370A
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Best Local S
Matches 10
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SOPTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 349
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09343011B
patent No. 6300473
GENERAL INFORMATION:
APPLICANT: Stephane Richard
TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL
TITLE OF INVENTION: SAM68-LIKE MAMMALIAN P
FILE REFERENCE: A32561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 19413
LENGTH: 217
TYPE: PRT
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Patent No. 6551795
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/343,011B
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: CA 2265271
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 38.
                                                                                274
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                                                                              DGYGGEYDDQTYEAYDNSYVTPTQSVPEYY 303
                                                                                                        DGGGGAYED----WSGEY----
                                                                                                                                       33.2%;
ilarity 36.7%;
Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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 Mismatches

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Pred. No. 93;
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Pred. No. 54;
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Pred. No. 23;
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LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-1
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APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
APPLICANT: STEINBACHER, Stefan
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STI
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER APPLICATION NUMBER: CETT/EP95/02626
EARLIER APPLICATION NUMBER: DET/EP95/02626
EARLIER APPLICATION NUMBER: DET/EP95/02626
EARLIER APPLICATION NUMBER: DES/ENGLES
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US-08-526-136-13
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Best Local Similarity
Thes 8; Conserve
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US-09-328-352-5411
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Best Local S
Matches 7
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5411
LENGTH: 229
TYPE: PRT
                                                                                                                                                                                          Sequence 13, Applion Patent No. 6107089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5411, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Towle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                        APPLICANT: Towle, Christine A. TITLE OF INVENTION: ANNEXIN XI
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                     CITY: Boston
                                                                    STREET:
                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                                                                                        3 GGGAYEDVWSGEYP 16
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                                                                      225 Franklin Street
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57.1%;
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70.0%;
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Pred. No.
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67;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 229;
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GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: PZ007P1

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT APPLICATION NUMBER: PCT/US98/11422

EARLIER APPLICATION NUMBER: FOT/US98/11422

EARLIER FILING DATE: 1998-06-04

EARLIER FILING DATE: 1998-06-06

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-205-258-745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 68
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acide
TYPE: amino acid
STRANDENESS:
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 745, Application US/09205258 Patent No. 6525174
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Best Local (
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,846
FILING DATE: 09-FEB-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-027015
FILLING DATE: 10-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-024045
APPLICATION NUMBER: JP 8-024045
                                                                         EARLIER
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                                                       APPLICATION NUMBER: 60/048,880 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896
                                                       FILING DATE: 1997-06-06
                                                                                                                                 APPLICATION NUMBER: 60/048,881 FILING DATE: 1997-06-06
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                  APPLICATION NUMBER: 60/049,020 FILING DATE: 1997-06-06
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82 DGGCSGGAYDIIGSGE 97
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milarity 62.5%;
Conservative
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60/048,876
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Pred. No.
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SOFTWARE: PatentIn Ver. (SEQ ID NO 745)
LENGTH: 105
TYPE: PRT
CRGANISM: Homo sapiens
US-09-205-258-745
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                             EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
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EARLIER FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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APPLICATION NUMBER: 60/048,917
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31155
LENGTH: 338
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7483
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US-09-252-991A-31155
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 69, Application US/09020846 Patent No. 6322965
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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APPLICANT:
APPLICANT:
                                           ZIP: 2007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       APPLICANT: HASEGAWA, Akira
TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                            STREET: 3000 K St
CITY: Washington
                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                STATE: D.C.
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Jocal Similarity 42.9%; Pred. No.
168 9; Conservative 2; Mismatc
             APPLICATION NUMBER: US/0 FILING DATE: 09-FEB-1998
                                                                                                                                                                                                                                                   ADDRESSEE:
CLASSIFICATION:
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                                                                                                                                                                                                                                  3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                         CHIBA, Yukie
YAGI, Shintaro
                                                                                                                                                                                                                                                                                                                                                                                KASHIWAKUMA,
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: YAMAGUC
APPLICANT: KASHIWA
APPLICANT: CHIBA,

APPLICANT: YAMAGUCHI, Kenjiro
APPLICANT: KASHIWAKUMA, Tomiko
APPLICANT: CHIBA, Yukie
APPLICANT: YAGI, Shintaro
APPLICANT: HASEGAWA, Akira
TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE

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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606
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US-09-252-991A-30606
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                                    US-09-020-846-68
                                                     RESULT 9
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PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30606
LERGITH: OF SEQ ID NOS: 33142

RIFLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30606
Sequence 68, Appli
Patent No. 6322965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6%;
Best Local Similarity 62.5%;
Matches 10; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
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REGISTRET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                           337 DGDGDAHDMPLWLCSVWTGESGFLYKLDL 365
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                                                                                                                                                                               10;
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                                                                                                                                          DGGGGAYE-----DVWSGEYPEYYAMDV 23
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                  Application US/09020846
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1996
                                                                                                                                                                             33.6%; Score 45; DB 34.5%; Pred. No. 95; tive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP 9-027015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 396
                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                Length 410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-882-329-2
RESULT 4
US-08-183-213-2
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                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amin
                                                                                                                                          Matches
                                                                                                                                                          Best Local
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PSM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 AV
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 34.3%;
Local Similarity 42.1%;
hes 8; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UPFILING DATE: 19920513
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
STRANDEDNESS: Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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    Application US/07882329
    5308765

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                                                                      59
                                                                                                                                                          Similarity
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                                                                                                      GGGAYEDVWSGEYPEYYAMDV 23
                                                                    GHGRSSQVWDGHDMDHYADDV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                           1: Pseudomonas putida
MR-2068 (FERM BP-3846)
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Numazawa, Ryozo

RYENTION: ESTERASE GENES, ESTERASE, RECOMBINANT

NVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT

NVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE

VENTION: CARBOXLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID

NVENTION: TRANSFORMANTS
                                                                                                                                                                                                                                                                                                                                              276 amino acids
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                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                       33.6%;
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ER: 7005-046-999
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Pred. No. 2.
                                                                                                                                                        Score 45; DB 1; Length 276; Pred. No. 60;
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                                                                                                                                          Mismatches
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US-09-328-352-7483; Sequence 7483, Application US/09328352; Patent No. 6562958
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                                       GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/183,213
FILING DATE: 14-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08183213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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NUMBER OF SEQ ID NOS:
SEQ ID NO 7483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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APPLICANT: Numazawa, Ryozo

TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT
TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT
TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID
TITLE OF INVENTION: TRANSFORMANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 07/882,329
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 869-8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas putida STRAIN: MR-2068 (FERM BP-3846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                   59 GHGRSSQVWDGHDMDHYADDV 79
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 9; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                  $ $ $ $ $
5 5 5 5 5
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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134
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB
   US-09-562-737-12
US-09-252-991A-29606
US-07-882-329-2
US-08-183-213-2
US-09-328-352-7483
US-09-252-991A-3165
US-09-252-991A-316606
US-09-252-991A-19413
US-09-252-991A-19413
US-09-252-991A-19413
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-09-328-352-5411
US-08-252-391A-25819
US-08-914-375C-79
US-08-914-375C-71
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Sequence 12, Appl Sequence 25606, A Sequence 2, Appli Sequence 2, Appli Sequence 31155, Ap Sequence 31155, Ap Sequence 31606, A Sequence 68, Appl Sequence 1745, Appl Sequence 19413, A Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 110, Appli Sequence 130, Appli Sequence 130, Appli Sequence 29, Appli
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RESULT 2 US-09-252-991A-29606 US-09-252-991A-29606 Sequence 29606, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 29606 LEEGTH: 1287 TYPE: PRT	Query Match 34.3%; Score 46; DB 4; Length 659; Best Local Similarity 34.6%; Pred. No. 1.2e+02; Matches 9; Conservative 3; Mismatches 4; Indels 10; Gaps 1; Matches 9; EDVWSGEY	RESULT 1 US-09-562-737-12 ; Sequence 12, Application US/09562737 ; Patent No. 6428967 ; Patent No. 6428967 ; Patent INFORMATION: APPLICANT: Herz, Joachim APPLICANT: Gotthardt, Michael APPLICANT: LDL Receptor Signaling Pathways CURRENT FILING DATE: 2000-05-01 INMERS OF SEQ ID NOS: 132 SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 12 LENGTH: 659 TYPE: PRT ORGANISM: Artificial Sequence PEATURE: OTHER IMFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Sequence	
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RESULT 15
US-09-840-459-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE

FURRENT APPLICATION NUMBER: US/10/062,254

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/630,346

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 60/156006

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: 60/156899

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/157287

PRIOR APPLICATION NUMBER: 60/157287

PRIOR APPLICATION NUMBER: 60/169767

PRIOR APPLICATION NUMBER: 60/169767

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/17054

PRIOR APPLICATION NUMBER: 60/17258

PRIOR APPLICATION NUMBER: 60/171515

PRIOR APPLICATION NUMBER: 60/171515

PRIOR FILING DATE: 1999-12-22

PRIOR FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: 60/171515

PRIOR APPLICATION NUMBER: 60/171515

PRIOR FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: 60/171515

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US-10-062-254-246
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Sequence 77, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LAROSS, Gregory J.
APPLICANT: Horvath, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 375
SOFTWARE: Microsoft Office 97
SEQ ID NO 246
LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
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                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                               359 NSGGGFGRDCFVWSPQYPYAYA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AYYDILTGYYLYYYYMDV 119
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Zheng, Peizhong
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Falco, Saverio Carl
Fang, Yiwen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morgante, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miao, Guo-Hua
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                                                                                                                                                                                                                                                                                                                                                                                     DB 14; Length 389;
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Search completed: December 30, 2003, 11:45:23 Job time : 4.93258 secs

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APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Keefe, Theresa
ITILE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
ITILE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES
ITILE OF INVENTION INVEST
CURRENT PILLY DATE: 2001-02-02
PRICE REPLICATION NUMBER: US/09/840,459
CURRENT FILLING DATE: 2001-02-02
PRICE RELING DATE: 2001-02-03
PRICE RELING DATE: 2001-02-03
PRICE REPLICATION NUMBER: 09/497,625
PRICE REPLICATION NUMBER: 09/21,781
PRICE FILLING DATE: 1999-07-22
PRICE REPLICATION NUMBER: 09/21,781
PRICE FILLING DATE: 1998-07-23
PRICE FILLY DATE: 2000-02-03
PRICE FILLY
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RESULT 10 US-09-880-748-1695 8

GAYYDILTGYYP--YGMDV 115

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                                                                                                                             ; ORGANISM: Homo sapiens
US-09-880-748-1698
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US-09-880-748-1698
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US-09-880-748-1695
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1695
LENGTH: 252
Type:
                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1698
LENGTH: 252
                                              Matches
                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                          TYPE: PRT
                                          11; Conservative
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Similarity 57.9%;
GAYEDVWSGEYPEYYAMDV 23
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                                                            38.8%;
                                      Score 52; DB Pred. No. 21; 2; Mismatches
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Pred. No. 21;
                                                            DB 11; Length 252; 21;
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                                        Indels
                                      2;
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                                      Gaps
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; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-839
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25
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US-09-880-748-839
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2172
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-2172
Query Match 37.3%; Score 50; DB Best Local Similarity 55.6%; Pred. No. 40; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                      SEQ ID NO 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 839, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2172
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 3239 SOFTWARE: PatentIn Ver. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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GAYYDILTGYYP--YGMDV 115
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55.6%;
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Pred. No. 3
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                                                 DB 11; Length 256;
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     Indels
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RESULT 6 US-09-880-748-926

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US-09-880-748-926
밁
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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APPLICANT: Ruben et al.
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                                                                                           Query Match 38.8%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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Best Local Similarity
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TYPE: PRT
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FILE REFERENCE: PF523
                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    LENGTH: 252
101 SYYDILTGYYVHYYGMDV 118
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milarity 57.9%;
Conservative
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Pred. No.
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Pred. No. 21;
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1674
LENGTH: 252
TYPE: PRT
ORGANIAM: Homo sapiens
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1646
LENGTH: 252
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Best Local (
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Best Local Similarity
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
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5 GAYEDVWSGEYPEYYAMDV 23
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Pred. No.
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Pred. No.
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US-09-880-748-2860
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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Best Local Similarity 57.9
Matches 11; Conservative
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1777
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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-09-880-748-1777
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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NUMBER OF SEQ ID NOS: 3239
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523
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PRIOR FILING DATE: 2001-03-21
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Similarity 54.5%;
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Pred. No. 7;
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/279,349
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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US-09-880-748-918
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US-09-880-748-2743
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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Best Local :
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SEQ ID NO 918
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Publication No. US20
GENERAL INFORMATION:
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TYPE: PRT
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Local Similarity 50.0%;
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                                         5 GAYEDVWSGEYPEYYAMDV 23
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                                                                                          Conservative
                                                                                                         38.8%;
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Pred. No. 21;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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7: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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9: /cgm2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
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10: /cgm2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR RILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 3082
LENGTH: 21
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-880-748-3082
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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GDFGDY-DILTGYYPVYYGMDV 21
                                                                                             41.4%;
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Search completed: Job time : 8.4822

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21-MAR-2001;
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                                                                                                                                                                     cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be edministered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                               This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben
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                                                                                                                                                           of the invention.
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17-OCT-2000;
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CAMBRIDGE ANTIBODY TE
                                                                            Similarity
GAYYDILTGYYP--YGMDV 118
                             GAYEDVWSGEYPEYYAMDV 23
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57.9%;
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RESULT 13 ABP45663

RESULT 14 ABP45684 ID ABP4

ABP45684 standard; Protein; 252

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                                                                                                                                                                            and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 reprethe antibodies and fragments of the antibodies described in the mel
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16-MAR-2001; 2001US-276248P.
16-MAR-2001; 2001US-277379P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies against B Lymphocyte Stimulating
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17-OCT-2000;
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                                                                              Similarity
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GAYYDILTGYYP--YGMDV 115
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                                                                Conservative
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immune disorders -
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les described in the method
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RESULT 10
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21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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; 2001US-293499P.
                                                                                                  Conservative
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                                                                                                                                DB
22;
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GAYYDILTGYYP--YGMDV 17

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ABP46732
ID ABP4
XX ABP4
XX ABP4
XX ABP4
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XX ABP4
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XX Comm
XX ABP4
XX Comm
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                                                                                                                      Query Match
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Matches
                                                                                                                                                                                                                                                                                                                         proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant ELyS expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP41990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell
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17-OCT-2000; 2000US-24081EP.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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                                                                                                                         Similarity
9; Conser
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                                                                                                                                                   38.8%;
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Pred. No.
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                                                                                                                   Mismatches
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GAYYDILTGYYP--YGMDV GAYEDVWSGEYPEYYAMDV 23 Matches

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Indels

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Gaps

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Similarity

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RESULT 9
ABP44907
AX ABP4
XX ABP4
XX ABP4
XX BLy8
XW Lumc
XW Systi
KW Systi
KW Systi
KW Comm
XX BLy8
XW Homc
XX Cla
PR 15-1
PR
                                                                                                                                                                                                                                                             CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the cc tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, cc antirheumatic and antiAIDS activity and can be used in vaccines to and so may be used to detect and quantitate the presence of BLyS in coincided with aberrant expression of BLyS. The antibodies bind to BLyS cand so may be used in this way to diagnose disease cc associated with aberrant expression of BLyS. They may also be cadministered to treat diseases associated with aberrant BLyS expression cc and activity such as cancer, immune, and autoimmune disorders and coincided coincided common variable immunodeficiency (CVID) and caquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the content of the articular and the content of the content of the articular and the content of the co
Query Match
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17-OCT-2000; 2
16-MAR-2001; 2
21-MAR-2001; 2
25-MAY-2001; 2
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                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel antibodies that immunospecifically bind to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies against B Lymphocyte Stimulating
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                                                                                                                                                                                                                                        antibodies and
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                                                                                                                        249 AA;
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2000US-240816P.
2001US-276248P.
2001US-277379P.
2001US-293499P.
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                                                                                                                                                                                                                                        fragments of the antibodies described in the method
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38.8%;
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Score 52; DB
Pred. No. 22;
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                                         Length 249;
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GDFGDY-DILTGYYPVYYGMDV 21 GGGGAYEDVWSGEYPEYYAMDV

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RESULT 6
ABP45766
                                                                                                 This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell collection and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiAIDS activity and can be used in vaccines to cinhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease CC administered to treat diseases associated with aberrant ELyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthitis, cimmunodeficiency (cVID) and CC communodeficiency (systemic lupus erythematosus, rheumatoid arthitis, considered immunodeficiency (systemic lupus erythematosus, rheumatoid arthitis, considered erythematosus, rheumatoid arthitis, considered erythematosus, rheumatoid
Query Match
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Matches 12
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17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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                                                                                              Sequence
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                                                                                                                                             invention.
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
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                                                                                                 253
  Conservative
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                        41.4%;
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  2
                        Score 55.5;
Pred. No. 7
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    Mismatches
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Gaps
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RESULT 7
ABP46849
IID ABP46849
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IID ABP46849
AX ABP4
XX ABP4
XX ABP4
XX ABP4
XX BLys
KW Huma
XX BLys
KW Gomm
KW Homc
KW Homc
KW Homc
KW Homc
XX Homc
CX Homc
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                                                                                                                                                                                           This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell continuous and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC cinhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to disgnose disease CC administered to treat diseases associated with aberrant ELyS expression and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, C immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC define antibodies and fragments of the antibodies described in the method CC of the antibodies and fragments of the antibodies described in the method
Query Match
Best Local S
Matches 11
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114799/15.
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                                                                                                                         Sequence
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                                                                                                                                                                                  of the invention.
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                                    Similarity
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CAMBRIDGE ANTIBODY TI
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2001US-276248P.
2001US-277379P.
2001US-293499P.
      Conservative
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                                 38.8%;
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      2
                                    Score 52;
Pred. No. 1
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               Mismatches
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                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        j polypeptides, useful for 
immune disorders -
                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilbert
            4
                                                               Length 17;
               Indels
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               <u>ب</u>
               Gaps
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Human gene

SEQ

ID NO:236

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CC AAH19170-AAH19250 represent cDNAs corresponding to 27 human secreted protein genes, and AAG62156-AAG62235 represent the proteins they encode. CC AAG62236-AAG62236 represent human secreted protein fragments. The genes CC their corresponding secreted proteins are useful for preventing, creating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of the CC ahlory autoimmune diseases (e.g., theumatoid arthritis), inflammation, CC allergies, neurological disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Altheimer's disease, CC gastingons's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound the allergiands or binding partners, and in chemotaxis, and can be used to a sa food additive or preservative to modify storage properties. CC alleviating symptoms associated with the disorders mentioned above, and CC indiagnostic immunoassays e.g., radioimmunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the disclosure of the invention.
Query Match 44.4%;
Best Local Similarity 50.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; chemotasis; food additive; expression; bioliculture; chemotasis; food additive; expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 62; 594pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel 27 isolated human secreted proteins and polynucleotides encoding them useful for treating, diagnosing, preventing Alzheimer's disease, Parkinson's disease, AIDS, rheumatoid arthritis, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-335835/35
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30-JUN-2000; 2000US-0215131.
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Score 59.5; DB Pred. No. 0.92; 2; Mismatches
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                                                                                                This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease administered to treat diseases associated with aberrant ELyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
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17-OCT-2000; 2000US-240816P:
16-MAR-2001; 2001US-276248P:
21-MAR-2001; 2001US-277379P:
25-MAY-2001; 2001US-293499P:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
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                                                                           invention.
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Conservative

41.4%;

Score 55.5; I Pred. No. 0.43 2; Mismatches

DB).43;

23;

Length

21;

7:

Gaps

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Sequence

21

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Example 4; Fig

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61pp;

Sequence

23 AA;

Similarity

100.0%;

Score 134; DB 21; Pred. No. 3.9e-12;

Length

23;

0

hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein CDR3 fragment which is used in the method of the invention.

This invention describes a novel polynucleotide (I) (and complements and

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RESULT 2
AAY50950
ID AAY5
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Matches 23
                        This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilla A patients. This sequence represents the human anti-factor VIII antibody clone IT-2 protein which is used in the method of the invention.
                                                                                                                                                                                                      New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human anti-factor VIII antibody VH clone IT-2 encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY50950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY50950 standard; Protein; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
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                                                                                                                                                                              Example 4; Fig 4A; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                     08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1999
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                                                                                                                                                                                                                                                                                                                         (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
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; VH gene.
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Sequence

132 AA

AAG62284 ID AAG XX AC AAG XX DT 18-

AAG62284 standard;

Protein;

129

18-JUL-2001 AAG62284;

(first entry)

RESULT 4

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RESULT 3
AAV50953
ID AAV50953
XX AAV50953
XX AAV50953
XX AAV50953
AC AAV5
XX AAV5
XX AAV5
DE Huma
XX Huma
XX Homo
XX Homo
XX Homo
XX Homo
YN W099
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                                                                                                                                                                                                                                                                                                hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them polypeptides of the invention and the antibodies generated from them antibodies in hemophilia A patients. This sequence represents the human anti-factor VIII antibody VH IT-2 protein which is used in the method
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hemophilia A
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                                                                                                                                                                                                                  Sequence
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23; Conserv
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ilarity 100.
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Listing first 45 summaries
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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493.415 Million cell updates/sec
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52	52	52	55.5	55.5	59.5	134	134	134	Score
38.8	38.8	38.8	41.4	41.4	44.4	100.0	100.0	100.0	% Query Match
249	20	17	253	21	129	132	132	23	% Query Match Length DB
23	23	23	23	23	22	21	21	21	
ABP44907	ABP46732	ABP46849	ABP45766	ABP47071	AAG62284	AAY50953	AAY50950	AAY50957	ID
Human BLyS binding		Human BLyS binding		Human BLyS binding			Human anti-factor	Human anti-factor	Description

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

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RESULT 1
AAY50957
ID AAY50957
ID AAY50957
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Huma
XX Homo
XX H
                                                                                                                                                                                           WPI; 2000-053102/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; VH protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY50957 standard; Protein; 23
                                                                                                                                                                                                                                                                               Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1999.
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RESULT 3
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       DR REAL REAL PROPERTY OF THE P
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Matches 90
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; BCC02040; AAH20240.1; -.
RINTERPRO; IPR007110; Ig-like.
RINTERPRO; IPR00306; Ig_MHC.
RINTERPRO; IPR00306; Ig_V.
RPfam; PP00047; ig; 5.
RPfam; PP00047; ig; 5.
RPART; SM00406; IGV; 1.
RPROSITE; PS0035; IG_LIKE; 5.
RPROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW; 60C7P5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBWUK1;
QBWUK1;
01-MAR-2002 (TrEMBLrel. 2:
01-MAR-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL91;
01-MAY-2000
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL91
                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                  "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                              Young D.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                        CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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Immunol. Immunopathol. 87:184-192(1998)
AF035023; AAD56259.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
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                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                         Kalis N.N.,
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                                                                                                                  carditis
                                                                                                                                                                                         Berney S.M.,
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RESULT 4
Q9UL71
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Matches 93
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 92; Conserv
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NON TER
SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N.,
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PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR007110;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fetus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            foung D.C.
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                                                                                    GIMVIVS
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                                          ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
  ADSVXGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKV-TTIYDR---
                                                                                                                                                                                                                                                                    121
121 AA;
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                                                                                                                                                                               68.8%; ilarity 73.0%; Conservative 1
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                                                                                                                                                                                                                                                 121
13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12843 MW; D0633949F2AC149D CRC64;
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; Ig_MHC.
; Ig_v.
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73.2%;
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Pred. No. 3.5e-39;
                                                                                                                                                                               Score 457.5; DB 4
Pred. No. 5.1e-39;
3; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95:
   100
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                       456
446.5
443.5
439.5
437.5
437.5
427
427
419.5
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457.5
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830525 seqs, 258052604 residues
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1: sp_archea:*
  QVQLVQSGGGLVQPGKSLRL....
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_fungi:*
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Q8WUX1
Q9WL71
Q9UL71
Q9HCC1
Q9HCC1
Q8TC77
Q96BB9
Q9UL93
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         O8wu38 homo sapien
O8wuk1 homo sapien
O9u191 homo sapien
O9u171 homo sapien
O9hcc1 homo sapien
O8tc77 homo sapien
O9hb9 homo sapien
O9u193 homo sapien
O9u193 homo sapien
O9u190 homo sapien
O9u190 homo sapien
O9u190 homo sapien
O9u190 homo sapien
O9u110 homo sapien
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sapien
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45	44	43	42	41	40	39	38	37	36	35	3. 4	S S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
302.5	303.5	304	308.5	310.5	313	313	319	325.5	325.5	327.5	330	330	333	337	339.5	342	351.5	358.5	365	371	374.5	376	378	381.5	381.5	384.5	397	409.5
45.5	45.6	45.7	46.4	46.7	47.1	47.1	48.0	•	48.9	49.2	49.6	•	50.1	50.7	51.1	51.4	•	53.9	•	•	•	•	•	•	57.4	57.8	59.7	61.6
146	150	241	119	142	500	159	121	484	125	614	482	124	124	124	112	437	480	521	298	484	486	95	469	479	131	119	487	104
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Q924R8	Q9Y298	Q921A6	Q9UL94	Q924Q1	Q9BRV0	Q96QS0	Q99NG4	Q99LA6	Q9UL95	Q96GA6	Q91X92	Q9N0W6	Q9N0W4	Q9UL92	Q9UGP3	Q9R1A4	Q91XE1	Q8N4Y9 .	OSAND60	Q8VEA0	Q91Z07	Q9ULB6	Q8R3V9	Q91WP5	Q9ULB8	Q920E7	Q99KA4	Q9UL87
Q924r8 mus musculu	Q9y298 homo sapien	Q921a6 mue mueculu	Q9u194 homo sapien	Q924q1 mus musculu	homo	homo	4 mus	Bnw	homo	Q96ga6 homo sapien	Q91x92 mus musculu	Q9n0w6 oryctolagus		Q9u192 homo sapien	homo	Q9rla4 mus musculu	1 mus	homo	Q9qyf0 mus musculu	a n	Bru	Q9ulb6 homo sapien	9 mu 6	8nu	homo	7 mus	900	Q9ul87 homo sapien

ALIGNMENTS

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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC021276; AAH21276.1; -.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003106; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 4.

R SMART; SM00406; IGV; 1.

R SMART; SM00406; IG LIKE; 2.

R PROSITE; PS05035; IG_MHC; 2.

R PROSITE; PS05035; IG_MHC; 2.

R PROSITE; PS05035; AB; 62967 MW; FD072344033AC530 CRC64;

SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 96; Conserv
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Q8WU38;
01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2003 (TrEMBLrel. 23, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Toneil;
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ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTALYYCAKH--GSGSYIGYYYGMDVWGQGT 137
                                                  ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                 EVOLVESGGELVOPGRELRLSCAASGFTFDDYAMHWVROAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                       QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIH#VRQAPGEGLE#VSGVT#SGTTIGF
                                                                                                                                                                                                                                                                                                                          75.5%; Score 502; DB 4; Length 573; llarity 76.2%; Pred. No. 1e-42; Conservative 12; Mismatches 16; Indels
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Last sequence update)
Last annotation update)
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Best Local S
Matches 74
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PIR; A02056; A3HUBR.

QO; GO:0005576; C:extracellular; NAS.

QO; GO:0003532; F:antigen binding activity; NA;

R GO; GO:0003525; P:immune response; NAS.

R InterPro; IPR0037110; Ig-like.

R InterPro; IPR003596; Ig_MHC.

InterPro; IPR003596; Ig_V.
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Best Local S
Matches 77
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Immunoglobulin V region.
DOMALN 1 108 IG.
NON_TER 115 115
SEQUENCE 115 AA.
                                                                                                                                                                                                         DOMAIN
MOD RES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
SMART; SM00406. TC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putnam F.W., Liu Y.-S.V., Low T.L.K.;
"Primary structure of a human 1gA1 immunoglobulin. I
IgA1 protease, digestion, Fab and Fc fragments, and
amino acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region BUR.
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                 SMART; SM00406; ĪGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic DOMAIN 1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN BUR).
MEDLINE=79151016; PubMed=107164;
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P01773;
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SMART; SM00406; IGv;
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l Similarity 61.1%;
77; Conservation
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                                                                                            Conservative
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                                                                                                                                                                                  12981 MW;
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59.2%;
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Pred. No. 9.5e-34;
9; Mismatches 19; Indels 11
                                                                                                               Score 386.5; DB 1
Pred. No. 4.1e-33;
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                                                                                            Mismatches
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Search completed: December Job time: 6.75548 secs

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10:55:53

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RESULT 15
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IT 21-UI
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                                                                                                                                                                                                                                                                                                                                                                                                                Wasserman R.L., Capra J.D.;
"primary structure of the variable regions of two canine immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
-I- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01784;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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MEDLINE=77242268;
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region GOM. Canis familiaris (Dog).
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    !- SIMILARITY: Contains 1 immunoglobulin-like

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                                                                                                                                                                                                                                                                                               h 57.4%; Score 382; DB 1; Similarity 61.9%; Pred. No. 1.1e-32; 78; Conservative 17; Mismatches 19
                                                                                                                                                                                             MVTVSS 126
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  114
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Last annotation update)
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SETTING DESCRIPTION OF THE PROPERTY OF THE PRO
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HV3F_HUMAL
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GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activit
GO: GO:0003825; P:antigen bending activit
Interpro: IPR007110; Ig-like.

Interpro: IPR007110; Ig-like.

Interpro: IPR003006; Ig_MHC.

Interpro: IPR003006; Ig_MHC.

Interpro: IPR003596; Ig_v.

Pfam; PF00047; 19; 1.

SMART; SM00406; IGv; 1.
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21-JUL-1986
15-SBP-2003
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DOMAIN
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=81101090; PubMed=6450418;
                                                                                                                                                                                                                                                                     HUMAN
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EMBL; M35415; AAA58735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region BUT.
19 heavy chain (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure and multiplicity of genes for the human imm heavy chain variable region."; Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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SEQUENCE
                                                                       Eukaryota;
Mammalia;
                                                                                                                                                                                                                                           P01767;
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Immunoglobulin
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pbulin V region; Signal; 3D-structure.
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                                                                  ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20
117
117 AA;
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update,
ain V-III region VH26 precursor.
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                                                                                                                                                                                                                                                                     STANDARD;
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76.3%;
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Pred. No.
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IG-LIKE.
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Best Local S
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SEQUENCE
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(Complete amino acid sequence of the alpha 2 heavy chain IRComplete amino acid sequence of the alpha 2 heavy chain IRCOMPLETA (2) allotype.";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-I- MISCELLANBOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALREGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV3D_HU
P01765;
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Immunoglobulin V region.
DOMAIN 1 111
NON_TER 115 115
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SMART; SM00406; IGv;
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                                                                     -!- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02048; H3HUTL. HSSP; P01772; 2FB4. GO: GO:0005576; C:extracellular; NAS. GO: GO:0003823; F:antigen binding activity; NAS. GO: GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                 Wang A.-C., Wang I.Y., ruderwesty ....., "Immunoglobulin structure and genetics. Identity regions of a mu and a gamma2 chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updating heavy chain V-III region TIL.
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Torano A., Putnam F.W.;

    -!- SIMILARITY: Contains 1 immunoglobulin-like domain

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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                  Biol.
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GO:0003823; F:antigen binding activity; NAS.
GO:0005855; P:immune response; NAS.
erpro; IPR007110; Ig-like.
erpro; IPR003006; Ig_MHC.
erpro; IPR00396; Ig_v.
                                                                                                                                                                                                                                       ions of a mu and a gamma2 chain."
Biol. Chem. 252:7192-7199(1977).
MISCELLANEOUS: THE SEQUENCES OF
OF IGM AND IGG2 ISOLATED FROM A
GAMMOPATHY ARE IDENTICAL. THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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76; Conservative
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Pred. No. 5.9e-34;
4; Mismatches 15;
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MEDLINE=77100368; PubMed=401950;
Milstein C., Secher D.S.;
SEQUENCE, AND DISULFIDE BONDS.
MEDLINB-83289131; PubMed=6884994;
MEDLINB-83289131; PubMed=6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                       Ig heavy chain V-III region Homo sapiens (Human).
                                                                                     NCBI_TaxID=9606;
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n; PP00047; 19; 1.
SM00406; IGv; 1.
The LIKE; 1.
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                  Primates;
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DN -> ND (IN REF. )
W -> H (IN REF. 2)
Y -> W (IN REF. 2)
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Pred. No. 2.3e-35;
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                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic DOMAIN

1 112 IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marquart M., Deisenhofer J., Huber R., Palm W.; "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE=81072295; PubMed=7441755;
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PDB; 2IG2; 12-JUL-89.
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 GPDYWGQGTPVTVSS
                                                                   ADSVKGRFTISRDNSKNTLFLOMDSLRPEDTGVYFCA-----RDGGHGFCSSASCF 111
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Pred. No. 2.
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RESULT 11
HV3C_HUMAN
ID HV3C_HUMAN
AC P01764;

STANDARD;

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HV3A HUMAN
ID HV3A HUMAN
AC P01762;
DT 21-JUL-1986
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P01763;
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"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLAYED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ig heavy chain V-III region WEA.
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PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

DOMAIN

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IG-LIKE.
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HSSP; P01772; 2FB4.
SG; GO:0005576; C:extracellular; NAS.
GO; GO:0003B23; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                       MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLVDSGGGLVBPGGSLRLSCSASGFTFSANDMNWVRQAPGKGLEWLSFIGGSGSTIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAPDIWGGGT 120
                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRNBSKNSLYLQMSSLRAEDTAVYYCARGWLLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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     01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
12256 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 414; DB 1; 65.1%; Pred. No. 5.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D88294FB418A07B7 CRC64;
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                                                            122
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Best Local S
Matches 75
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NON_TER
SEQUENCE
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15-SEP-2003 (Rel. 42, Last annotation updat)
Ig heavy chain V-III region TRO.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuscBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     HV16 MOUSE STANDARD; PRT; 136 AA.
201783;
201783;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 21 precursor (Fragment).
"Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                           BSDOW
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (MYELOMA PROTEIN TRO) . WEDLINE=76023781; PubMed=809331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                         MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                         Baltimore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSALAT
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122 /
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illarity 59.5%;
Conservative 2:
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13472 MW; 2E21A11DA04D80F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 412; DB 1;
Pred. No. 9.8e-36;
                                                                                                                Reth
                                                evident
                                                                       contribution to the NPb family
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                                                in a gamma
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                                                                                                                Rajewsky
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                                                region.";
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Best Local S
Matches 83
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                  MEDLINE-79124695; PubMed-420800; Chiu Y.-Y.H., Lopez de Castro J.A., Pc "Amino acid sequence of the VH region cryoimmunoglobulin IgG Hil."; Biochemistry 18:553-560(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat ig heavy chain V-III region HIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV3J_HUMAN STANDARD;
P01771;
21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), II: the amino acid sequence of the H-chain (m
type), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                      -1- SIMILARITY: Contains
                                                                                                                                                                                    -!- MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0006955; P:immune response; NAS.
                P; P01772; 2FB4.
GO:0005576; C:extracellular; NAS.
GO:0003523; F:antigen binding activity; NAS.
GO:0006955; P:immune response; NAS.
                                                                                                                A02054; G1HUHL.
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                                                                                                                                                                                    THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
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; Pred. No. 5.3e
12; Mismatches
                                                                                                                                      immunoglobulin-like
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                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                      domain
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Best Local S
Matches 77
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Best Local S
Matches 81
                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:000575; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
1 112
INTERPORATION OF THE PYRROLLER.
DOMAIN
1 112
INTERPORATION OF THE PYRROLLER.

GOMAIN
1 112
INTERPORATION OF THE PYRROLLER.

GOMAIN
1 112
INTERPORATION OF THE PYRROLLER.
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InterPro; irac.

Pfam; PF00047; ig; 1.

Pfam; PF000406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

IG-LIKE.

IG-LIKE.

PYRROLIDONE CARBOXYLIC

PYRROLIDONE CARBOXYLIC

----AR CRC.
                                                                                                                                                                       MOD_RES
NON_TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region GA.
Homo sapiens (Human)
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACROGLOBULIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=74175307; PubMed=4208843;
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                                                                                                            Similarity
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121 AA;
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122 AA;
                                                                                      Conservative
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13166 MW;
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13566 MW;
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                                                                                                          63.0%;
61.1%;
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                                                                                      24;
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                                                                                                          Score 419;
Pred. No. 1
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Pred. No. 8e
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                                                                                      Indels
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Best Local Similarity
Matches 82; Conserv
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1
Immunoglobulin v region.
DOMAIN
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HUMAN
HV3U_1
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Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 18:4054-4067(1979).
--- MISCELLANEOUS: THIS GAMMA-1 MYBLOMA PROTEIN HAS A DELETION IN
HINGE REGION. THERE ARB NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The crystallizable human myeloma
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region NIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=80020920; PubMed=114208;
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                        Homo sapiens (Human)
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-JUL-1986 (Rel. 01, Last sequence up-
-SEP-2003 (Rel. 42, Last annotation heavy chain V-III region DOB.
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0000585; P:immune response; NAS.
erPro; IPR007110; Ig-like.
erPro; IPR003006; Ig_MHC.
erPro; IPR003596; Ig_V.
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120 AA;
Metazoa;
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                                                                                                                                                                     STANDARD;
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13440 MW;
  Chordata; Craniata; Vertebrata;
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65.1%;
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Pred. No. 2.5e
18; Mismatches
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                                                                  update)
on update)
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?.5e-38;
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  Euteleostomi;
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RESULT 4
HV3T HV3T
AC P01.7
DT 21.-J
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DE IG h-mo
OC Euka
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ON NOB1
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RP SEQU
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Best Local S
Matches 84
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MOD RES
DISULFID
NON TER
SEQUENCE
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Prom; Pro0406; IGv; 1.

SMART; SM00406; IGv; 1.

PROSITE; P850835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

Immunoglobulin V region; Pyrrolinone Carboxylic acid.

DOMAIN

1 112

PYPRONITONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Toppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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NCBI_TaxID=9606;
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HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activity; NAS.
G0; G0:0006955; P:immune response; NAS.
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I; Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                        P01781;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region GAL.
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MEDLINE=77070269; PubMed=826475;
                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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     MEDLINE=75059123;
                                  SEQUENCE
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     PubMed=4803843
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Primates;
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Pred. No. 3.8e
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PYRROLIDONE CARBOXYLIC ACID
                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Maximum DB seq length: 200000000
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                             SwissProt_41:*
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		ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGOG - - - - -	GFTFGDYAIHWVRQA : : GFTFSNYAMHWVRQP	e 444; DB l; Length . No. 4.8e-39; ismatches 17; Indel	A42D0F17D252F1C2 CRC64	PYRROLIDONE CARBOXYLIC ACID					NAS.	NAS.		1 immunoglobulin-like domain	S ISOLATED	9-3243 (1980) .	ole region of a human			Craniata; Vertebrata; I Catarrhini; Hominidae;	•	tion update)	O O	; 122 AA.		ALIGNMENTS				NOUSE	MOUSE MOUSE	ASUON E	HUMAN
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RESULT 15
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; Sequence 69145, Application US/09791537
; GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 69145
LENGTH: 122
TYPE: PAT
ORGANISM: Homo Bapiens
US-09-791-537-69145
Search completed: December 30, 2003, 11:38:31 Job time: 192.162 secs
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SEQUENCE 18, Application PC/TUS0305128

GENERAL INFORMATION:

APPLICANT: Dyax Corporation, et al

TITLE OF INVENTION: MGC-PEPTIDE COMPLEX BINDING LIGANDS

FILE REFERENCE: 10280-034W01

CURRENT APPLICATION NUMBER: PCT/US03/05128

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: US 60/358,994

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NO 18

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENCTH: 120
Sequence 18, Application US/10371942
; GENERAL INFORMATION:
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
APPLICANT: Reiter, Yozam
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 18
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 102506
LENGTH: 118
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CURRENT FILING DATE: 2001-02-22
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llarity 82.4%;
Conservative
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Sequence 19813, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 19813

LENGTH: 132
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; TYPE: PRT
; ORGANISM: Homo s
US-10-371-942-18
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US-09-791-537-19813
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                                             US-09-791-537-31924
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                                                                                                       CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
SEQ ID NO 31924
                                                                                                                                                                                                                                                                                      Sequence 31924, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity
Best Local Similarity
               Query Match
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
TITLE OF INVENTION: METHODS OF USB THEREOF
FILE REPERENCE: 261/210
                                                                            LENGTH: 11
TYPE: PRT
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                                                             ORGANISM: Homo sapiens
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80.7%;
80.8%;
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Pred. No. 1e-42;
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Pred. No. 1.3e-42;
Score 502; DB 22;
Pred. No. 1.3e-42;
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RESULT 8
US-09-791-537-102505
; Sequence 102505, Application US/09791537
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-791-537-68722
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US-09-791-537-106428
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SOFTWARE: Patentin version 3.0
SEQ ID NO 106428
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 68722
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT PPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bionomix, Inc.
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                                                                                                                             ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKERVRGVMVN--WGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Debe, Derek
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Pred. No. 4e-43;
8; Mismatches 13;
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Pred. No. 3.8e-43;
7; Mismatches 13
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RESULT 10 US-09-791-537-102506

; Sequence 102506, Application ; GENERAL INFORMATION:

US/09791537

APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek

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; TYPB: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31283
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US-09-791-537-31283
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US-09-791-537-102505
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Best Local
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APPLICANT: Danzer, Joseph
TITLE OP INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OP INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPILLOATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBITITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
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Local Similarity 81.5%;
121
                                    117 TVSS 120
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                                                                                                                                                       EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                           EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGQLWSSD-YWGQGTLVTVSS 118
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                                                                           ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDYNYYDSSGYYSLDYWGQGTLV
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83.2%;
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Pred. No. 4.6e-43;
7; Mismatches 12
                                                                                                                                                                                                                                   Score 506; DB 22;
Pred. No. 5.4e-43;
7; Mismatches 12;
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RESULT 2
US-09-674-752-46
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; ORGANISM: Homo sapiens
US-09-674-752-46
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US-09-791-537-87993
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APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 87993
LENGTH: 121
TYPE: PAT
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GENERAL INFORMATION:
APPLICANT: Voorberg, Johannes
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Best Local
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-09-791-537-87993
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1 EVQLVBSGGGLVQPGRSLRLSCVDSGLTPSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                   th 83.3%; similarity 81.7%; 98; Conservative
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                                                                                                                                   Score 518; DB 22;
Pred. No. 3.2e-44;
6; Mismatches 16;
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PRC
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT TILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 31853
LENGTH: 121
TYPE: PRT
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US-09-791-537-69157
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Best Local S
Matches 97
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 69157
LENGTH: 117
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Best Local Similarity
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
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Pred. No. 2.6e-43;
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Pred. No. 2.8e-43; 
7; Mismatches 11
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Perfect score:
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/ Cgm2_6/ptodata/1/paa/US083_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US085_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US085_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US086_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US086_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US089_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US089_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US090_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US090_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US093_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US094_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US094_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US095_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US096_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US0978_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US098_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US098_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US098_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US098_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US101_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
/ Cgm2_6/ptodata/1/paa/US106_COMB.pep:*
     120
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_6/ptodata/1/paa/US081_COMB.pep:*
_6/ptodata/1/paa/US082_COMB.pep:*
                                                                                                                                                                                                                                                                                                 _6/ptodata/1/paa/US60
     20 US-09-674-752-36
                                                                                                                                    SUMMARIES
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                                               Description
Sequence 36, Appl
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ALIGNMENTS

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; ORGANISM: Homo sapiens US-09-674-752-36
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US-09-674-752-36
                                                                                                                      SEQ ID NO 36
LENGTH: 120
TYPE: PRT
                                                                                                                                                                                                                               Sequence 36, Application US/09674752

GENERAL INFORMATION:
APPLICANT: Voorberg, Johannes
TITLE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With
TITLE OF INVENTION: Inhibitor
FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US
CURRENT APPLICATION NUMBER: US/09/674,752
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: BCT/NL99/00285
PRIOR APPLICATION NUMBER: EP 98201543.0
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1998-05-08
Query Match
Best Local Similarity
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1
                                                                                                                                              120
    100.0%;
    Score 622; DB 20;
Pred. No. 8.6e-55;
                           Length 120;
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Search Job tim	дь	ঠ	Db	ð
Search completed: December 30, 2003, 11:45:24 Job time : 25.7352 secs	61 ADSVKGRFTISHDNSKNTLYLOMNSLRAEDTAVYYCARDAAVTAEGWGKGTLVTVSS 117	61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS 120	1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHMVRQAPGKGLEMVAVISYDGSIKYY 60	1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60

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US-10-041-860-211
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-211
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: ABGENIX.051A CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 211
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Gazit, Richard
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FILE REFERENCE: ABGUIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 127
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 211, Application US/10041860 Publication No. US20030157109A1
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ORGANISM: homo sapiens
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Local Similarity 74.8%;
121
                                     114 TLVTVSS 120
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                                                                                                                                                                      1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
                                                                                                           ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAK-----DLIESNIAEALWGQG 113
                                                                                                                                                QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWYDGNDKYY
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                                                                       ADSVKGRFTVSRDNSKNTLYLOMNSLRAEDTAVYYCARGYYYDSSDYLYYYYGMDVWGQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSSDYLYYYYGMDVWGQG 120
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                                                                                                                                                                                                                                        79.3%;
74.8%;
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Pred. No. 2.8e-40;
8; Mismatches 17;
                                                                                                                                                                                                                          Score 493.5; DB 1:
Pred. No. 2.8e-40;
B; Mismatches 17
                                                                                                                                                                                                                                                                DB 12; Length 127;
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RESULT 14

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Gaps

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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 331
TENERGY SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                   ORGANISM: Homo sapiens US-09-880-748-1912
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-331
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                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
PRIOR PELLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-27
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILLING DATE: 2001-05-25
PRIOR FILLING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1912, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 331, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
Query Match 79.3%;
Best Local Similarity 79.2%;
Matches 95; Conservative
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                                            LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADSVKGRPTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSSDYLYYYYGMDVWGQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAK------DLIESNIAEALWGQG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 493.5; DB 12; Length 127; 74.8%; Pred. No. 2.8e-40; ative 8; Mismatches 17; Indels 7;
  Score 493.5; DB:
Pred. No. 5.6e-40
9; Mismatches 1:
                                                  DB 11;
                                                Length 240;
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APPLICANT: Es van, Helmuth
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Steffan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACII
TITLE OF INVENTION: TRANSPORTER
FILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/10/235,175
CURRENT APPLICATION NUMBER: US/9/3/315,926
PRIOR APPLICATION NUMBER: US/9/9/315,926
PRIOR APPLICATION NUMBER: US/9/9/315,926
PRIOR PILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98201593.3
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR APPLICATION NUMBER: BP 98201693.3
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SCOTTMARE: Patentin version 3.0
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; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-10-235-175-80
                                                                                                               SOPTWARE: PatentIn Ver. 2.0; SEQ ID NO 512; LENGTH: 249; TYPE: PRT; ORGANISM: Homo sapiens US-09-880-748-512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-880-748-512
                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
Query Match 79.6%;
Best Local Similarity 77.0%;
Matches 97; Conservative
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Best Local Similarity 78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feat
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
TYPE: PRT
ORGANIEM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09880748
o. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Score 495; DB 11; Length 249; Pred. No. 4.2e-40; 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 495; DB 12;
Pred. No. 4.2e-40;
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     6,
     Gaps
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER: 0F SEQ ID NOS: 3239
SOCTWARE: PAECENTIN Ver. 2.0
LENGTH: 249
                                                                               GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
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US-09-880-748-1109
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; ORGANISM: Homo sapiens
US-09-880-748-1109
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US-10-041-860-33
; Sequence 33, Application US/10041860
; Publication No. US20030157109A1
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Publication No. US20030059937A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 96; Conserv
                    APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
APPLICANT: Peng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Mcber, Richard
APPLICANT: Bezabah, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARASYYDILTGYYKGAFDIWGQGT 120
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US-10-325-694-150
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        CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR EILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR APPLICATION NUMBER: 08/692,084
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TITLE OF INVENTION: RECEPTORS AND USES THEREOF
FILE REFERENCE: 38164000
CURRENT APPLICATION NUMBER: US/10/325,694
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/99/403,107
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 152
SOFTMARE: PATENTIN Ver. 2.1
SEQ ID NO 150
LENGTH: 138
TYPE: PRT
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Matches
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-10-325-694-150
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FILING DATE: 1996-08-08
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o. US20030148463A1
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76.4%;
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Pred. No. 1.6e-40;
8; Mismatches 15
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APPLICATION NUMBER: 60/27,379
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR APPLICATION NUMBER: 60/210,310
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR PRILING DATE: 2001-03-16
PRIOR PRILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1394
TENCTTH: 252
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Best Local S
Matches 97
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PRIOR PTILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030059937A1
GENERAL INFORMATION:
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Best Local Similarity
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                       112 QGTLVTVSS 120
121
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                                                                                                    61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEA------LWG 111
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97; Conserv
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                                                                                                                                                                                                                                              97; Conservative
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KGTLVTVSS 129
                                                                                                                                                                                    EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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nilarity 80.8%;
Conservative
                                                                                                                                                                                                                                                                 79.7%; Score 495.5; DB 1
75.2%; Pred. No. 3.8e-40;
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Pred. No. 1.7e-40;
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                                                                                                                                                                                                                                                                                      DB 11;
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US-10-235-175-80
US-10-235-175-80, Application US/10235175
Sequence 80, Application US/10235175
Publication No. US20030166287A1
GENERAL INFORMATION:

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US-10-269-805-21
Sequence 21, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLLNER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-21
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US-10-325-694-144
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SOFTWARE: PATENTIN VER. 2.1
SEQ ID NO 144
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                       Query Match
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CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/403,107
PRIOR FILING DATE: 1999-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KUFER, PETER APPLICANT: RAUM, TOBIAS
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Local Similarity 79.7%;
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121
                                                                                                                                                                                                                                     98; Conservative
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                                      118 VSS 120
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                                                                                                        61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAK---DLIESNIAEALWGQGTLVT 117
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VSS 123
                                                                           ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPVDFDYGDYAIDYWGQGTLVT 120
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77.2%;
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                                                                                                                                                                                                                                Score 498.5; DB 15; Length 123; Pred. No. 8.9e-41; 6; Mismatches 16; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 499.5; DB 1
Pred. No. 8.1e-41;
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
NUMBER: 0F SEQ ID NOS: 3239
SOPTWARE: PAECHEIN Ver. 2.0
LENGTH: 252
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                                                                                   ORGANISM: Homo sapiens US-09-791-153A-63
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US-09-880-748-1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-791-153A-63
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Deshpande, Rajendra

APPLICANT: Hitz, Anna

APPLICANT: Boyle, William

APPLICANT: Sullivan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                            SOPTWARE: PatentIn version 3.0
SEQ ID NO 63
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/09791153A Publication No. US20030103978A1
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Best Local (
Query Match 80.0%;
Best Local Similarity 80.8%;
Matches 97; Conservative
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                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                    APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
FILE REFERENCE: A-633A
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                             TYPE: PRT
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1 Similarity 75.2%;
97; Conservative
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Pred. No. 1.9e-40;
9; Mismatches 14;
  Score 497.5; DB 11;
Pred. No. 1e-40;
5; Mismatches 11;
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                                              Length 113;
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                493.5
493.5
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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622
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Match Length
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/cgn2_6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pep:*
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                US-09-972-656-76
US-10-325-694-144
US-10-269-805-21
US-09-80-748-1731
US-09-80-748-1731
US-10-315-694-150
US-10-315-694-150
US-10-010-729-7
US-09-880-748-1394
US-10-235-175-80
US-09-880-748-1109
US-09-880-748-1109
US-10-041-860-331
US-10-041-860-331
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                                                                                                                                                                                                                                                                                                            Description
                Sequence 76, Appl
Sequence 114, App
Sequence 21, Appl
Sequence 1731, Ap
Sequence 150, Appl
Sequence 150, Appl
Sequence 150, Appl
Sequence 134, Appl
Sequence 80, Appl
Sequence 512, Appl
Sequence 512, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	<u>3</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
4.	485.5	5	486	486	486	486	486	487	487	487	488	488	488	488	488.5	488.5	489	489	490	490	490	490	490	490		491	9		493
78.0	78.1	78.1	78.1	78.1	78.1	•	•	78.3	•		•		•	•		78.5	•	•		78.8	•	•	78.8	8	8		79.0	•	•
122	241	123	254	254	251	251	122	249	249	249	254	252	247	118	451	238	252	249	249	249	249	247	241	241	119	122	123	109	248
10	11	15	11	11	11	11	15	11	11	11	11	11	11	12	15	11	11	11	11	H	11	11	11	11	12	15	15	12	11
-09-144-	US-09-880-748-2055	-10-243-	US-09-880-748-1428	US-09-880-748-981	US-09-880-748-982	US-09-880-748-952	US-10-269-805-53	-748	11	US-09-880-748-911	US-09-880-748-977	US-09-880-748-1519	US-09-880-748-924	US-10-120-377-78	-382-	US-09-880-748-1931	US-09-880-748-1627	US-09-880-748-1117	US-09-880-748-1115	US-09-880-748-1102	US-09-880-748-397	US-09-880-748-1330	US-09-880-748-1901	US-09-880-748-1887	20		US-10-269-805-1	US-10-309-764-1	US-09-880-748-1890
68, A ₁	e 20	e 2,	14:	e 981	æ	e 952,	e 53,	e 1956,	e 1119	e 911,	e 977,	e 1519	e 924,	e 78,	17,		1627	1117	Sequence 1115, Ap		397,	1330,	Sequence 1901, Ap	Sequence 1887, Ap	e 76	•	e 1, 7	e 1,	Sequence 1890, Ap

ALIGNMENTS

RESULT 1 US-09-972-656-76

GENERAL INFORMATION:

Sequence 76, Application US/09972656 Publication No. US20030099647A1

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US-09-972-656-76
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 76
                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OP INVENTION: Pully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OP INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
FILE REFERENCE: A-799
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 227
TYPE: PRT
                                                                                                                                                                                                                                                                        Match 80.5%; Score 501; DB 11; Length 227; Local Similarity 77.4%; Pred. No. 1e-40;
121
                                       117 TVSS 120
                                                                                                                     61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLI----ESNIAEALWGQGTLV 116
                                                                                  61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCASDLVLTMTSRRAAFDIWGQGTMV 120
                                                                                                                                                                  1 QVQLVETGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                      1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
                                                                                                                                                                                                                                                    96; Conservative
TV8S 124
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RESULT 2

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                                                                                                                                                                                                                                                                   The present invention describes a virus-like particle or gene delivery controls (I) provided with a ligand capable of binding to a human amino calls transporter. (I) is used to deliver genes to human cells or primate cells that express the hCAT1 amino acid transporter, such as endothalial, haematopoietic or smooth muscle cells, as part of a gene therapy regime. CC The vectors are especially useful for providing local applications of cadenoviral vector to patients with restenosis following balloon cC angioplasty, where smooth muscle cells need to be transduced with ceNOS CC cDNA, for example. (I) may also be used to pseudotype recombinant type C constitution (I) may be used in functional genomics where transduction of as many cell types as possible is required. The new gene delivery vehicles transduce DNA more efficiently and specifically into tissues that are compared to a wildtype adenoviral vector. This increased specificity results in lower multiplicities of infection which can occur with prior callow DNA to be transduced into cells that are in low abundance in cell mixtures and tissues, which increases their efficiency for use as gene concreases the potential host cell range of these vehicles. The present correspent inventions.
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New gene therapy vectors, useful for treating balloon angioplasty patients -
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                                                                                                                                                                                                                                                           present invention.
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                                                                      319 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 378
                    61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                             ch 79.6%; Score 495; DB 21; Length 490; Similarity 78.3%; Pred. No. 6e-39; 94; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                           490 AA;
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Search completed: December 30, 2003, 10:54:35 Job time : 38.6861 secs

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AAY56287
ID AAY56
XX AAY56
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XX O8-FE
DT O8-FE
XX HCAT1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel antibodies that immunospecifically bind to Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1014-1015; 3148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                AAY56287;
                                                                                                                              AAY56287 standard; Protein; 254 AA
                               HCAT1 clone 25 antibody variable heavy chain protein sequence.
                                                                08-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM,
                                                                                                                                                                                                            121
                                                                                                                                                                                                                                          115 LVTVSS 120
 cationic
                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                              MVTVSS 126
                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGYYDILTGYSYYGMDVWGQGT
                                                                                                                                                                                                                                                                                                      ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKD-----LIESNIAEALWGQGT
                                                                                                                                                                                                                                                                                                                                     QVQLVESGGGVVQPGRSLRLSCAASGPTFSSYGMHWVRQAPGKGLEWVAAISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
 amino
                                                                                                                                                                                                                                                                                                                                                                                                                   79.6%;
77.0%;
acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH,
 transporter; hCAT1; targeted delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 495; DB 23;
Pred. No. 2.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                      6.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                       114
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밁 ð 밁 ঠ

Synthetic.

Homo sapiens

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RESULT 15
AAY56637
ID AAY56637
AC AAY56
XX 22-FB
XX 22-FB
XX V1rus
KW human
KW targe
XX Homo
OS Synth
XX X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a virus-like particle or gene delivery vehicle comprising a ligand capable of binding to a human amino acid transporter. The method is useful for the target delivery of substances to cells e.g. gene therapy. A human cationic amino acid transporter (hCATI) targeted adenovirus is useful for local applications of adenoviral vector e.g. in patients with restenosis following balloon angioplasty where smooth muscle cells need to be transduced with an adenoviral vector carrying the CeNOS cDNA. More efficient transduction of tissues can be carried out therefore resulting in lower multiplicity's of infections that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells. AAZ38737 to AAZ38770, and AAY56264 to AAY56287 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene delivery; virus-like particle; retroviral envelope molecule;
infection; gene therapy; restenosis; balloon angioplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New virus-like particle or gene delivery vehicle, useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP959136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                smooth muscle cell; transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 16; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                     targeted delivery;
                                                                                                                                                        Virus-like particle; ligand; gene delivery; envelope protein; hCAT1; human cationic amino acid transporter 1; retrovirus; adenovirus;
                                                                                                                                                                                                                            hCAT1 binding human antibody molecule protein sequence
                                                                                                                                                                                                                                                                          22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                 AAY56637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INTR-) INTROGENE BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-001283/01.
)B; AAZ38770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLVESGGGLVQPGRSLRLSCVDSGLTESSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-0201693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98EP-0201693.
                                                                                                                                     gene therapy; balloon angioplasty
                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.6%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                   490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 495; DB 21;
Pred. No. 2.8e-39;
9; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                   ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC neurite outgrowth, regeneration, remyelination and neuroprotection in C central nervous system (CNS). (1) is capable of inducing remyelination, CC promoting cellular proliferation of glial cells, and promoting Ca2+CC signaling with oligodendrocytes. An humanised antibody to (1) can be CC selected from antibody sHIGMY2 (LYM 22), ebwHigM MsI19D10, ebw HigM CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (1) is useful for stimulating CC remyelination of CNS axons, stimulating proliferation of glial cells in CC CNS axons, or treating demyelinating proliferation of glial cells in CC CNS. (1) is preferably useful for treating a demyelinating disease of CNS in a mammal in need CC for a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a cC neural disease of CNS. (1) is preferably useful for treating ademyelinating disease, or a post-neural disease of CNS. (1) is also useful for stimulating tremyelination of CNS axons. The CC (1) is also useful for stimulating remyelination of CNS axons. The cc antibodies are useful for preventing infection by a bacterium, virus or condition in a subject. Methods where (1) is administered to a patient CC already disease, amyotrophic lateral sclerosis (ALS), a virus or condition disease, anyotrophic lateral sclerosis (ALS), a virus or condition of disease, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents cc the sHigM22 heavy chain variable region clone A amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 97
                                                                                                                                                                                                      BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel neuromodulatory agent (a human IgM monocional antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
                     15-JUN-2001; 2001WO-US19110
                                                              10-JAN-2002
                                                                                                       WO200202641-A1
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                       common variable
                                                                                                                                                                                                                                                                                                                                      Human BLyS
                                                                                                                                                                                                                                                                                                                                                                             19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                      ABP45383
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45383 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a neuromodulatory agent (I) capable of promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFAISRDNAKUTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLTADDTAVYYCAKGVTGSPTLD-YWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                 binding scFv SEQ ID 1394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; 219pp; English.
                                                                                                                                                                                     immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 495.5; DB 23; Pred. No. 1.1e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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Best Local (
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to dispose disease associated with aberrant BLyS expression and activity such as cancer, immune, and activity may also be
                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunostimulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficie systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                           Human
                                                                                                                                                                         19-AUG-2002
                                                                                                                                                                                                      ABP44501;
                                                                                                                                                                                                                                     ABP44501 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2066-2067; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ibodies against B Lymphocyte Stimulating polypeptides, useful diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                  112 QGTLVTVSS 120
                                                                                                                                         BLyS binding scrv SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMJWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
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CAMBRIDGE ANTIBODY T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEA-----LWG
                                                                                                                                                                                                                                                                                                                   KGTLVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRPTISRDNSKNTLYLOMNSLRAEDTAVYYCAKBESYYDILTGYYVHYYGMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-273499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                         (first
                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                         entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 495.5;
Pred. No. 2.5
                                                                                                                                           512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                       $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5e-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                              immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                111
                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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Homo sapiens

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RESULT 10
AAY44995
JD AAY44995
AC AAY44
XX AAY44
AX AAY HD70,
XW EPCAN
KW HD70,
KW EPCAN
KW IL-2,
KW ANEL,
KW ANEL,
KW ANEL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the left chain of a heterominibody comprising HD70 single-chain Fv (scFv) fragment N-terminally linked human CH1 domain which bears at its C-terminus the human inflammaton cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), a hexahistidine sequence for ease of purification. HD70 scFv specifically recognises the human epithelial cell adhesion molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2; interleukin-2; Ck-domain; kappa light chain constant domain; heterominibody; multifunctional compound; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; prevention; antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY44995 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanomas and sarcomas.
                                                                                                                                                 WPI; 2000-195265/17
N-PSDB; AAZ50588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HD70scFv-Ck-interleukin 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200006605-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HD70;
                                                            New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis -
                                                                                                                                                                                                                                                                                                   (MICR-)
                                                                                                                                                                                                                                                                                                                                                          28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EpCAM) also called
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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97; Conserv
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      10,
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166pp;
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Pred. No. 4.7e-39;
8; Mismatches 15;
                                                                                                                                                                                                                                      ₽A,
                                                                                                                                                                                                                                   Borschert K,
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the human inflammatory
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RESULT 11
ABB07169
ID ABB077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HigM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide antiparkinsonian; neuroprotective; nootropic; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells e.g. lymphomas and leukaemias, or melanomas and sarcomas
                                      WPI; 2002-066596/09
N-PSDB; ABA94216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200185797-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                         (MAYO-) MAYO FOUND MEDICAL EDUCATION
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Pred. No. 4.7e-39;
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This is the amino acid sequence of the human D4.5 heavy chain variable region, used in the method of the invention. for providing receptors that can be used for targeting antigens in humans without being immunogenic themselves. Such receptors can be used for treating
                                                                      Claim
                                                                                                            Production of anti-human antigen receptors combination of functionally rearranged VH and
                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW80815 standard; Protein; 138
                                                                                                                                                                                                                             (RAUM/)
                                                                                                                                                                                                                                                                        14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of human D4.5 heavy chain variable region.
                                                                                                                                                                                                 Kufer P,
                                                                                                                                                                                                                                                                                                  14-APR-1998;
                                                                                                                                                                                                                                                                                                                                22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; auto-immune
                                                                                                                                                                                                                                                                                                                                                            WO9846645-A2
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                                                                      9; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                 D4.5 heavy chain variable region; receptor; antigen; auto-immune disease; graft rejection; allergy; matory disease; endocrine disease; degenerative disea
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                                                                                                                                                                                                                             KUFER P.
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97; Conser
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                                                                                                                                                                                                   Raum T;
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76.4%;
                                                                                                a recombinant vector
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Pred. No. 9.3e-40;
B; Mismatches 15
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Best Local
The patent discloses heterominibodies which are multifunctional compounds produceable in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises, a CHI-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CI-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (poly)peptides having different receptor or ligand functions, where further at least two of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF; granulocyte/macrophage colony stimulating factor; heterominibody; CH1-domain; multifunctional compound; heavy chain constant domain; immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis; antiproliferative; prevention; treatment; malignant; haematopoietic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases such as tumours or auto-immune diseases, graft rejection after transplantation, infectious diseases by targeting cellular receptors as well as allergic, inflammatory, endocrine and degenerative diseases by targeting key molecules involved in the
                                                                                                                                                                                                                                                                                                                                  New multifunctional compounds useful for preventing and/or treating malignant cell growth and for detection and diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195265/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kufer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric Homo sapie
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW15522 standard; Protein; 115 AA.
                                                                  Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosi immune and inflammatory disease
                                                                                                                                                                        Bacon L, Gr
Tempest PR,
                                                                                                                                                                                                                                    19-JAN-1996;
06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macrophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW15522
                                                                                                                             N-PSDB; AAT60369
                                                                                                                                        WPI; 1997-215360/20.
                                                                                                                                                                                                                                                                        07-OCT-1996;
                                                                                                                                                                                                                                                                                                23-APR-1997
                                                                                                                                                                                                                                                                                                                     GB2305921-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor beta-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TGF beta-2 scFv antibody 2A-H11 VH
                                            Claim 4; Fig
                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRETISRDNSKNTLYLQMNSLTAEDTAVYYCAKGVTGSPTLD-YWGQGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIBSNIAEALWGQGTLVTVSS
                                                                                                                                                                                        Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                          een JA, J
Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                           2a(i); 184pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens;
                                                                                                                                                                                                                                    96GB-0001081.
95GB-0020486.
                                                                                                                                                                                                                                                                       96GB-0020920
                                                                                                                                                                                                                                                                                                                                                                             note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                               note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             label= CDR1
                                                                                                                                                                                                                                                                                                                                                         label=
                                                                                                                                                                                                                                                                                                                                                                                          label=
                                                                                                                                                                                     Jackson
                                                                                                                                                                          JE,
                                                                                                                                                                                                                                                                                                                                           "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                        CDR3
                                                                                                                                                                                                                                                                                                                                                                                         CDR2
                                                                                                                                                                          on RH, John
Vaughan TJ,
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                                                                                                                                                                            Johnson KS, Po
n TJ, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta-2; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
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                                                                                                                                                                          ms AJ;
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                                                                                                                                                                                                                                                                                                                                                                              region
                                                                               of fibrosis
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                                                                                                                                                                                 gene (AAT60369) obtained by panning a phage antibody library produced from cloned germline V genes and synthetic CDRs. The antigen-
and/or beta-2 can be used to counter the adverse effects of TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-
c angioplasty restanosis, scleroderma, vascular disorders, cataract, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases (or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigenbinding domains. These are highly specific, have low dissociation.
                                                                        Query Match
Best Local S
Matches 97
                                                                                                                                                 Sequence
                                   μ
                                                                                            Similarity
                   EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
 EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY
                                                                                                                                                     115
                                                                            Conservative
                                                                                                                                                   ξ
                                                                                            79.8%;
                                                                            6
                                                                        Score 496.5; DB 1
Pred. No. 8.3e-40;
6; Mismatches 12
                                                                                                              DB 18;
                                                                            12;
                                                                            Indels
                                                                                                              Length
                                                                                                                  115;
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                                                                            Gaps
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AAY17954 standard; Protein; 127
                         61
                                  61
                        ₹
                                    120
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Human D4.5 heavy chain variable region 04-AUG-1999 (first entry)

Binding site autoimmune di disease; domain; BSD; epitope; isease; scFv-antibody; fusion protein; therapeutic; cancer; single-chain Fv.

Homo sapiens

WO9925818-A1

27-MAY-1999

16-NOV-1998; 98WO-EP07313.

(KUFE/) KUPER

17-NOV-1997;

97EP-0120096

Borschert K, Kufer ٣ Lutterbuese æ Raum H

WPI; 1999-338004/28. N-PSDB; AAX77236.

Phage display system for identification retaining capacity to bind an epitope of binding site domains

Disclosure; Fig 3.1; 152pp; English.

RESULT 7
AAY17954
ID AAY1
XX AAY1
XX AAY1
XX Bind
XX Bind
XX Bind
XX Bind
XX Huma
XX Huma
XX Home
XX H The invention relates to a method of identifying binding site domains (BSD) that retain the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bior multivalent polypeptide. The method comprises (a) testing a panel of BSD displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, where the fusion

This polypeptide sequence comprises the VH domain of human antibody 2A-H11 (also known as 6H1), which is specific for transforming growth factor (TGF) beta-2. It is encoded by

8CFV

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Examphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the Ct tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have Ctycostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity of BLyS. The antibodies bind to BLyS cinhibit the expression and activity of BLyS. The antibodies bind to BLyS cand so may be used to detect and quantitate the presence of BLyS in CC and so may be used may be used in this way to diagnose disease CC associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression cC and activity such as cancer, immune, and autoimmune disorders and cdiseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, cc immunodeficiency (e.g. common variable immunodeficiency (CVID) and cc difficulties and fragments of the antibodies described in the method contributions and fragments of the antibodies described in the method contributions.
                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                        Matches
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16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BLyS binding scFv SEQ ID 1731.
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2468-2469; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2000;
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                                                                                                                                                                                                                                                                                  Local
      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
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                                                                                                                                                                                                                                                    l Similarity
97; Conser
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CAMBRIDGE ANTIBODY TO
                                                                                                                                                         EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
                                          ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIE-----SNIAEALWG
                                                                                                                            QVQLVESGGGVVQPGRSLRLSCAASGFTPSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILTGYYYYYGMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                252 AA;
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2001US-27624BP.
2001US-277379P.
2001US-293499P.
                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                           80.1%;
75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TECHNOLOGY.
                                                                                                                                                                                                                                                    9,
                                                                                                                                                                                                                                                 Score 498.5; DB 23;
Pred. No. 1.3e-39;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaughan T,
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                                                                                                                                                                                                                                                                                                            Length 252;
                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                              Gaps
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120
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δ. 밁 ঠ

Best Local Similarity

80.0%;

Score 497.5; DB 23; Pred. No. 6.9e-40;

Length 119;

Query Match

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The invention provides a neuromodulatory agent (I) capable of promoting coentral nervous system (CNS). (I) is capable of inducing remyelination, coentral nervous system (CNS). (I) is capable of inducing remyelination, coentral nervous system (CNS). (I) is capable of inducing remyelination, coentral nervous system (CNS). (I) is capable of inducing remyelination, coentral remyelination of glial cells, and promoting Ca2+ coentral nervous system (CNS). (I) is useful for mannised antibody to (I) can be coentral coentral remyelination of CNS axons, or treating demyelinating proliferation of glial cells in coentral coentral remyel. (I) is capable of binding to structures and cells within coentral coentral remyelinating disease of CNS (I) is preferably useful for treating a demyelinating disease of CNS (I) is preferably useful for treating a demyelinating disease of CNS (TMEV) or for treating a human being having multiple sclerosis, or a post-neural disease of CNS. (I) is also useful for stimulating the proliferation of glial cells from mixed cell culture. (I) is also useful for stimulating remyelination of CNS axons. The condition in a subject. Methods where (I) is administered to a patient causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient causeful for treating multiple sclerosis, Parkinson's disease, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the shights the shights have close a sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; viantiparkinsonian; neuroprotective; nootropic; vulnerary.
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          post-infectious encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodriguez M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2000; 2000US-0568351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB07186 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Fig 17; 219pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-066596/09
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Matches 120;
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hybridizable polynucleotide (I) (; hybridizable polynucleotides) comprising a contiguous coding for a human antibody with factor VIII specific; hemostatic activity. (I) is useful a primer or probe presence of inhibitory antibodies directed against far polypeptides of the invention and the antibodies gene) are useful in compositions for neutralizing factor VII antibodies in hemophilia A patients. This sequence repared to the invention of the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the antibodies generated the properties of the invention and the properties of the invention and the antibodies generated the properties of the invention and the properties of the invention and the antibodies generated the properties of the invention and the invention and the properties of the invention and the properties of the invention and the invention
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N-PSDB; AAZ43865.
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tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant anti-human TNF-alpha monoclonal antibody consisting of a heavy (H) chain and a light chain. The recombinant anti-human TNF-alpha human monoclonal antican be produced stably in a high purity and in a large amount.
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 12-13; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant anti-human TNF-alpha human monoclonal antibody produced stably with a high purity, and in large amounts
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tumour necrosis factor; light
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No. 3.8e-41;
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AAY50963
    New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                           WPI; 2000-053102/04.
                                                                                                                                                                                                                                  08-MAY-1998;
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ALIGNMENTS

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Homo sapiens
                                        Human; heavy chain; antibody; factor VIII; hemostatic;
hemophilia A; scFv; A3-C1.
                                                                                                        Human FVIII antibody A3-C1 scFv heavy chain protein B35
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C TISSUE=Mammary gland;

I Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T.

A Isogai T., Ota T., Nishikawa T., Ishii S., Kawai-Hio Y.

A Suzuki Y., Nagai K., Sugano S., Ishii S., Kojima S., Nagai Yamamoto J., Wakamateu A., Nakamura Y., Kojima S., Nagai Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S.,

A Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

"NEDO human cDNA sequencing project.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ database EMBL, AKO74651; BAC11114.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.

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SMART; SM00409; IG; 4.

SMART; SM00409; IG; 1.

SMART; SM00406; IGv; 1.

SMOSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG MHC; 1.

Hypothetical protein.

SEQUENCE 493 AA; 53224 MW;
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Q8NCL6;
Q8NCL6;
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Q1-QT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-QT-2002 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90170.
HOMO sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
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119 AA; 13025 MW; F6E904044381CA7C CRC64;
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EMBL; BC021276; AAH21276.1; -.
InterPro; IPR0070110; Ig-1ike.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; 19; 4.
R SMART; SM00406; IGv; 1.
R PROSITE; PS0035; IG_MHC; 2.
R PROSITE; PS00290; IG_MHC; 2.
Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                             EMBL; AF035042; AAD56278.1; --
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UL72; PRELIMINARY;
Q9UL72; PTEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 23,
                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis
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89; Conserv
Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein.
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                                                                     12872 MW;
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71.8%;
67.2%;
72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 436; DB 4; Length Pred. No. 2.4e-37; 6; Mismatches 25; Indel
Score
Pred.
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                                                                     B4D1A5944B2D5CCA CRC64;
418;
No.
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RESULT 13
Q91Z05
ID Q91Z0
AC Q91Z0
AC Q91Z0
DT 01-DE
DT 01-MA
DE Hypot
GN AUU6 14
OS Mus n 1
OC Eukar
OC Mamma
OX NCB1 |
RN [1] -
RN [1] -
RN [1] -
RN SECTAL
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Best Local S
Matches 83
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Q91205;
C91205;
Q91205;
Q91206;
Q91206;
Q91206;
Q91207;
Q91208;
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(0920B7, O920B7, O920B
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SMART; SM00406; IGv; 1.

PROSITE; PS00199; CYTOCHROME C; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS00290; IG MHC; 1.

Hypothetical protein.

SEQUENCE 473 AA; 51946 MM; CF1
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Submitted (JUL-2001) to the EMI
Submitted (JUL-2001) to the EMI
EMBL; BC010327; AAH10327.1; -.
MGD; MGI:2144967; AU044919.
InterPro; IPR000345; CytC heme
InterPro; IPR007110; Ig-Ilke.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Atkin J.D., Tape A., Jenning "Definition of the Idiotope in Mammalian Cells.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                          Chordata;
Rodentia;
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69.2%;
                                             Jennings I
diotope of 1
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Pred. No. 2.4e-35;
9; Mismatches 26;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF625F008932AF12 CRC64;
                                         I.G., Horaitis O.,
Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                             Antibodies
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                                                                                                                                                                                                                             ¿ Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                         region
                                                                               R.G.
                                             Expressed
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RANDER PRESENTATION OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유 성
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Best Local S
Matches 90
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EMBL; BC024289; AAH24289.1; -.
InterPro; IPRO03006; Ig_-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig__v.
InterPro; IPRO03596; Ig__v.
Pfam; PPF00047; ig; 4.
PROSITE; PS00406; IG_-LIKE; 4.
PROSITE; PS00406; IG_-MHC; 2.
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Cres 01-JUN-2002 (TrEMBLrel. 21, Lass 01-MAR-2003 (TrEMBLrel. 23, Lass Hypothetical protein. Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Primates; C
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Q9UL91;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                            (l)
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE;
NON_TER
NON_TER
SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Spleen;
                                                                                                                                                                                  Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van Young D.C.,
                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies
fetus.";
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                                                       100406; ĪGv; 1.
PS50835; IG_LIKB;
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73.8%;
  12843 MW;
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, Last sequence up
, Last annotation :
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Pred. No. 4.4e-38;
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Catarrhini; Hominidae;
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FDLWGRGTLVTV
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RESULT 11
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ID Q8WU3
AC Q8WU3
DT 01-W3
DT 01-W3
DT 01-W3
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Best Local S
Matches 89
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I logai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

IA logai T., Ota T., Hayashi K., Shiratori A., Sudo H.,

IA Wishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

IA Wagatauma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

IA Watanabe S., Kimura Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

IA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

IA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

IA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

IA Ninomiya K., Iwayanagi T.;

INEDO human cDNA sequencing project.";

INEDI; RAC27379; BAB55072 1;

InterPro; IPR003106; Ig MHC.

InterPro; IPR003106; Ig MHC.

InterPro; IPR003596; Ig MHC.

InterPro; IPR003596; Ig MHC.

INTERPROSITE; PS00835; IG_LIKE; 4.

PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 87
Q8WU38;
Q8WU38;
01-MAR-2002
01-MAR-2002
01-MAR-2003
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical protein FLJ14473.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 494 AA; 5
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87; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.1%; Score 436; DB 4 llarity 71.3%; Pred. No. 2e-37; Conservative 10; Mismatches
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Pred. No. 1.9e-38;
8; Mismatches 20
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(TrEMBLrel. (TrEMBLrel.

20, 23,

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Q9UL71;
Q9UL71;
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01-MAY-2000 (TrEMBLrel. 13, Create on the control of the 
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                                                                                        "Myosin-reactive autoantibodies in fetus.";
Clin. Immunol. Immunopathol. 87:184
EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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EMBL; AF035030; AAD56266.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Dfam. DF0A071:10; 11
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut-
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
NCBI_TaxID=9606;
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01-MAY-2000
                                                                                                                                                                                                                                                Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                             P.L.,
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Pred. No. 6
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Catarrhini; Hominidae;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ da
EMBL; BC015760; AAM15760.1; -.
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InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 5.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_MHC; 3.
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SMART; SM00406; IGV; 1
PROSITE; PS50835; IG_I
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Q96BB9; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo agiens (Human)
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                       Hypothetical protein sequence 597 AA;
                                                                                                                                                                                                                                                                                                      TISSUE=B-cell;
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Similarity 71.2%;
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                                                        ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKD-----LIESNIABALWGQGTL
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121 AA;
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71.3%;
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                                                                                                                            Score 444.5; DB 4;
Pred. No. 3.3e-38;
8; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Q9UL90;
01-MAY-2000
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Q9UL93;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
MYOSIN-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
"Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAR-2003
 InterPro;
InterPro;
                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. EMBL; AF035024; AAD56260.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin-reactive
                      Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AP035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus."
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                                                          fetus.";
                                                                      "Myosin-reactive autoantibodies
                                                                                Wu X., Liu B., Van der Young D.C.;
                                                                                          MEDLINE=98277139; PubMed=9614934;
Wn X.. Liu B., Van der Merwe P.L.,
                                                                                                                                          NCBI_TaxID=9606;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                   SEQUENCE FROM N.A.
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IPR007110; Ig-like IPR003006; Ig_MHC.
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113 AA;
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(TIENHBLrel. 13, Last sequence update)
(TIENHBLEL. 23, Last annotation update)
Live immunoglobulin heavy chain variable
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80.8%;
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Pred. No. 1.2e-44;
4; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae;
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RESULT 4
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01-NOV-1999
01-MAR-2003
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MEDLINE=96071149; PubMed=7475288;

MEDLINE=96071149; PubMed=7475288;

Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,

Lichtenstein A.K., Berenson J.R.;

"A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers."

Leukemia 9:1948-1953(195).

EMBL; S80860; AAD14339.1; -.

HSSP; P01772; 2284.
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 1.
NON TER 1 1 1
SEQUENCE 147 AA; 15768 MW;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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SMART; SM00406; IGv; 1.
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                                                                                                     ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEAL----
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  QGTLVTVSS
                                     QGTLVTVSS
                                                                                   AGSVKGRFTISRDNSKNTLYLOMTSLRVEDTAVYYCAKD-
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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116 AA; 12434 MW;
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79.0%;
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    126
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Primates;
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69.8%;
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Pred. No. 2.3e-43;
                                                                                                                                                                                                                                                     Score 461; DB 4;
Pred. No. 9.4e-41;
3; Mismatches 14
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Mismatches 16
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria:*
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4: sp_human:*
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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48.4	48.6	48.6	48.7	49.0	49.0	•	50.2	50.3	50.7	51.2	51.4	51.6	53.3	54.1	54.2	54.3	54.8	54.8	55.9	56.0	56.9	58.7		59.9	62.0	63.7	64.0	65.8
141	159	146	145	463	145	145	139	145	112	484	125	121	104	521	124	124	437	124	484	480	298	469	131	486	479	487	95	499
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Q924q4 mus musculu	Q96q80 homo sapien	Q924q3 mus musculu	Q924r4 mus musculu	Q991c4 mus musculu	Q924r3 mus musculu	Q924q6 mus musculu	Q924r5 mus musculu	Q924q9 mus musculu	OMO	Bru	Q9u195 homo sapien	Q99ng4 mus musculu	Omo		Q9u192 homo sapien	oryc	Q9rla4 mus musculu	Q9n0w4 oryctolagus	Q8vea0 mus musculu	Q91xe1 mus musculu	Bn	Bnw	Omo		Q91wp5 mus musculu	mu8	homo	homo

ALIGNMENTS

RESULT	77 1
ij	08WUK1 PRELIMINARY; PRT; 613 AA.
AC	
Ŋ	2002 (TrEMBLrel. 20, Created)
ဌ	(TrEMBLrel.
PT	Last annotation
BG	Hypothetical protein.
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გ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
႙	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
õ	D=9606;
R	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Tonsil;
₽ A	Strausberg R.;
RL	Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC020240; AAH20240.1;
DR	
DR	
DR	••
DR	19; 5.
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DR	
DR	PROSITE; PS00290; IG_MHC; 3.
₹	Hypothetical protein.
SQ	SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
5	Query Match 82.5%; Score 513; DB 4; Length 613;
Ma	Best Local Similarity 81.7%; Pred. No. 2e-45; Matches 98; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
?	1 EVOLVESCEST VODESPSIDISCYPEST TERSSYCHUMUNDADADADA TO TAVAVIA Y TONNAYY 60
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밁	20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79
?	61 ADGVZGDENTGERVAKANTI VI OMNGI TIRRVAKAVGERTI IRRVAKANGERTAKANGERT 120
문	80 ADŚVKGRFTIŚRDNSKNTLYLOMNSLRAEDTAVYYCAKDWSEGVETFDIWGQGTMVTVSŚ 139

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RESULT 15
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AC P0177
DT 21-JU
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Best Local S
Matches 81
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PO1775;
PO1775
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21-JUL-1986 (Rel. (
21-JUL-1986 (Rel. (
15-SEP-2003 (Rel. 4
SEQUENCE.

MEDLINE-75046755; PubMed=4139708;

Capra J.D., Kehoe J.M.;

"Structure of antibodies with shared idiotypy: the complot the heavy chain variable regions of two immunoglobulianti-gamma globulins.",

Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN
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Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy: the composit the heavy chain variable regions of two immunoglobul:
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
MCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WIT)
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
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81; Conserv
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ADSVNGRFTISRNDSKNTLYLLMNSLQAZBTALYYCARDAGPYVSP:
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119 A
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01, Last sequence update)
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NTI-GAMMA

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Search completed: December Job time : 6.43379 Becs
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SMART; SM00406; IGv; 1.
SMORTT; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN 1 112
NON TER 119 119
SEQUENCE 119 AA; 12858 MM
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PIR; A02058; MAHULY.
HSSP; P01772; 2FB4.
GO; GO:00005576; C:extracellular; NAS.
GO; GO:0001823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                    2 VQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYYA 61
                                                                                                                                                                        . Similarity 79; Conserv
                                                      DSVNGRFTISRNDSKNTLYLQMNGLQAZVSAIYYCARDAGPYVSPTFFAHMGQGTLVT 119
                                                                           DSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDL--IBSNIAEALWGQGTLVT 117
                                                                                                               VQLLESGGGLVQPGGSLRLSCAASGFTFSASAMSWVRQAPGKGLEWVAWKYENGNDKHYA 61
                                                                                                                                                                                                              1 112
119 119
119 AA; 12858 MW; D6338098794DCF5E CRC64;
                                                                                                                                                                          Conservative
                                                                                                                                                                     62.9%; Score 391; DB 1; I
66.9%; Pred. No. 2.4e-34;
tive 11; Mismatches 26;
             30,
             2003,
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               10:55:53
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RESULT 12
HV3F HUMAN
ID HV3E HUMAN STANDARD; PRT;
AC P01767;
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequenc
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DE Ig heavy chain V-III region BUT.
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Matches 79
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Pfam; PF00047; 1g; 1.

Pfam; PF00047; 1g; 1.

PROSITE; PS50835; IG LIKE; 1.

Temunoglobulin V region; Pyrrolidone carboxylic acid.

Temunoglobulin V region; Pyrrolidone CARBOXYLIC ACI

   Immunoglobulin 'DOMAIN 115 SEQÜENCE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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HSSP; P01772; 2FB4.
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                               "Complete amino acid sequence of the alpha 2 heavy cha 19A2 immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-i- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2)
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
                                                                                                                                                                                                                                                                                                                         HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                             PIR; A02050; A2HUBU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torano A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=78137069; PubMed=416441;
Torano A., Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM AGAINST 3.4-PYRUYLATED GALACTOSE AND ISOLATE WALDENSTROM'S MACROGLOBULINEMIA.
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obulin V region.
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Pred. No. 1.6e-35;
                                                      IG-LIKE.
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RESULT 13
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Matches 79
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Best Local (
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PS5085; IG_LIKE; 1.
Immunoglobulin V region.
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21-JJL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOO.
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NON_TER
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McCumber L.J., Capra J.D.;
MrcCumber anino-acid sequence of a canine mu chain
Mrc complete anino-acid sequence of a canine mu chain
Mol. Immunol. 16:565-570(1979).
MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A M
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A M
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wasserman R.L., Capra J.D.; rprimary structure of the variable immunoglobulin heavy chains."; Biochemistry 16:3160-3168(1977).
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MEDLINE=77242268; PubMed=407924;
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Mammalia; Eutheria; Carnivora;
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HSSP; P01772; 2FB4.
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79; Conservative
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117 AA;
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Pred. No. 2.5
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Pred. No. 3.8e-35;
9; Mismatches 22;
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RESULT 14 HV3M_HUMAN ID HV3M_HUMAN

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Best Local
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                             ASDOW S
MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth Baltimore D.;
                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Buropean Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contermodified and this statement is not removed. Usage by entities requires a license agreement (See http://www.icor send an email to license@isb-sib.ch).
                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81101090; PubMed=6450418; Matthyssens G., Rabbitts T.H.;
                                               SEQUENCE FROM N.A.
                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                             P01783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure and multiplicity of genes for the human heavy chain variable region.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                         GDSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAK 117
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117 AA;
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nilarity 79.6%;
Conservative
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                                                                                          Craniata; Veri
Sciurognathi;
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               Imanishi-Kari
                                                                                              Vertebrata; Eute
thi; Muridae; Mur
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SON THE TRANSPORT OF THE PROPERTY OF THE PROPE

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MEDIINE=83273707; PubMed=6410398; Goni F., Frangione B.; Goni F., Frangione B.; "Amino acid sequence of the Fv region of a human monoclonal : (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

SEQUENCE

NCBI_TaxID=9606;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region WEA.

update)

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P01763;
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pDB; IIGC; 03-JUN-95.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv;
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"Molecular analysis of spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=77100368; PubMed=401950; Adetugbo K., Milstein C., Secher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 17-136.
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
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D SEGMENT.
JH4 SEGMENT.
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Pred. No. 9.4e-36;
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GO; GO:0003823,
GO; GO:0006955; P:immune
GO:0006955; P:immune
R InterPro; IPR003106; Ig_MHC.
JR InterPro; IPR003506; Ig_v.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
Tmmunoglobulin V region; Glycoprotein; Pyrrolidone carb xylic acid
Tmmunoglobulin V region; Glycoprotein; Pyrrolidone CARBOXYLIC ACI
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P01773;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region BUR.
Homo sapiens (Human)
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SEQUENCE 116 AA; 12730
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding actions
GO; GO:0006955; P:immune response; NAS
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EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLE
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F:antigen binding activity;
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67.2%;
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Pred. No. 4.2e
10; Mismatches
                                                                                         Score 416.5; 1
Pred. No. 4.9e
12; Mismatches
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4.2e-37;
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4.9e-37;
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NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region DOB.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                      Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                               GO; GO:000
InterPro;
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HSSP; PO1772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding act
GO; GO:0003823; P:immune response; NA
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deletion."
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Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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HINGE REGION. THERE ARE
DISULFIDE BONDS.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 immunoglobulin-like
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                                                                                                                        ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS
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01, Created)
01, Last sequence 42, Last anno
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Primates;
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ARE NO LIGHT-HEAVY OR INTER-
                                                                                                                                                                                                                                                                                                                                                                              binding activity; response; NAS.
                                                                                                                                                                                                                                                        MW; 880DDE307C4B2627 CRC64;
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InterPro;

IPR003006;

InterPro; IPR003596;

Ig_v. Ig-like.

InterPro; IPR007110;

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Best Local S
Matches 77
                                            InterPro; IPRO07110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-8tr
DOMAIN
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NON_TER
SEQUENCE
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P01772;
  MOD_RES
DISULFID
                                                                                                                                                                                                                                               PDB; 2FB4; 12-JUL-89.
PDB; 2TG2; 12-JUL-89.
GO; GO:0005576; C:extracellular; NF
GO; GO:0003823; F:antigen binding a
GO; GO:0003825; P:immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND DISULFIDE BONDS.

MEDILINE=83289131; PubMed=6884994;

MEDILINE=83289131; PubMed=6884994;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Home.
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Immunoglobulin V region; Pyrrolidone carboxylic
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81072295; PubMed=7441755;
Marquart M., Deisenhofer J., Huber R., Palm W.;
"Crystallographic refinement and atomic models of the in'
immunoglobulin molecule Kol and its antigen-binding frag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.-JUL-1986 (Rel. 01, Created)
21.-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
15 heavy chain V-III region KOL.
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                                                                                                                                                                                                                                                                                                                                                                                                          J. Mol. Biol. 141:369-391(1980).
-I- SIMILARITY: Contains 1 immunoglobulin-like domain
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                                                                                                                                                                                                                                                                                                                                                                                  A02055; G1HUKL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
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122 AA;
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nilarity 63.1%;
Conservative 2
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13166 MW; 74E5B6959E84100A CRC64;
                                                                         3D-structure; Pyrrolidone carbo ylic
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Pred. No. 1.3e-39;
4; Mismatches 19
                          PYRROLIDONE CARBOXYLIC ACID
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                                                    IG-LIKE
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21-JUL-1986 (Rel. 01, Last sequer
15-SEP-2003 (Rel. 42, Last annot;
7- heavy chain V-III region GAL.
                                                                                                                                                                                                                    MEDLINE-75059123; PubMed-4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metroglobulin Gal.), II: the amino acid sequence of the H-chain (metro
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 9.
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RESULT 3
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AC P01771;
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HSSP; P01772; 2PB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.
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P01770;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region NIE.
21-JUL-1986 (Re)
21-JUL-1986 (Re)
15-SEP-2003 (Re)
15 heavy chain 1
Homo sapiens (H
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PROSITE;
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"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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DOMAIN
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bulin V region; Pyrrolidone carboxylic acid
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                                                                                                                                                           ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCAR-IRDTAMFFAHWGQGTLVTVSS
          (Rel. 01, Created)
(Rel. 01, Last sequen)
(Rel. 42, Last annota
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    (Human)
                                                                                     STANDARD;
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71.7%;
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                             Last sequence update)
Last annotation update)
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Pred. No. 6.2e-41;
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PYRROLIDONE CARBOXYLIC ACID
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RESULT 4
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P01769;
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SMART; SM00406; IGv; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic DOMAIN
1 112 IG-LIKE.
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"Amino acid sequence of the
cryoimmunoglobulin IgG Hil.
Biochemistry 18.553-560(197
                                                                                                                                                                               Florent G., Lehman D., Putnam F.W.; "The switch point in mu heavy chains Biochemistry 13:2482-2498(1974).
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Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Chiu Y.-Y.H., Lopez de Castro J.A.,
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Mammalia; Eutheria;
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003B23; F:antigen binding acti
GO; GO:0006955; P:immune response; NAS
                                                                                      MACROGLOBULIN.
-|- SIMILARITY: Contains 1
PIR; A02052; M3HUGA.
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MEDLINE=74175307; PubMed=4208843;
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Primates;
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119 SS 121 SS	1 QV	atch cal s 89	Homo sapiens (Hum Eukaryota; Metazo Mammalia; Eutheri [1] SEQUENCE Lehman D.W., Putn "Amino acid seque location of a pos proc. Natl. Acad!- MISCELLANEOUS pATIENT WITH -!- SIMILARITY: C PIR, A02051; M3HU HSSP; P01772; 2FB GO; GO:0005576; C GO; GO:00323; F GO; GO:00323; F GO; GO:0047; ig SMART; SM00406; I TRESPROSTE; PS59835; Immunoglobulin V DOMAIN NON_TER 122 AN NON_TER 121 NON_TER 122 NON_TER 12	LT 1 HUMAN HV3G HUMAN P01768; 21-JUL-1986 21-JUL-1986 21-JUL-1986 15-SEP-2003 Ig heavy ch	358.59 358.59 357.55 355.55 355.55 355.55
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Cipacies; Chain V region - human (fragment)
Cipacies; Chor sapiens (man)
Cipate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Cipate: 22-Nov-1999
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Ig heavy chain precursor V region (mu) - human (fragment C; Species: Homo sapiens (man)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text C; Accession: S70442
R; Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, Mol. Immunol. 29, 1363-1373, 1992
A; Title: IgM kappa/lambda EBV human B cell clone: an ear A; Title: new Kappa/lambda EBV human B cell clone: an ear A; A; Cession: S70442; MUID:93024508; PMID:1383695
A; Accession: S70442
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuss: 1-133 <TIM>
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIP:64470)
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A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: A49028
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A;Residues: 1-140 <CUI>
C;Superfamily: immunoglobulin V region; immuno;
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                       QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVLQAPGKGLEWVAVIWYDGSNKYY 60
                                                                                                                                                                                                                  EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHIVGATYFDYWGQGTLVTVSS
                                                                                              ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR-RLTIAAAGNFDYWGQGTLA 119
                                                                                                                                        ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEA----LWGQGTLV 116
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123
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78.3%;
                                                                                                                                                                                                                                                                                                           78.1%;
78.2%;
                                                                                                                                                                                                                                                                                   Score 485.5;
Pred. No. 1.4e
6; Mismatches
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Pred. No. 8.8e-39;
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PMID:1383695
                                                                                                                                                                                                                                                                                                         5.5; DB 2;
. 1.4e-38;
                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                        Indels
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submitted to the EMBL Data Library, October 1994

A; Description: Molecular characterization of natural human anti-Sm autoantil

A; Reference number: $48797

A; Accession: $48797

A; Accession: $48797

A; Accession: $48797

A; Cross-references: EMBL: Z46379; NID: 9587147; PIDN: CAA86512.1; PID: 91340168

A; Cross-references: EMBL: Z46379; NID: 9587147; PIDN: CAA86512.1; PID: 91340168

A; Cross-references: EMBL: Z46379; NID: 9587147; PIDN: CAA86512.1; PID: 91340168

A; Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A; Title: The repertoire of human germline V(H) sequences reveals about fifty

A; Reference number: $26885; MUID: 93021117; PMID: 1404388

A; Accession: $26885; MUID: 93021117; PMID: 1404388
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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S48797
                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021
A;Cross-references: EMBL:Z14177; NTD:g31020; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31701
C;Accession: S31701
C;Accession: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S31701
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 94; Conserv
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Best Local 9
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61 ADSVKGRPAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGTLVTVSS
                                                                                         20
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                                                                                                                       96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKD--LIESN-----IAEALWGQ 112
                                                                                      QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
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75.0%;
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78.3%;
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Pred. No. 2e-38;
8; Mismatches
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Pred. No. 1.5e-38;
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
                                                                                                                                                                                                                                                      R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
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A; Residues: 1-121 < MAR>
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                                                                                                                                                            Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; P;Superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin
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Best Local
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                                                                          Matches
                                                                                                        Query Match
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                                                                                         Similarity
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                          EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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                                                                                                                                             immunoglobulin homology
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78.7%;
                                                                                       79.3%;
80.2%;
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                                                                  Score 493.5; DB 2
Pred. No. 2.3e-39;
6; Mismatches 17
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Pred. No. 2.1e-39;
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                                                                                                      DB 2;
                                                                      17;
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                                                                      Indels
                                                                                                     Length 121;
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RESULT 9

$31117

Ig heavy chain - human

C.Species: Homo sapiens (man)

C.Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C.Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C.Accession: S31117

R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992

A.;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUJD:92111633; PMID:1730252

A.;Accession: S31117

A.;Accession: S31117

A.;Accession: S31104
                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31579
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity opera A;Reference number: S31585
A;Accession: S31579
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                                                                                                                                                                                     A;Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
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Pred. No. 6.1e-39;
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20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.P.
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse the property of the 
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Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: P36005
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C;Species: Homo sanior
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C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Gene: GDB:IGH@; IGHDY1
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A; Residues: 1-119 <SCH>
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;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
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2, 247-251, 1992
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Pred. No. 3.5e-40;
7; Mismatches 14
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                              Score 500; DB 2;
Pred. No. 5.6e-40;
7; Mismatches 17
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Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
C;Accession: G36005
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
A;Cross-references: EMBL:Z31686; vegion; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Steywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A;Title: In vitro assembly of repertoires of antibody chains A;Reference number: $46390; MUID:94254092; PMID:8196048
                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: GB:M34031
C;Genetics:
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G36005
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                                                                                                                                                                   A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                       R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
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               1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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79.7%;
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Pred. No. 1.8e-39;
7; Mismatches 13
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Pred. No. 6.5e-40;
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ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEAL---WGQGTLVT 117

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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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622
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72.9	72.9	72.9	73.0	73.0	73.1	73.1	73.2	73.2	73.3	73.4	73.6	73.7	73.8	74.0	4.0
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ALIGNMENTS

RESULT 1 S31603 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: S31603 R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992 A;Description: Mechanisms that generate human immunoglobulin diversity operate from A;Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;30-113/Domain: immunoglobulin homology <IMM> A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-132 <CUI> 밁 S 밁 श्च A; Reference number: S31585 A; Accession: S31603 Query Match Best Local Similarity Matches 98; Conserv 13 16 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMMWVRQAPGKGLEWVAVISYDGSNKYY 76 1 BVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY ADSVKGRPAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIABALWGQGTLVTVSS 120 ADSVKGRFTISRDNSKNTLYLOMNGLRAEDTAVYYCAKDLF---YYFDYWGQGTLVTVSS Conservative 80.8%; Score 502.5; DB 2 Pred. No. 3.6e-40; 5; Mismatches 14 14; Indels ้ -: Length 132; ω •• Gape 75

Ig heavy chain - human
[c;Species: Homo sapiens (man)
[c;Species: Homo sapiens (man)
[c;Species: Homo sapiens (man)
[c;Species: Homo sapiens (man)
[c;Species: Accession: S31116
[c;Accession: S31116
[c;Accession: S31116
[c] Immunol. 22, 247-251, 1992
[a,Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem a,Reference number: S31104; MUID:92111633; PMID:1730252
[a;Accession: S31116
[a;Accession: Accession: Acce

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FILE REFERENCE: 2183-4080US
CCURRENT APPLICATION NUMBER: 109-05-20
CCURRENT PILLING DATE: 1399-05-20
PRIOR APPLICATION NUMBER: EP 9201593.3
PRIOR PRIOR APPLICATION NUMBER: EP 9201593.3
PRIOR PRIOR OATE: 1399-05-20
PRIOR PILLING DATE: 1399-05-20
PRIOR DATE: 1499-05-20
PRIOR DATE: 1
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                                                                 Sequence 1
Patent No.
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Best Local Similarity
Matches 87; Conserv
                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
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APPLICANT:
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LENGTH: 121 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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FRAGMENT TYPE:
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NAME: DECORTÍ, GÍULÍO A., J
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY.
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STATE: Massa
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INVENTION: Human Antibodies that Bind Human TNFa
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                                                                                 Application US/09540018
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Salfeld, Jochen G.
Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
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Mankovich, John A.
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internal
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Pred. No. 1.4
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-540-018-10
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                                                                                                                                                  RESULT 15
                                                                              ; GENERAL INFORMATION:
                                                                                                sequence 80, Application US/09315926A Patent No. 6498027
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLB OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
                                                         APPLICANT: Es van, Helmuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018
FILING DATE: 31-MARCH-2000
CLASSIFICATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 08-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                           116 LVTVSS 121
                                                                                                                                                                                                                                              121 MVTVSS 126
                                                                                                                                                                                                                                                                               61 ADSVEGRFAVSRDNAKNALYLOMNSLRPEDTAVYYC----TKASYLSTSSSLDNWGQGT 115
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                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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INVENTION: Human Antibodies that Bind Human TNFa
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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White, Michael
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Mankovich, John A.
McGuinness, Brian T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schoenhaut, David
Vaughan, Tristan J.
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                70.3%; Score 467.5; DB 4; 69.0%; Pred. No. 1.4e-37;
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RESULT 12
US-08-599-226-10
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Sequence 10, Application US/08599226
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 residues
                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fUSE5 fusion phage construct
CLONE: V13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB:
FILING DATE: June 28, 1996
CLASSIFICATION: 435
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CURRENT APPLICATION DATA:
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APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/983,607 FILING DATE: April 27, 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 06520-8114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1i1
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: heavy chain
                                                                                         111 PVTVSS 116
                                                                                                                           121 MVTVSS 126
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                                                                                                                                                                                                                                                                    1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                         92; Conservative
                                                                                                                                                             ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                    Connecticut
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                                                                                                                                                                                                                                                                                                     70.5%; Score 469; DB 3; 73.0%; Pred. No. 1.1e-37; ative 11; Mismatches 13
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RESULT 13
US-09-125-098-10
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Best Local Similarity
Matches 87; Conserv
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TRLEPAX: (617)227-10:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                           121 MYTYSS 126
                                                              116 LVTVSS 121
                                                                                                                          61 ADSVEGRPAVSRDNAKNALYLQMNSLRPEDTAVYYC----TKASYLSTSSSLDNWCQGT 115
                                                                                                                                              61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGOGT 120
                                                                                                                                                                                                         1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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Mankovich, John A.
McGuinness, Brian T.
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                                                                                                                                                                                                                                                    70.3%; Score 467.5; DB 3
69.0%; Pred. No. 1.4e-37;
ative 17; Mismatches 17
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                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                      Length 121;
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                                                                                                                                                                                                                                                        Gaps
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Sequence 10, Application US/09125098 Patent No. 6258562 GENERAL INFORMATION: APPLICANT: Salfeld, Jochen G. APPLICANT: Allen, Deborah J.

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Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION UMBER: US/08/652,816A
PILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.8
PRIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9206318.9
PILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 9525004.9
PILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICANT: McClefferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
                     FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
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                                                                                                                                                                                                  FILING DATE: 23-MAY-1996 PRIOR APPLICATION DATA:
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STRANDEDNESS:
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Local Similarity 73.8%;
les 93; Conservative 1
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 amino acida
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MBER: US 08/244,597
01-JUN-1994
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Pred. No. 4.7e-38;
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CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
SEQ ID NO 75
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
US-08-918-148-75
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Best Local S
Matches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 75,
Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Adams, Camellia APPLICANT: W. APPLICANT: Carter, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acid
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                         Local Similarity
115
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                              121 MVTVSS 126
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                                                                                     61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
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                                                                                                                                                                                                     ch 70.7%; Score 470; DB 4; Length 245;
l Similarity 73.8%; Pred. No. 1.7e-37;
93; Conservative 12; Mismatches 13; Indels
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                                                                                                                                                      1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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MVTVSS 120
                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-----RWSGEDAFDIWGQGT
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                                                                                                                                                                                                       Gaps
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US-08-983-607-28

Sequence 28, Application Patent No. 6140470 GENERAL INFORMATION:

US/08983607

COUNTRY:

D.C.

TRY: United States 20037-3202

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US-08-665-202-30
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TELEX: 6491103
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
PILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide -07-942-245-24
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
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MEDIUM TYPE: Ploppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING THE THE TOTAL OF T
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APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                       FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
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NAME: Hunter, Tom
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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                     38,498
     02307B-061410
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/09/315,574
PILING DATE: 20-MAY-99
CLASSIFICATION: 530
CLASSIFICATION: 530
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LENGTH: 123 amino acid
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
                                                                                                                                        APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 123 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Four Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 LVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 MVTVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 73.8
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09315574
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73.6%; Pred. No. 4.7e-38;
tive 11; Mismatches 19
                                                                                             02307E-061411
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                                                                                                                                                                                                                 RESULT 5
                                                                                        GENERAL INFORMATION:
APPLICANT: Salfeld
APPLICANT: Allen,
APPLICANT: Hoogen
                                                                                                                                                        Sequence 2, Application US/09540018
Patent No. 6509015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 73.0 Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE DOCKET NUMBER: BEI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227,7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TBLBFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
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PRIOR APPLICATION NUMBER:
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ADDRESSEE: LAHIVE & COCKPIELD
STREET: 60 State Street, suite 510
                                                         APPLICANT:
                                                                          APPLICANT:
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TITLE OF INVENTION: Human Antibodies that Bind Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                  LVTVSS 121
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Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T.
Roberts, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                    Hoogenboom, Hendricus
Kaymakcalan, Zehra
                                                                                                        Allen,
                                                                                                                         Salfeld,
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                                                                                                       Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.2%; Score 486.5; DB 3; 73.0%; Pred. No. 2.2e-39; tive 14; Mismatches 15;
                                                                                                                         Jochen G.
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                                                                                          R.J.M.
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US-07-942-245-24
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                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                    APPLICANT: E
APPLICANT: E
APPLICANT: E
APPLICANT: E
APPLICANT: C
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540 CLASSIPTOTE
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PILING DATE: 31-MAPOTE
CLASSIPTOTE

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PILING DATE: 31-MAPOTE
PILING DATE: 31-MAPO
                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BI-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
APPLICATION NUMBER: US/01
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
PRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palane
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                      ADDRESSEB: Sughrue, Mion, Zinn, N
STREET: 2100 Pensylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/07942245
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60 State Street, suite 510
                                                                                                                                                                                                                       GUILD
                                                                                                                                                                                                                                                                        REES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 227-5941
                                                                                                                                                                                                                                           ROGUSKA,
                                                                                                                                                                                                                                                                                                 SEARLE,
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                                                                                                                                                                                                                                                                                                                                        PEDERSEN,
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internal
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SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
522
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73.0%;
                                                                                                                                                                                                                 Stephen M.J.
Anthony R.
Michael A.
Braydon C.
                                                                                                                                                                                                                                                                                                                                        Jan T.
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                                Zinn, Macpeak & Seas
venue, N.W.
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121 MVTVSS 126

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RESULT 2
US-08-958-201-8
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/0
PILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
                                                        Sequence 2, Application US/08599226
Patent No. 6090382
GENERAL INFORMATION:
APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-958-201-8
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APPLICANT: Williams, Andrew J
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: 2D
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                                            APPLICANT:
                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 76.4%; Score 508; DB 2; Length 120; Similarity 76.2%; Pred. No. 1.9e-41; 96; Conservative 14; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARPL----YPKG-TQYDFWGQGT
                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAPDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Marshall O'Toole Gerstein Murray & Bo
6300 Sears Tower, 233 South Wacker Drive
Allen, Deborah J.
Hoogenboom, Hendricus I
Kaymakcalan, Zehra
Labkoveky, Boris
Mankovich, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-599-226-2
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US-09-125-098-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local :
Matches 9
                                                                GENERAL INFORMATION:
APPLICANT: Salield
APPLICANT: Holgenb
APPLICANT: Hoogenb
APPLICANT: Kaymakc
                                                                                                                                                      Sequence 2, Applic Patent No. 6258562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/599,226
FILING DATE: 08-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMB: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: BBI-043
REFERENCE/DOCKET NUMBER: BBI-043
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT:
APPLICANT:
                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
                 APPLICANT:
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                             116 LVTVSS 121
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                                                                                                                                                                                                                                                                                                                                 61 ADSVEGRETISRDNAKNSLYLQMNSLRAEDTAVYYCA----KVSYLSTASSLDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                  61
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92; Conserv
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                                                                                                                                                                       Application US/09125098
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Schoenhaut, Dav
            Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T.
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                                                                  Allen, Deboran v.
Hoogenboom, Hendricus R.J.M.
Zehra
Roberts, Andrew J.
                                                                                                                      Salfeld,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.2%; Score 486.5; DB 3 73.0%; Pred. No. 2.2e-39;
                                                                                                                        Jochen
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
    455.55
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seq length: 2000000000
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                December 30, 2003, 10:47:45; Search time 12.7945 Seconds (without alignments) 416.677 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                      QVQLVQSGGGLVQPGKSLRL.....RRGVAAFDIWGQGTMVTVSS
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Copyright (c) 1993 - 2003 Compugen Ltd.
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131
121
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248
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119
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SUMMARIES
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Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl.
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452.5 68.0 125 3 US-09-240-274-151 452 68.0 120 2 US-07-934-373C-4 452 68.0 120 3 US-08-146-206C-4 452 68.0 120 4 US-08-146-206C-4 452 68.0 120 4 US-08-146-206C-4 451.5 67.9 127 3 US-09-240-274-27 451.5 67.9 249 4 US-10-039-785-53 451.5 67.7 125 2 PCT US-31-10555-1 450.5 67.7 125 5 PCT US-31-1055-1 450.5 67.7 245 4 US-08-918-148-78 449 67.5 120 4 US-08-918-148-78 449 67.5 120 4 US-09-025-7698-38 449 67.5 120 4 US-09-025-7698-63 449 67.5 120 4 US-09-025-7698-63 449 67.5 281 4 US-09-25-7698-18 449 67.5 281 4 US-09-25-7698-18 449 67.5 120 4 US-09-025-7698-18 449 67.5 120 4 US-09-025-7698-18	45	44	43	42	41	40	39	38	37	36	35	4	ω W	32	u L	30	29	
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3 US-09-240-274-151 2 US-07-934-373C-4 2 US-08-146-206C-4 4 US-08-146-206C-4 4 US-08-240-274-27 4 US-09-240-274-27 4 US-10-039-185-53 3 US-09-983-607-32 2 US-08-983-10555-1 5 PCT-US93-10555-1 4 US-08-918-148-78 4 US-08-918-148-78 4 US-09-25-7698-38 4 US-09-025-7698-63 1 US-09-025-7698-178 4 US-09-025-7698-178	117	281	128	120	120	123	245	125	125	140	249	127	124	120	120	120	125	
US-09-240-274-151 US-08-437-642B-4 US-08-437-642B-4 US-08-146-206C-4 US-09-240-274-4 US-09-240-274-7 US-10-039-785-53 US-08-983-607-32 US-08-98-1198-7 US-08-98-1198-7 US-09-025-7698-63 US-09-025-7698-63 US-09-025-7698-17 US-09-025-7698-17	_	4	w	4	4	4	4	v	N	w	4.	w	w	4	w	N	w	
	US-07-942-245-36	US-09-025-769B-178	US-09-240-274-1	US-09-025-769B-63	US-09-025-769B-38	US-09-560-198A-2	US-08-918-148-78	PCT-US93-10555-1	US-08-428-197-1	US-08-983-607-32	US-10-039-785-53	US-09-240-274-27	US-09-240-274-4	US-08-146-206C-4	US-08-437-642B-4	US-07-934-373C-4	US-09-240-274-151	
	36,	178	1,	63,	38,	2	78,	1,	1	32,		27,	4	٠,	4.	4	151	
363, 278, 278, 278, 278, 278, 278, 278, 278	36, App.	178, App	Appl:	Appl	Appl	App1:	78, Appl	App1	Appli	Appl	App	Appl	Appli	App1	Appli	Appli	, Ap	;

ALIGNMENTS

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                                                                                                                                                              Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 60/
APPLICATION NUMBER: US 60/
PILLING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application Patent No. 5977319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                                                                                                                                                                                                                    TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: 2Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
                                                                                                                                                                                                                                                                                                             LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
61
                                       61
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), Application US/08958201
5977319
                       ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALLYYCALPYINSSNYRRGVAAFDIWGOGT
                                                                                EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                       QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARPL----YPKG-TQYDFWGQGT
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                76.5%; Score 509; DB 2; 76.2%; Pred. No. 1.5e-41; tive 14; Mismatches 10
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                                                                                                                                                                10;
                                                                                                                                                                                                       Length 120;
                                                                                                                                                                  Indels
                                                                                                                                                                6
                                                                                                                                                                Gaps
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Sequence 76, Application US/09972656

; Bedlication No. US20030099647A1

; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
APPLICANT: Deshpande, Rajendra
ITILE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PACENTIN Ver. 2.0
SEQ ID NO 1324
US-09-880-748-1324
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US-09-972-656-76
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                                                                                                                                                                                                                                                        Query Match 72.6%; Score 483; DB 11; Length 227; Best Local Similarity 73.0%; Pred. No. 1.3e-39; Matches 92; Conservative 17; Mismatches 15; Indels
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                                          121 MVTVSS 126
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                                                                                  13
                                                                                                               61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                                                     1 QVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
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  MVTVSS 124
                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASDLVLTMTSRR--AAFDIWGQGT 118
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Search completed: December 30, 2003, 11:45:24 Job time : 28.0219 secs

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APPLICANT: Fischkoff, Steven
APPLICANT: Chartash, Elliot
TITLE OF INVENTION: Use of TNP-a Antibodies and Anc
FILE REFERENCE: BBI-186
CURRENT APPLICATION NUMBER: US/10/133,715
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LEMGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: CTUEN UNDERFORMETON COLORS
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US-10-133-715-2
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Best Local Similarity
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                                                                                        Matches
                                                                                                                              Query Match
                                                                                                                                                                            OTHER INFORMATION: D2E7 heavy chain variable region -10-133-715-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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PILING DATE: 07-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                        l Similarity
92; Conserv
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                      QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHIDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCA----KVSYLSTASSLDYWGQGT 115
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TYPE: amino acid
TYPE: linear
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FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 60/031,476
FILING DATE: 25-NOV-1996
                                                                                        Conservative
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                                                                                                        73.2%;
73.0%;
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73.0%; Pred. No. 2.8e-40;
tive 14; Mismatches 15
                                                                                   Score 486.5; DB 12; Length 121;
Pred. No. 2.8e-40;
4; Mismatches 15; Indels 5;
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APPLICANT: WILTON, Alison, J.
TITLE OF INVENTION: Human Antibodies That Bind Human
FILE OF INVENTION: TUPAlpha
FILE REFERENCE: BBI-043CPACN2
CURRENT APPLICATION NUMBER: US/10/302,356A
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 09/540018
PRIOR APPLICATION NUMBER: 08/590226
PRIOR APPLICATION NUMBER: 08/599226
PRIOR APPLICATION NUMBER: 08/599226
PRIOR FILING DATE: 1996-02-09
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                        Sequence 1324, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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US-10-302-356A-2
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Publication No. US20030219438A1
GENERAL INFORMATION:
APPLICANT: SALERLD, Jochen G.
APPLICANT: ALLEN, Deborah J.
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APPLICANT:
APPLICANT:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Mutated human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              92; Conservative
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MANKOVICH, John A.
MCGUINNESS, Brian T.
ROBERTS, Andrew J.
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KAYMAKCALAN, Zehra
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WHITE, Michael
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SCHOENHAUT, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                73.2%; Score 486.5; DB 1 73.0%; Pred. No. 2.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
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                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-59
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LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 59
LENGTH: 227
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                                                                                                                                                                        Query Match
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PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 154
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CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Deshpande, Rajendra APPLICANT: Hitz, Anna
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING
FILE REFERENCE: A-633A
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APPLICANT: Hitz, Anna
APPLICANT: Boyle, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Score 488.5; DB 1
Local Similarity 73.8%; Pred. No. 1.8e-40;
198 93; Conservative 13; Mismatches 17
                                                                                                                                                      Local
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                                                                                                                               Similarity
93; Conserv
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                                                                 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGBGLEWVSGVTWSGTTIGF 60
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Sullivan, John
                                            EVOLLESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGRIGY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hitz, Anna
ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                                                                  Conservative
                                                                                                                             73.5%; Score 488.5; DB 11; Length 227; 73.8%; Pred. No. 3.6e-40; tive 13; Mismatches 17; Indels 3;
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: PATENTING DATE: 2.0
SEQ ID NO 1416
LENGTH: 252
TYPE: PRT
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US-09-880-748-1416
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US-09-801-185A-2
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1416, Application US/09880748 Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09801185A publication No. US20030092059A1 PUBLICANTION:
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 73.3%; Score 487.5; DB 11; Length Local Similarity 71.2%; Pred. No. 5.1e-40; neb 94; Conservative 14; Mismatches 15; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LVIVSS 124
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                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                         STREET: 28 State Street
                                                                                                                                       COUNTRY: USA
                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                              ADDRESSEE:
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       Version #1.25
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLy
FILE REFERENCE: PF523
CURRENT APPLICATION UNMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/210,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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US-09-880-748-1427
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US-09-880-748-1427
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1427
LENGTH: 254
TYPE: PRT
                                                                                                                                      Sequence 6, Application US/10447331
Publication No. US20030219434A1
GENERAL INFORMATION:
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Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
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Best Local
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FILE REFERENCE: GENENT.122A
CURRENT APPLICATION NUMBER: US/10/447,331
CURRENT FILING DATE: 2003-05-28
                                                        APPLICANT: Carter, Paul J.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: DIAGNOSIS
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Similarity 71.9%;
92; Conservative 1
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;; Pred. No. 2.3e-40;
16; Mismatches 18;
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                                                                                 CANCER THERAPY
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Best Local Similarity
Thes 95; Conserve
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PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 922
FIRMSTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 122
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PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/122262
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                         Local
                                                              108 RGVAAFDIWGQGTMVTVSS 126
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                                                                                                                             61 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCA------
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                                                                                                                                                                                                         1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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                                                                                                                                                                                                                                                                                     73.5%; Score 489; DB 11; Length 251; 67.6%; Pred. No. 3.6e-40;
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PRIOR FILING DATE: 2000-02-03
PRIOR PPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 88
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 88,
Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50, Application US/08779457 Publication No. US20020193571A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reefe, Theress
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LaRosa, Gregory J. APPLICANT: Horvath, Christop
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kin
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
**NORPRESER: Caractech Inc.
**TOTRESER: Caractech
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                           ZIP: 94080
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
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Newman, Walter
Jones, S. Tarran
                                                                                                                                                                                                         California
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RESULT 4
US-09-880-748-1926
JS-09-880-748-1926
JS-09-80-748-1926
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                                                                            US-09-880-748-1926
                                                                                                                                                                                                                                                                                                                             CURRENT PILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 00/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/667
PILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: 08/585
PILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PF523
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SOPTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/667197
                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ADSVXGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
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97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
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DB 11; Length 245;
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Query Match

75.7%;

Score 503.5;

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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                             489.5
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
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Match Length DB
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    GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
US-09-880-748-1926

US-09-880-748-1427

US-10-447-331-6

US-09-880-748-92

US-09-880-748-92

US-09-791-153A-66

US-09-880-748-1416

US-09-801-185A-2

US-09-801-185A-2

US-10-133-715-2

US-10-133-715-2

US-10-302-356A-2

US-09-880-748-1324

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               Sequence 65, Appl
Sequence 80, Appl
Sequence 50, Appl
Sequence 1926, Ap
Sequence 1427, Ap
Sequence 6, Appl
Sequence 6, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 2, Appl
                                                                                                                                                                                                                                                                                                                                     Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
467.5	467.5	467.5	467.5	467.5	467.5	467.5	467.5	468	468	468	469	469	469	469	469.5	469.5	471	J	472.5	472.5	•		473	474	475	475	476	481	483
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244	244	244	225	121	121	121	119	367	248	136	249	122	122	116	259	121	239	239	296	296	290	290	239	239	239	128	248	251	251
11	11	11	11	12	12	11	15	12	11	12	11	15	15	15	11	12	11	11	12	12	12	12	11	11	11	15	11	11	11
-09-880-748-	-09-880-	-09-88	-09-453-234-6	-10-302-	-10-13	-09-801	-644C-	-10-045-		-10-045-	9-880-	-10-269	-10-269-805-	US-10-091-300-24	-09-880	-10-010-	US-09-880-748-937	-09-880-748-	US-09-949-039-75	-09-969-	9	-09-969-7480	US-09-880-748-2022	US-09-880-748-2015	-09-880-748-203	US-10-269-805-29	US-09-880-748-1890	-09-880-748-154	-09-880-748-132
e 28	e 164,	e 82,	e 68,	e 10,	e 10,	e 10,	Φ	e 453, A	e 1974,	e 487, 1	e 110	<u></u>	7,	Sequence 24, App	e 1664,	æ	e 937, F	e 2023	e 75,	e 12,	e 2, App	e 2, App	e 202	e 2015,	e 2038,	e 29, Ap	e 1890,	e 15	e 1320,

ALIGNMENTS

S ঠ ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-791-153A-65 US-09-791-153A-65
; Sequence 65, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION: 吊 맑 밁 S CURRENT APPLICATION NUMBER: US/09/791,153A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/511,139
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin version 3.0
SEQ ID NO 65
LENGTH: 132 Query Match 77.0%; Score 512; DB 11; Best Local Similarity 75:0%; Pred. No. 9.9e-43; Matches 99; Conservative 12; Mismatches 15; APPLICANT: Deshpande, Rajendra
APPLICANT: Hitz, Anna
APPLICANT: Boyle, William
APPLICANT: Boyle, William
APPLICANT: Sullivan, John
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
FILE REFERENCE: A-633A 121 115 IWGQGTMVTVSS 126 61 ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAA-----FD 114 61 1 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY ADSVKGRPTISRDNAKNSLYLQMNSLRAEDTALYYCAKDGYSSGWYGIAVAGVQWLVYFD Length 132; Indels 6 Gaps 60 60

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to continibit the expression and activity of BLyS. The antibodies bind to BLyS in the solution of BLyS in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and conditioney (e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (eyc.) and activity such as cancer, immune, and autoimmune disorders and conditioney (e.g. common variable immunodeficiency (CVID) and conditioned immunodeficiency (eyc.) and activity such as cancer, immune (AIDS)). ABP43990-ABP47228 represent confirming and invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the invancional fragments of the antibodies described in the method confirming the firming t
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Best Local S
Matches 92
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Region
                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                          LU20; human; antibody; VH domain; decay accelerating factor; DAF; phage display; subtractive panning; lung cancer; lung carcinoma; lung adenocarcinoma; therapy; diagnosis.
                                                                                            Region
                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human anti-DAF antibody LU20 heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNSKNTLYLQWNSLRAEDTAVYYCTRGYEYYDILTGYNELGAFDIWGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAQLVQSGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWYSGISWNSGSIGY
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                                                                                                                                                               /note= "hypervariable loop 50..66
                                                                                               /note= "complementarity determining region
53..56
                                                                  /note=
                                                                                                                                                                                                                                                       /label= CDRI
                                                                                                                                          /label= CDRII
                                                                                                                                                                                                                               /note= "complementarity determining
                            'label= CDRIII
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"complementarity determining region
                                                                     "hypervariable loop residues
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                                                                                                                                                                                    region"
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Making antibodies (e.g. anti-decay accelerating factor antibody) for diagnosing or treating e.g. lung cancer comprises identifying an antigen that is differentially expressed on the surface of two or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1999;
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TLVTVSS
                                     TMVTVSS 126
                                                                                               ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSS-NYRRGVAAFDIWGQG 119
                                                                                                                                                    EVOLVETGGGLVQPGRSLRLSCAASGFTFEDYGMHWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                                          QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                           ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCARDAPSGSYGY----
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                                                                                                                                                                                                                           73.5%; Score 489; DB 21; 74.8%; Pred. No. 2.3e-39; tive 12; Mismatches 14.
                                                                                                                                                                                                                                                               Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (BST) sequences, corresponding to human secreted proteins. AAY64651 to AAY65438 represent the BST-related proteins corresponding to AAZ42265 AAZ43052. The 5' ESTs can be used for producing secreted human gene
                                                                                                                                                                                 N-PSDB; AAZ42351.
                                                                                                                                                                                                                                     Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                            09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                           09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; identification.
                                                                                          Claim 3;
                                                                                                                          Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                  2000-038446/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST related polypeptide SEQ ID NO:898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTLVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADSVRGRETISRDNAKNSLYLOMNSLRAEDTATYYCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                      Page 627; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                        98US-0057719.
98US-0069047.
                                                                                                                                                                                                                                                                                                                                                             99WO-IB00712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.7%; Score 503.5; DB 75.2%; Pred. No. 2e-40;
                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                     Giordano
                                                                                                                          sequence tag sequences used in and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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ABP45416
ID ABP4
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc products. They can be used to identify and isolate 5' untranslated cc regions (UTRs) and upstream regulatory regions which control the clocation, development stage, rate, and quantity of protein synthesis, as cc well as stability of mRNA. The ESTs are also useful as probes for cc chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in cdiagnostic procedures to identify individuals having genetic diseases cc resulting from abnormal gene expression. The products may also be used in cc used for directing extracellular secretion of a polypeptide can be compared to the proteins encoded by the ESTs can be compared to the proteins encoded by the ESTs can be contained a variety of human conditions. Secreted proteins have cc raluable. AAZ42249 to AAZ4264 and AAX64644 to AAX64650 represent cx sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                        BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                             16-JUN-2000; 2000US-212210P: 17-OCT-2000; 2000US-240816P: 16-MAR-2001; 2001US-276248P: 21-MAR-2001; 2001US-277379P: 25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BLyS binding scFv SEQ ID 1427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
WPI; 2002-114799/15
                                Ruben SM,
                                                                                                                                                                                                                15-JUN-2001; 2001WO-US19110
                                                                                                                                                                                                                                               10-JAN-2002.
                                                                                                                                                                                                                                                                               WO200202641-A1.
                                                                                                                                                                                                                                                                                                                                            common variable immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP45416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP45416 standard; Protein; 254
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                               HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCA-----LPYINSSNYRRGVA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFDIWGQGTMVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMDVWGQGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADSVKGRPTISRDNAKNSLYLOMNSLRTEDTAFYFCAKARGLFSDTWPYXH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGITWNSGXIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AA;
                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.1%; Score 492.5; DB 2
70.4%; Pred. No. 1.3e-39;
tive 11; Mismatches 12
                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                  TECHNOLOGY.
                                Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                   Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 149;
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ARESULT 11
AAW24063
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AAW24063
AC AAW24
AC AAWA4
AC AAWA
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The present sequence is an agonist antibody clone to the human WSX receptor, which can be used to identify and purify ligands and cativators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to contake in an obese mammal. WSX receptor ligands can be used to reputation or differentiation of lymphoid, myeloid or crythroid blood cell lineages. This is useful when a mammal, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; WSX receptor; clone #17; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; arteriosclerosis; Type I diabetes; polycystic ovarian disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSX receptor and related antibodies and ligands - used products for diagnosis and therapy, e.g. for improving haematopoiesis or for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW24063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 14; Pages 122-123; 219pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-372864/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9725425-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human WSX receptor agonist antibody clone #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1998
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96US-0585005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US00325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.0%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chiang NY,
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Pred. No. 5.8e-41;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, in resistance, hypercholesterolaemia, hypertriglyceridaemia, and cholelithiasis.
                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2000; 2000US-212210P:
17-OCT-2000; 2000US-240816P:
16-MAR-2001; 2001US-276248P:
21-MAR-2001; 2001US-277379P:
25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BLyS binding
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systemic lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                          CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
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                                                                                                                                                                                   2699-2700; 3148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erythematosus; rheumatoid arthritis; CVID; A:
immunodeficiency; acquired immunodeficiency
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77.0%;
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Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                    Vaughan T,
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have

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antirheumatic

immunosuppressive, immunost: lc and antiAIDS activity and

can be used in vaccines

24-MAY-2002

(firet

entry)

16-OCT-2001

(first entry

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RESULT 10
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                         fused to a fluorescent protein. The method comprises constructing a scrv antibody library composed of phage clones expressing scrv antibody on their surface, screening this library with an antigen, extracting the gene for scrv antibody from the selected phage clones and inserting it into an expression vector that expresses the gene fused to a fluorescent protein. Also described are: (1) a fusion protein comprising the scrv antibody fused to a fluorescent protein; (2) immunological assays using the fusion protein of (1); (3) an expression vector encoding the fusion protein of (1), and (4) a kit for producing the fusion protein of (1). The fusion protein can be used in immunoassays and immunostaining.

Immunological assays using the fusion protein do not require a secondary or tertiary antibody. Direct intracellular and even in vivo assays are possible. ABL49521 to ABL49591 and ABB06276 to ABB06276 represent
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing scFv antibody fused to a fluorescent protein, useful for immunoassay and immunostaining, comprises expressing a scFV gene (extracted from selected clones) fused to a fluorescent protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-098058/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Construction, scFV antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VH3-4 amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for producing a scFv antibody fused to a fluorescent protein. The method comprises constructing a sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunological assay.
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                                                AAE07025 standard; Protein; 119 AA
                                                                                                                                    115
                                                                                                                                                                     121 MVTVSS
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                                                                                                                                                                                                                                                                                           1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF :||||:||||||||::|: :||: :||:
                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 82-83; 105pp; Japanese
                                                                                                                                                                                                                                                                         EVOLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                                                                        ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKGPSGSFD-----
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protein; antigen binding; immunostaining; fusion protein;
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                in the exemplification of the present invention
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                           Score 508; DB 23;
Pred. No. 3.4e-41;
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                                                                                                                                                                                                                                                                                                                                               Mismatches
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AAE07025;

Sequence

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CC The patent discloses a numanistic anticopy of the patent discloses a numanistic anticopy of the control of the patent discloses a numanistic anticopy for CC-chemokine receptor 2 CC (CCR2), comprising an antigen binding region of non-human origin. The cand at least a portion of an immunoglobulin of human origin. The comprising are useful for inhibiting the interaction of CC humanised antibodies are useful for inhibiting the interaction of CC acell expressing CCR2. They are useful for inhibiting or treating CCR leukocyte trafficking, for treating CCR2-mediated disorders such as reumatoid CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis, CC and for inhibiting restenosis. They are useful in therapy or disgnosis, CC and for inhibiting restenosis. They are useful in therapy or disgnosis, CC and for the manufacture of a medicament for treating CCR-2 mediated CC disease. They are also useful for treating allergy, anaphylaxis, CC mediated allergic reaction, shock, stenosis, allograft rejection, CC disease, asthma, inflammatory glomerulopathies, acquired cintervention, including angioplasty and/or stent placement in a mammal. CC Humanised antibodies are also useful for inhibiting narrowing of the CC used and antibodies are also useful for inhibiting narrowing of the CC a vessel in a mammal, preferably associated with vascular intervention. The present sequence is human heavy chain variable (VH) region, UBI-24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple scierosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 173; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488888/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larosa GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2001; 2001WO-US03537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157226-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              discloses a humanised antibody or its antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR2
/note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newman W,
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                                                                                                                                                                                                                                               This sequence represents a VH domain complementarity determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0x10^-8M for estradiol, and a dissociation constant of at least 500-fold higher for the steroid hormones selected from estriol, testosterone, dihydrorestosterone, progesterone, estriol-3-sulphate and estriol 3-beta-di-glucuronide, where the polypeptide comprises an antibody VH domain. The sbps can be used in an immunoassay for determining the presence or absence of estradiol in a sample. They can be used for monitoring estradiol levels, e.g. during the menstrual cycle, in hormone replacement therapy and for disgnosing ostrogen secreting them of the sbps can provide for disgnosing ostrogen secreting of the standard process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estradiol; complementarity determining region; CDR; estriol-3-sulphate; antibody antigen binding domain; steroid hormone; estriol; testosterone; dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide; menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacem
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy and for diagnosing oestrogen secreting tumours
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                           ADSVXGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAPDIWGQGT 120
                                                                                                    QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Column 23-24; 26pp;
 MVTVSS 126
                                                                                    RVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
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76.2%;
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  ABB06276;
                                                       ABB06276 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing gene libraries and antibody libraries, involves selecting light chain that binds to a heavy chain product to produce a function formation, and producing a gene library of the light chain variable
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Okuno Y, Sł
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-2001
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Pred. No. 3.4e-41;
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                                                                                                                                                                                                                                                       This invention describes novel nucleic acid fragments that encode human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane protein, GPIIb/IIIa. The products of the invention are used for diagnosis (including monitoring and determining predisposition), prevention and treatment of autoimmune thrombocytopaenic purpura (AITP) and also for modulating binding of fibrinogen to thrombocytes (particularly to dissolve thrombi and/or prevent their formation, e.g. in cases of cardiac infarction or pulmonary embolism). Unlike murine antibodies, human antibodies (hab) do not induce adverse side effects
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                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 58-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human autoantibodies against platelet glycoprotein IIb/IIIa - used for diagnosis, treatment and p of autoimmune thrombocytopaenic purpura and for modulation fibrinogen binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-1998;
06-JUN-1997;
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                     ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINS---SNYRRGVAAFDIWGQ
                                                                  ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVKDMGSSVVATYN----AFDIWGQ
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                                                                                                                                       Conservative
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97DE-1023904.
97DE-1055227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
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1.8e-41;
hes 12;
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Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                     testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate estriol 3-beta-di-glucuronide, where the polypeptide comprises an antibody VH domain. The sbps can be used in an immunoassay for determining the presence or absence of estradiol in a sample. They could for monitoring estradiol levels, e.g. during the menstrual cycl hormone replacement therapy and for diagnosing oestrogen secreting tumours. The sbps can provide for discrimination between estradiol a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a VH domain complementarity determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0x10^8M for estradiol, and a dissociation constant of at least 500-fold higher for the steroid hormones selected from estriol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacement therapy and for diagnosing oestrogen secreting tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody antigen binding domain; steroid hormone; estriol; testosterone;
dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Estradiol, complementarity determining reantibody antigen binding domain; steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VH domain CDR of anti-estradiol antibody.
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 25-26; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                other related steroids.
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                                                                                                           EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                                                                                                                                 QVQLVQSGGGLVQPGKSLRLSCAASGFTEGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
||||:||||||||::|: :||: :||:
                                        ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
     ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARPL----
                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                                                Conservative
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Pred. No. 2.7e-41;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                       20;
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Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cell line 3D6 (87110301; Porton Down) produced the product of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant protein which binds to complex vire HIV-1 - contains variable region of antibody decell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavy chain of 3D6 anti-HIV antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR20057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR20057 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ20068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-DEC-1991
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/label= Framework_1
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Pred. No. 1.3e-41;
1; Mismatches 14
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-1 gp41 and also
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ker. The
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ved from 3D6
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RESULT 5
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Best Local S
Matches 99
                                     Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis; blood platelet membrane protein; predisposition; prevention; treatment; autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombi; thrombocyte; cardiac infarction; pulmonary embolism; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The variable region of the heavy chain is used in a recombinant protein with the variable region from the kappa light chain of 3D6, the two V regions being joined by a linker. The recombinant protein binds to HIV gp160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D cell line, used for detecting HIV-1 antigen
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                                                                                                     Human anti-GPIIb/IIIa
                                                                                                                               07-SEP-1999
                                                                                                                                                                                 AAW90286 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ20067 and AAQ20068.
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              Homo
                                                                                                                                                       AAW90286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-007468/01.
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                                                                                                                                                                                                                                                                                                                 ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYC--ALPYINSSNYRRGVAAFDIWGQ
                                                                                                                                                                                                                                                                                                                                                      EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGY
                                                                                                                                                                                                                                                GTMVTVSS 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 AA;
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                                                                                                                               (first entry)
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86..117
/label= Framework_3
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                                                                                                                                                                                  Protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                        77.6%; Score 516; DB 13; 77.3%; Pred. No. 2.6e-41; ive 11; Mismatches 14
                                                                                                    antibody heavy chain protein from phagemid AI-X40
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; heavy chain; hemophilia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human FVIII antibody heavy chain variable region B18 protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY50967 standard;
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                                                                                                  New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
                                                                                                                                                                                                                                                                                         07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the
                                                                                                                                                                                                                                                             08-MAY-1998;
                                                                                                                                                                                                                                                                                                                    18-NOV-1999
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                                                                        Example 8; Fig 9C; 61pp; English.
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                                                                                                                                                                                                       Score 665; DB 21;
Pred. No. 3.1e-56;
Mismatches 0;
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                                                   .abel= CDR_3_light_chain
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:l= Framework_2_light_chain
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                                                                                                 _Framework_3_light_chain
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Pred. No. 3.1e-56;
Mismatches 0;
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Maximum DB
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Maximum Match 10
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and is der
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493.415 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAY43254
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Human PVIII antibo
Human FVIII antibo
Recombinant sc3D6
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Human anti-GPIIb/I
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VH domain CDR of a
Amino acid sequenc
VH3-4 amino acid s
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472	472.5	•	472.5	•	472.5	472.5	473	474	474	475	476	476	479	480	480.5	481	481	481	483	486	486.5	486.5	487	487.5	8	487.5	8	38	489	489	_	92	8	505.5	ò
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239	519	296	291	290	123	117	239	239	117	239	248	120	118	118	121	251	131	127	251	246	121	121	118	252	248	146	126	227	251	122	254	149	245	241	119
23	23	23	23	24	18	23	23	23	15	23	23	22	22	22	17	23	23	23	23	23	24	18	22	23	22	24	22	22	23	21	23	21	23	18	22
ABP46012	19	ABG60637	ABG60632	ABP55318	AAW08582	AA015187	ABP46011	ABP46004	AAR52053	ABP46027	ABP45879	AAU02501	AAU02593	AAU02605	AAR88848	ABP45531	ABG76547	ABG76513	ABP45309	ABP45313	AAO16460	56	AAU02560	ABP45405	AAG65590	ABJ36923	AAU02623	AAU08385	ABP44911	AAY96065	54	AAY64737	591	2406	AAE07025
Human BLyS binding	Human secreted pro	Immunoglobulin rel	Immunoglobulin rel	Pelb/5AF/myc/6His	Human antibody C4.	Dig3 antibody heav		Human BLyS binding		Human BLyS binding	Human BLyS binding	Anti-adipocyte mon	Anti-adipocyte mon		Human antibody IM9	Human BLyS binding	HCV E1 antigen mon	HCV E1 antigen mon	Human BLyS binding	Human BLyS binding	Human anti-TNF-alp	Anti-TNF-alpha ant	Anti-adipocyte mon	Human BLyS binding	Anti-hEDRF antibod	CD40 mono	adipo	Anti-OPGbp antibod	Human BLyS binding	Human anti	. Human BLyS binding	Human 5' EST relat	BLyS	Human WSX receptor	Human heavy chain

ALIGNMENTS

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RESULT 1
AAY50961
ID AAY5
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hemophilia A; scFv; A3-C1.
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                                                                                                                                                                                               WPI; 2000-053102/04.
                                                                                                                                                                                                                                                                                  Voorberg JJ, Van Den Brink EN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1998;
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New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -

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LVTVSS 140 MVIVSS

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Q9UL72
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Best Local Similarity
Matches 88; Conserv
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Q9UL72;
Q1-MAY-2000
                                                                                                                                                 Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eur leostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AP035042; AAD56278.1; -.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
TISSUE-Mammary gland;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo J
                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 18
NON_TER 118 118
SEQUENCE 118 AA; 12872 MW;
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SMART; SM00406; IGv; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
[1]
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAFYYCA----RDRFGEFLFDYWGQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
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Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 419; DB 4;
Pred. No. 4.2e-35;
L1; Mismatches 19
                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalis N.N.,
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                                   Suzuki Y.,
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RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human CNA sequencing project.";
RT "NEDO human CNA sequencing project.";
RT EMBL, AKO27379; BAB55072.1; -.
DR EMBL, AKO27379; BAB55072.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig-v.
DR InterPro; IPR003596; Ig-v.
DR InterPro; IPR003596; Ig-v.
DR Ffam; PF00047; ig; 4.
DR PROSITE; P800290; IG_LIKE; 4.
DR PROSITE; P800290; IG_MHC; 1.
KW Hypochetical protein.
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 83; Conserv
                                                                 136
                                                                                             121 MVTVSS 126
                                                                                                                               80
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                                                                                                                                                                                                          1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                             RDSVKGRFTISRDNAKNSLYLOMNSLRVDDTAVYYCARDSCNGAI----CYGFSPWGQGT
                                                                                                                                               ADSVKGRPTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT
                                                                                                                                                                                           BVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYY
                                                                 LVIVSS
                                                                                                                                                                                                                                                            Conservative
 December 30,
7 secs
                                                                                                                                                                                                                                                                        62.7%;
65.9%;
                                                                                                                                                                                                                                                           14; Mismatches
                2003, 11:01:08
                                                                                                                                                                                                                                                                        Score 417; DB 4; Length 494; Pred. No. 4e-34;
                                                                                                                                                                                                                                                              25;
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RESULT 12
Q9UL84
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Best Local Similarity
Matches 84; Conserv
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Q9Y509;
01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                                                                                                             (1)
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                           Q9UL84 PRELIMINARY; PRT; 122 AA.
Q9UL84;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                     fetus.";
Clin. Im
                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers. Leukemia 9:1948-1953(1995).
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MEDLINE-96071149, PubMed-7475288,
Cao J., Vescio R.A., Rettig M.B.,
Lichtenstein A.K., Berenson J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
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                                             Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AF035030; AAD56266.1; -. HSSP; P01772; 2FB4.
                                                                                                                              Wu X., Liu B., Van der Merwe P.I
Young D.C.;
"Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                      InterPro;
                                                                                                                                                                                                                                                                                                                                                    (Fragment)
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IPR007110; Ig-like IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.2%; Score 427; DB 4; Length 147; 65.6%; Pred. No. 8.3e-36; Live 16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23,
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Last annotation update)
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                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 82
                                                                                                                                                                                               Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                              PÉAM; PF00047; ig; 4.

SMART; SM00409; IG; 4.

SMART; SM00409; IG; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG MHC; 1.

Hypothetical protein.

SEQUENCE 493 AA; 53224 MW;
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1

NON_TER 1 1 1

NON_TER 12 122

SEQUENCE 122 AA; 13579 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig. ike. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_cl. InterPro; IPR003596; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBNCL6;
QBNCL6;
QBNCL6;
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-QCT-2002 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90170.
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Mammary gland;
TISSUE-Mammary gland;
TISSUE-Mammary gland;
TISSUE-Mammary gland;
TISSUE-Mammary gland;
TISSUE-Mammary gland;
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Aotsuka S., Sasaki N.,
Masuho Y., Ono T., Okamo K., Yoshikawa Y., Aotsuka S., Sasaki N.,
Hattori A., Okumura K., Tuayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AK074651; BAC11114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                       ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
                                                                                               QVQLVESGGGVVLPGGSLRLSCAASGFRFRDYDMHMVRQSPGBGLEMVALIMYDGTKTYY
                                                                                                                       QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTVSS
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                                                                                                                                                                                                                                                                                                      53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                                            63.1%; Score 419.5; 65.9%; Pred. No. 2.2
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A Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003591; Ig-like.
R InterPro; IPR003597; Ig-Q1.
R InterPro; IPR003596; Ig_MHC.
R InterPro; IPR003596; Ig_W.
R InterPro; IPR003596; Ig_V.
R InterPro; IPR003596; Ig_V.
R SMART; SM00407; IG; 4.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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Young D.C.;
"Myosin-reactive autoantibodies in
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01772; 2FB4.
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116 AA;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLel. 23, Last annotation update)
tive immunoglobulin heavy chain variable
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n der Merwe P.L.,
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Primates;
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Last annotation update)
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Best Local :
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InterPro; IPR003006; Ig_MCC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Q9UL90;
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01-MAY-2000
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PROSITE; PS00290; IG_MHC; 1
Hypothetical protein.
SEQUENCE 499 AA; 53376 N
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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67.5%; Pred. No. 5.1e-37;
tive 14; Mismatches 14
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Catarrhini; Hominidae;
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Best Local S
Matches 86
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EMBL; AB049915; BAB16829.1; -.

HSSP; P01772; 2FB4.
InterPro; IPR001710; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_W.

Pfam; PF00047; ig; 1.

SMART; Swarz:
Strausberg R.;
Strausberg R.;
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                        QBTC77; PRELIMINARY;
QBTC77; CTEMBLrel. 21,
01-JUN-2002 (TEMBLrel. 21,
01-JUN-2003 (TEMBLrel. 23,
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Q9HCC1;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Single chain Fv (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Spleen;
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
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; SM00406; IGv; 1.
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112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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                                                                                                                                                                                                                                                                  Chordata;
Primates;
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Last sequence update)
Last annotation update)
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Pred. No. 6
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                                                                                                                                                                                                                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   471
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RESULT 8
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Best Local S
Matches 88
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Matches 90
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ date EMBL, BC015760; AAH15760.1; -.
Interpro; IPR0077110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
PMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50839; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                         Q96BB9;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                              Hypothetical SEQUENCE 59
                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
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SEQUENCE 471 AA; 51791 MW;
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Mammalia; Eutheria;
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136
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                                                        ADSVKGRFTISRDNAKNSLYLYMNSLRAEDTALYYCALP---YINSSNYRRGVAAFDIWG 117
                                                                                     EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY
                                                                                                   QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWSGTTIGF
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                     OCTMVTVSS
                                            ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTRE---
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QGTLVTVSS
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                                                                                                                                                                              65039 MW;
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19,
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Last annotation update)
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                                                                                                                                  Score 446.5; DB 4;
Pred. No. 4.9e-37;
7; Mismatches 17;
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Pred. No. 1.6e-37;
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                                                                                                                                                                              4FCA3AD8ECE263D9 CRC64;
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Best Local
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INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                             NUMBER OF SHAPE ADDRESS:
CORRESPONDENCE ADDRESS:
Cownsend and Townsend and Crew
ADDRESSEE: Townsend and Townsend and Crew
ADDRESSEE: Townsend and Townsend and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        APPLICANT: Willingham, Mark APPLICANT: FitzGerald, David
                                                                                                                                                                                TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
                                                                                                                                                                                                                      APPLICANT: Brinl
APPLICANT: Pai,
                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                        COUNTRY:
                                                                                         CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFAISRDNAKWTLYLOMNSLTIEDTAVYYCAKDLIESNIAEAL---WGQGTLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
                                       94105-1492
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                                                                           California
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2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
                                                            USA
                                                                                                                                                                                                                                       Brinkmann, Ulrich
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SURFACE RESIDUB VENEERING
ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.9%; Score 490.5; DB 1
79.5%; Pred. No. 1.1e-41;
tive 7; Mismatches 13
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Michael
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-331-398A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-331-397B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMB: Hunter, Tom
REGISTRATION NUMBER: 0152
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHAX: (415) 543-9603
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/08331397B
Patent No. 5981726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version :
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                COUNTRY: USA
ZIP: 94105-1492
                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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TOPOLOGY: li
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECULE TYPE: protein
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28-OCT-1994
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78.3%;
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Specific
Thereof
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56P1'CL Variable Heavy chain (V-H)"
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                 US/08/331,397B
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Pred. No. 2.7e-41;
                                                                                                                                                                                                                                                                                                                        Antibody Fragments,
                                                                                                                                                                                                                                                                                                                                            and Mutationally Stabilized Tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Migmatches
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                      Database
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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622
1 EVQLVESGGGLVQPG
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
Issued_Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQLVESGGGLVQPGRSLRL.....IESNIAEALWGQGTLVTVSS 120
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	26	25	24	23		21	20	19	18			15 4			12 4				80	7 4	6 4	σ 4	4	u A	2	4		Result
464.5	466	467	467	467	167.5	468	468	468	469	469.5		473.5	•	477.5	477.5	477.5	477.5	478.5	٠	485.5	•	486.5	•	486.5	•	495	Score	
74.7	74.9	75.1	75.1	75.1	75.2	75.2	75.2	•	75.4	•	76.0	٠	76.8	76.8	76.8	76.8	76.8	76.9	77.9	78.1	78.2	78.2	٠	78.2	•	79.6	Match	٠. ا
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US-09-240-274-151	US-09-240-274-149	US-09-240-274-26	US-09-240-274-6	-09-240-274-	US-09-240-274-140	US-08-468-671-2	US-08-259-372A-2	-09	US-09-079-029-11	US-09-240-274-23	US-09-240-274-9	-09-240-	US-09-240-274-22	US-09-240-274-21	-09	-09	-09-560-	US-09-560-198A-4	-09-025-769B-	US-09-560-198A-2	-09-227-	•	US-08-331-397B-46	-08-331-398A	US-07-942-245-35	US-09-315-926A-80	ID	:
15	e 149	26	6		140	ν,	'n	Sequence 4, Appli	11,	23,	,		22,	21,	20,	Sequence 8, Appli	į		24,	Sequence 2, Appli	e 46,	e 46,	46,	46,	35,	Sequence 80, App	ptio	

RESULT 2
US-07-942-245-35
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.

45	44	43	42	41	0	39	38	37	36	35	34	L)	32	<u>υ</u>	30	29	•
458.5	458.5	459	459.5	459.5	459.5	461	461	461.5	462	462	462	462	462	462	462	462	
73.7	73.7	73.8	73.9	73.9	73.9	74.1	74.1	74.2	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	
125	125	126	127	127	113	126	123	121	124	122	122	122	122	120	120	120	
N	N	w	w	w	w	w	w	w	w	σ	4.	w	N	4	ω	N	1
US-08-428-197-6	US-08-428-197-5	US-09-240-274-25	US-09-240-274-19	US-09-240-274-18	US-08-974-899-6	US-09-240-274-153	US-08-983-607-38	US-09-202-181-4	US-09-240-274-2	PCT-US93-07832-21	US-08-146-206C-21	US-08-437-642B-21	US-07-934-373C-21	US-08-146-206C-4	US-08-437-642B-4	US-07-934-373C-4	44 11 11 11 11 11
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ALIGNMENTS

	; NAME/KEY: mis ; OTHER INFORMA ; NAME/KEY: PEP ; LOCATION: (1) ; OTHER INFORMA US-09-315-926A-80 Query Match Best Local Simi Matches 94;	CURRENT AP CURRENT FI PRIOR APPLI PRIOR APPLI PRIOR APPLI PRIOR PILII PRIOR FILII PRIOR OF TILII PRIOR FILII PRIOR FILII PRIOR FILII PRIOR FILII PRIOR FILII PRIOR FILII SEQ ID NO 8 SEQ ID NO 8 SEQ ID NO 8 SEQ ID NO 8 FEATURE: FEATURE:	US-09-315-926A-80 US-09-315-926A-80 ; Sequence 80, Ap ; Patent No. 6498 ; GENERAL INFORMA ; GENERAL INFORMA ; APPLICANT: Ha ; APPLICANT: Ha ; APPLICANT: Ve ; TITLE OF INVEN
1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEMVAVISYDGNDKYY 60	NAME/KEY: misc feature OTHER INFORMATION: Description of Artificial Sequence: phage NAME/KEY: PEPTIDE LOCATION: (1)(248) OTHER INFORMATION: /note="hCAT1 amino acid sequence" 9-315-926A-80 79.6%; Score 495; DB 4; Length 248; set Local Similarity 78.3%; Pred. No. 9.18-42; tches 94; Conservative 9; Mismatches 17; Indels 0; Gaps	CURRENT APPLICATION NUMBER: US/09/315,926A CURRENT FILING DATE: 1999-05-20 PRIOR APPLICATION NUMBER: EP 99201593.3 PRIOR FILING DATE: 1999-05-20 PRIOR FILING DATE: 1999-05-20 PRIOR FILING DATE: 1998-05-20 RIOR FILING DATE: 1998-05-20 RIOR FILING DATE: 1998-05-20 ROPTWARE: Patentin version 3.0 EQ ID NO 80 LENGTH: 248 TYPE: PAT ORGANIEM: Artificial Sequence FEATURE:	ISULT 1 1-09-315-926A-80 3-09-315-926A-80 3-equence 80, Application US/09315926A Patent No. 6498027 GENERAL INFORMATION: APPLICANT: Be van, Helmuth APPLICANT: Havenga, Menzo APPLICANT: Havenga, Menzo APPLICANT: Verlinden, Stefan TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
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Q99LC AC O99LC AC O99LC AC O99LC DT 01-JU DT 02-JU DT 02-
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QBWY24
ID QBWY24
ID QBWY2
AC QBWY2
AC QBWY2
DT 01-MA
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InterPro; IPKUULL.
InterPro; IPKUULL.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGV; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; E
                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Sheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Theng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Index regulated in colorectal cancer.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283666; AAL36987.1; -.

InterPro; IPR003196; Ig-11ke.

InterPro; IPR003196; Ig-MHC.

InterPro; IPR003196; Ig_wHC.

InterPro; IPR003196; Ig_v.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99LC4 PRELIMINARY; PRT; 463 AA.
Q99LC4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBWY24;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNC66 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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23,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497
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                                                                                                                                                           Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                 SEQUENCE
140 VTVSS 144
                         110
                                                   80
                                                                             61
                                                                                                       20
                                                                                                                                                             74; Conservative
                                                                                                                                                                         Similarity
                                                                 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE------LDWFYIWGQGTM 109
                                                                                                       ÓBÓLBÓSGABVTKÞGASVKVSCKÁSGYTFIAYDINWVRÓAÞGÓGLEWMGWMNÞOTGNTEF 79
                                                                                                                       QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
                         VIVSS 114
                                                   AQKFQGRLTFSRDTSINTAYMYLSSLSTEDSAIYFCARGNLRGGRGFGYNWFDPWGHGTL 139
                                                                                                                                                                                                                  497 AA;
                                                                                                                                                                                                                  53665 MW; F24D08DFA5A663E5 CRC64;
                                                                                                                                                           62.6%; Score 373.5; DB 4; 59.2%; Pred. No. 1.2e-30; tive 17; Mismatches 23;
                                                                                                                                                               Indels
                                                                                                                                                                                       Length
                                                                                                                                                              11;
                                                                                                                                                              Gaps
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Search completed: December 30, 2003, 11:01:09
Job time: 27.7823 secs

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RESULT QREVDC9
ID QRE
DT QRE
DT 011
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KÖZÖNÖ Y., KÖZÖNÖ H., AZUMA T.;

"Direct Estimation of Relative Affinity by Flow Cytometry!

"Birect Estimation of Relative Affinity by Flow Cytometry!

Affinity Maturation of B Cell Antigen Receptors in Response

"Hydroxy-3-Nitropheny!)Acety! (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AB069915; BAB63931.1; -.

RINterPro; IPR007110; Ig-like.

RINterPro; IPR003006; Ig-MHC.

RINterPro; IPR003006; Ig-MHC.

RINterPro; IPR003596; Ig-V.

REART; SM00406; IGv; 1.

R SMART; SM00406; IGv; 1.

R PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q924Q0 PRELIMINARY; PRT; Q924Q0; (TrEMBLrel. 19, Created 01-DEC-2001 (TrEMBLrel. 19, Last se 01-MAR-2003 (TrEMBLrel. 23, Last an V165-D-J-C mu protein (Fragment). V165-D-J-C MU protein (Fragment). Wils musculus (Mouse).
SEQUENCE FROM N.A.

STRAIN=BALB/c;

Chernajovsky Y.;

Submitted (OCT-2001) (2)
                                                                                                                                                                                                                                                                                                              Q8VDC9
Q8VDC9;
01-MAR-2002
                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
Anti-MOG Z12 variable gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                           IGG2A.
                                                                                                                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AREFQGSVIMTADISTDIAYMELSSLRSDDTAVYYCAVPDPDAFDIMGQGTMVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFYIWGQGTMVTVSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAPDSNHLYFDYWGQGTTLTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.5%; Score 385; DB 11; 62.7%; Pred. No. 1.6e-32;
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                         the
                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
2a (Fragment).
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Last annotation update)
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                         EMBL/GenBank/DDBJ
                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C99D2433F2BAD8A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                            168
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ID QSBRVO
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AC QSBRV
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGV; 1.
SMOSITE; PS50835; IG LIKE; 4.
PROSITE; PS50835; IG MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TEEMBLrel 17, Cre
01-JUN-2001 (TEEMBLrel 17, Las
01-MAR-2003 (TEEMBLrel 23, Las
Hypothetical protein.
Homo sapiens (Human).
Elkaryota, Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/c;
Sembi P.;
"Targeting T cells to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BRV0;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
NON TER 168 AA; 18293 MW;
SEQUENCE 168 AA; 18293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted JAN-2002) to the ELEMBL; AJ416332; CAC94867.1; -
InterPro; IPR007110; Ig-ilke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2001) to the
EMBL; BC005951; AAH05951.1;
HSSP; P01789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                              Local Similarity
                         140
                                                                     107
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                                                                                                                                                                                                                                                                                           76;
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                                                                                                              GITVIVSS
                                                                     GIMVIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.7%;
ilarity 60.5%;
Conservative 2
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                                                                     114
                         147
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                                                                                                                                                                                                                                                                                                                                                                                 54154 MW;
                                                                                                                                                                                                                                                                                                              63.3%;
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Last sequence
Last anno
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Pred. No. 5.8e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                       Score 378; DB 4;
Pred. No. 4.2e-31;
5; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500
                                                                                                                                                                                                                                                                                       . 4.2e-31;
:cheв 23;
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                                                                                                                                                                                                                                                                                                                                  Length 500;
                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                        CELDWFY----IWGQ 106
                                                                                                                                                                                                                                                                                           14;
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RESULT 9
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A Airakwa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Airakwa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Airakwa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kucha K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrimi L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,
A Myroshaw-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Myroshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Hypothetical
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O9D8L4; PREMBLrel 17,
O1-JUN-2001 (TrEMBLrel 17,
O1-MAR-2003 (TrEMBLrel 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PÉAM; PF000047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW;
                                                                                                                               Q8VCX7
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:96443; Igh-1.
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MEDLINE=21085660; PubMed=11217851;
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IGH-1 OR 1810060009RIK.
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? (TrEMBLrel. 20, Las
} (TrEMBLrel. 23, Las
al 67.9 kDa protein.
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                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.9%;
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                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9DED57A514475FBB CRC64;
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Fukuda S.,
Imanaka I.,
Saito R.,
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Query Match
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Best Local S
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MGD; MGI:96448; Igh-6.
InterPro; IPR0077110; Ig'like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; Ig; 5.
SMARR; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW;
                                                                                                                                                                          Q9Y298;
Q9Y298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                           Signal.
                                                                                                                                       Blood 92:496-506(1998)
EMBL; AJ224083; CAA118:
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        196 VH.
                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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                                        SEQUENCE
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                                                                                PROSITE;
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Similarity
79; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                             QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY
                                                                               PS50835; IG_LIKE;
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150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
                                         16031 MW;
 65.2%; Score 389.5; DB 4
67.5%; Pred. No. 5.8e-33;
tive 11; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 390; DB 1
Pred. No. 3e-32;
                                                              POTENTIAL
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                                        563D164AB22802D5
                                                                                                                                                                                                                                                                                                                                                      150
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                     DB 4;
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BMBL; AF035019; AAD56255.1; -.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS0835; IG_LIKE; 1.

NON_TER 125 125
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Q9UL95;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96DKO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
SEQUENCE FROM N.A.

TISSUE-Gastric mucosa;
Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Ishibashi T., Kanehori K., Yosida M., Takiguchi S., Kusano J.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein FLJ25298. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
M.X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TERMBLEE). 13, Created)
01-MAY-2000 (TERMBLEE). 13, Last sequence update)
01-MAR-2003 (TERMBLEE). 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96DK0
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125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
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                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
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Pred. No. 2.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Catarrhini; Hominidae; Homo.
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RESULT 7

Q96CG
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AC Q96C
AC Q96C
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Best Local S
Matches 82
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Kawakami B., Nagai K., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKOSS027; BAB71633.1; -.

InterPro; IPR003006; Ig MHC.

InterPro; IPR00306; Ig MHC.

InterPro; IPR00396; Ig_v.

Pfam; PF00047; ig; 4.

SMART; SM00406; IGV; 1.

PROSITE; PS00835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SPOUENCE 496 AA; 53532 MM; C72EE1E247C86FED CRC64;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                             Piam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 159 AA; 17497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Homo sapiens putative microfibrillar protein with Ig-like mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY039025; ARX82649.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Q96QS0;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                      Similarity
GQGTMVTVSS 114
                                                                                                          SSVT
                                                                                                                                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79
                                                                                                                                                                                                                    QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVHLVQSGAELKMPGSSVKVSCKASANMFRSYAFTWVRQAPGQGLQWMGGIIPNFGAPNY
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                                                                                 SOKFOGRUTMTROTSTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFYYYGMDVW
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                                                                                                                                                                                                                                                                                             Conservative
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                   Score 404; DB 4; Length 159; Pred. No. 1.9e-34;
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Pred. No. 3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                  5D29537E881FAF02 CRC64;
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RESULT 3
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ID 29UL
AC 29UL
AC 29UL
AC 11-M
DT 01-M
DT 01
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Best Local Similarity
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InterPro; IPR007006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 124 124
                                                                                                                                                                                                                                                              Q9UL94
Q9UL94;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2000 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TremBLrel. 23, Last annotation update)
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. EMBL; AF035022; AAD56258.1; HSSP; P01772; 2FB4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates;
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Best Local S
Matches 84
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 86
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EMBL; BC009851; AAH09851.1; -.

RINterPro; IPR000005; HTHATAC.

RINterPro; IPR007110; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

RINterPro; IPR003096; Ig_WHC.

RINterPro; IPR003596; Ig_V.

R Pfam; PF00047; Ig; 5.

R SMART; SM00406; IGv; 1.

R PROSITE; PS00041; HTM ARAC_FAMILY_1; 1.

R PROSITE; PS00031; IG_LIKE; 5.

R PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96GA6 PRELIMINARY; PRT;
Q96GA6;
01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last seq
01-MAR-2003 (TEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical SEQUENCE 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1
NON_TER 119 119
SEQUENCE 119 AA; 13205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Young D.C.;
"Myosin-reactive autoantibodies in
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01810; 2FBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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114 S
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Similarity 70.6%; Pred. No. 6.5e-36;
84; Conservative 10; Mismatches 20;
                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                              AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL-----DWFYIWGQGTMVTVS
                                                                                                                                                                          OMOLVOSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMGWITPFNGNTNY
                                                                                                                                                                                                     QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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                                                      AQKFQDRVTITRDRSMNTAYMELSSLRSEDTAMYYCARGYSSSWDDAFDIWGQGTMVTVS
                                                                                                                                                                                                                                                                                                                                                                                                       al protein. 614 AA; 6
                                                                                                                                                                                                                                                                                          Conservative
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Last annotation update)
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                                                                                                                                                                                                                                                                                          Score 413.5; DB 4; Length Pred. No. 1e-34; 6; Mismatches 22; Indels
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Result
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Maximum
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Perfect score:
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Maximum Match 100%
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                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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597
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Copyright (c) 1993 - 2003
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sp_phage:*
sp_plant:*
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sp_bacteria:*
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sp_virus:*
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sp_bacteriap:*
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Compugen Ltd.
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Q9u192 homo
Q9u194 homo
Q96ga6 homo
Q96ga6 homo
Q96g80 homo
Q96g80 homo
Q96g80 homo
Q96g80 homo
Q94g80 homo
Q94g80 homo
Q94g90 mus
Q9y298 homo
Q924q0 mus
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58.8	•	•	59.0	•	•	59.1			•	59.5					59.8	•	60.3	60.3	60.3	60.4	60.6		٥.			61.2	61.6	62.3
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Q924 q 9	Q924r	Q924q;	Q924q7	Q8vcx4	Q921k	Q924q4	Q924p	Q924q1	Q8k17	Q924r6	Q924r8	Q8vij1	Q924r	Q9912	Q924r	Q8k0z4	Q924q	Q924r5	Q9z1c	Q9qxf	Q925e3	Q91wt	Q924pi	Q924q1	Q920e8	Q9qxe9	Q924p9	Q91v6
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Best Local S
Matches 95
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EMBL; AF035025; AAD56261.1; -.

HSSP; PO1810; ZFBJ.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_WHC.

InterPro; IPR00356; Ig_v.

Pfam; PP00047; Ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

NON_TER 116 116

SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 C
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UL89 PRELIMINARY; PRT; 116 AA.
Q9UL89;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                      etus.";
                                                                                                                                                                                                                                                                                                                                                                         Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                           95;
                      5
                                                                            Similarity
VQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNYAQKF 64
                                                                                                                                116 116
116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
                                                           Conservative
                                                       80.7%; Score 482; DB 4; Length 116;
81.9%; Pred. No. 8.8e-43;
tive 8; Mismatches 7; Indels
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                                                           Gaps
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380.5 378 376 373.5 373.5

musculu sapien

389.5 385

416.5 413.5 410.5 408 404 399.5

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HV01_MOUSE
ID HV01
AC P0174
AC P0174
AC P0174
DT 21_JU
DT 22_JU
DT 21_JU
DT
Search completed: December 30, 2003, 10:55:54 Job time : 6.1121 secs
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Matches 65; Conserv
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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NON TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V region MPC 11.

Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Zakut R., Cohen J., Givol D.;

Nucleic Acids Res. 8:4839-4840(1980).

-!- MISCELIANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.; Zakut R., Cohen J., Givol D.; "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                               61 NDNLKGKATITADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS
                                                                                                                                                                                                                                                             55 TDPFQGVYIKWERVTVSLKPSFNQAYMELVNLFNEDGAVYYCAREWKGQVNVNPFDYWGQ 114
                                                                                                                                                                                                                                                                                                                                             ch 57.9%; Score 345.5; DB 1; Length 121;
l Similarity 53.7%; Pred. No. 1.9e-28;
65; Conservative 24; Mismatches 25; Indels 7
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121 121
121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
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RESULT 13
HV51_MOUSE
ID HV51_MOUSE
AC P06330;
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-I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain V region AC38 205.12.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bothwell A.L.M.,
Baltimore D.;
                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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SMART; SM00406; IGv; 1
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MEDLINE-84182519; PubMede-6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) ev
lymphocytes is encoded by a large set
                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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1A6U; 27-MAY-98.
1A6W; 15-JUL-98.
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bulin V region; Signal;
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                                                                                                                                                                                 STANDARD;
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Paskind M., Reth
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JH2 SEGMENT.
BY SIMILARITY
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Pred. No. 4.9e-29;
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FRAMEWORK.1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK.2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                       1B57DD4FD0C9F465 CRC64;
                                                                                                                                                                                                                                                                                                                                        Mismatches
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M., Beyreuther K., Rajewsky K.; 
) expressed at high frequency in 
set of antibody structural gener
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RESULT 14
HV1E_HUMAN
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                                                                                    SOUTH TERMS OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
Query Match 58.0
Best Local Similarity 56.3
Matches 72; Conservative
                                                                                                                                 InterPro, IPKv.,
pfam; pP00047; ig; 1.
pfam; pR000406; IGv; 1.
smarr; sm00406; IGv; 1.
rmoSITE; pS50835; IG LIKE; 1
rmoSITE; pS50835; IG LIKE; 1
light region; Py:
                                                                                  MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                     888
                                                                                                                                                                                                                                                                                                                                                                                   -|- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02044; M1HUSI. HSSP; P01825; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews D. M., Capra J.D.;
Andrews D. M., Capra J.D.;
"Amino acid sequence of the variable regions of heavy chains
"Amino acid sequence of the variable regions of heavy chains
"Amino acid sequence of the variable regions of heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Bep-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-I region SIE.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_v.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 3:517-523(1984).
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 20:5822-5830(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE=82046599; PubMed=7028111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01761;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01789; 1MCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV18 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunoglobuln
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLOBULIN ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACKFOGRVTITADESTSTAYMELSTLISEDTAVYYCE----LDWFYIWGOGTMVTVSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUGLOGSGPELVKPGASVKISCKASGYTFTDYYMMVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGABVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 AA;
                                                                                    124
124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104
118
96
118
12934
                                                                                    13732 MW;
                      58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.8%;
                                                                                                                                                                         Pyrrolidone carboxylic
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Pred. No. 5.2e-29
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B 4 D 4
                        Score 346;
Pred. No. 1
                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                     IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAS ISOLATED FROM AN IGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                      62CED4573BDEF59F
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                                                                                                                                                                                                                                                                                                                                                activity; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                        1.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                         CRC64;
                                                                                                                                                                           acid
                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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12;

Mismatches

24;

Indels

20;

Gaps

u T

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A POR DE DE COCOCCERTE DE COCCCECCE DE COCCCE DE COC
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7.1
                                                                                                                               SEGMENT, JH2.

-i- SIMILARITY: Contains 1 immunoglol
HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR007106; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
IMMUNOGlobulin V region; Hybridoma.
DOMAIN 111 IG-LIKE
NON TER 120 120
SEQUENCE 120 AA; 13307 MW; FF04E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region 36-65.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vermammalia; Butheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=83131846; PubMed=6186498;
Siekevitz M., Gefter M.L., Brodeur P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.

SMART; SM00406; IOv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Hybridoma; Signal.

SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";
Eur. J. Immunol. 12:1023-1032(1982).
-i- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME OF THESE VERGIONS HAVE REARRANGED TO THE SAME OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00493; AAA38128.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 S 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYDFDYWGQGTPLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 60.7%;
Similarity 58.7%;
71; Conservative 2
   Similarity 70; Conserv
                                                                                                                            120
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
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20
20
140
140
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains 1 immunoglobulin-like domain.
                                                                                                       120
13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15514 MW;
   59.7%; Score 356.5; DB 1
58.3%; Pred. No. 1.4e-29;
bive 20; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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Pred. No. 4.2e-30;
1; Mismatches 22;
                                                                                                                                                                                                    IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                 DB 1;
                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 140;
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                                                                    120;
   7;
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   Gaps
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RESULT 12
RV07 MOUSE
ID HV07 M
AC P01751
DT 21-JUL
DT 21-JUL
DT 15-SEP
DE 1G hea
OS Mus mu
OC Eukary
OC Mammal
OX NCBI T
RN [1]
RP SEQUEN
RC STRAIN
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Best Local S
Matches 70
                                                                   HV07 MOUSE STANDARD; PRT; 139 AA.

P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region B1-8/186-2 precursor.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebr;
Mammalia; Eutheria; Rodentia; Sciurognathi; Mur:
NCBI TaxID=10090;
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DISULFID
NON_TER
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG heavy chain V region AC38 15.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P06329;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M.,
"A V region determinant (idiotope) e:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02037; MHMS15.
HSSP; P01810; 2FBJ.
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Similarity 58.3%;
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105
120
96
                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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Pred. No. 3.3e-29;
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SQ TTTT
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HV12_MC
RESULT
HV13_MC
ID _HV
AC PO
DT 21
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Best Local
                                                     MOUSE
HV13 MOUSE
P01757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV12 MOI
P01756;
                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete amino acid sequence of a mouse mu heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
-i- MISCELLANBOUS: THE SEQUENCE OF THE LIGHT PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                              CARBOHYD
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55. MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amoutation update)
Ig heavy chain V region MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V region J558.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: Contains 1 immunoglobulin-like
PIR; A02039; MINS4E.
                                                                                                                                                                                                                                                                                             Immunoglobulin
                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kehry M.R., Fuhrman J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                P00047; 15, 1, SM00406; IGV; 1.
SM00406; IGV; 1.
E; P850835; IG LIKE; 1.
oglobulin V region; Glycoprotein.
1 16 IG-LIKE.
N 196 BY SIMILARITY.
N 196 N-LINKED (GLCNAC...
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                                                                                                                                                             AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL----DWFYIWGQGTMV
                                                                                                                                 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC--ELDWFY-IWGQGTMVTVSS 114
                                                                                                                    NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS
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22
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                                                                STANDARD;
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59.0%;
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                                                                                                                                                                                                        Score 367.5; DB 1
Pred. No. 1.1e-30;
5; Mismatches 20
                                                                PRT;
                                                                                                                                                                                                                                                  3CF8ACE4BE447E41 CRC64;
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ches 20;
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Best Local
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).

-I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS,
WHICH OCCUR IN THE D AND J SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schilling J., Clevinger B., Davie J.M., "Amino acid sequence of homogeneous ant rearrangements in heavy chain V-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria;
                                                                                                                                    "Somatic mutation in genes for the variable immunoglobulin heavy chain."; science 216:309-311(1982)
                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                              P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THIS PROTEIN BINDS
-!- SIMILARITY: Contains 1 immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                            Capra J.D.;
                                                                                                                                                                                           MEDLINE=82152818; PubMed=6801765; Sims J., Rabbitts T.H., Estess P.,
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=A/J;
                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                       SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
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117 AA;
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Contains 1 immunoglobulin-like
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Rodentia;
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59.0%;
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BY SIMILARITY
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Best Local
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pffam; PF000407; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
ITMUNOGLOBULIN V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human
immunoglobulin epsilon chain expressed in a myeloma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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NON_TER
                                                                                         888
                                                                                                                                                                                                                                       Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
(Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
-i- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy, chain '''. region ND precursor (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
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PIR; S00476; HVHU35.
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                                                                                                                                                                        HSSP;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            InterPro;
P; P01789; IMCP.
GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0006955; F:immune response; NAS.
erPro; IPR007110; Ig-1ike.
erPro; IPR003006; Ig_MHC.
erPro; IPR003596; Ig_V.
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117 117
117 AA; 13009 MW;
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Pred. No. 4.7e-3:
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Matches 76
Query Match
                                                               Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin V region.
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-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02022; G1MSAA.
HSSP; P01772; 2EB4.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                         Capra J.D., Nisonoff A.;

"Structural studies on induced antibodies with defined idiotypic specificities. VII. The complete amino acid sequence of the heavy chain variable region of anti-p-azophenylarsenate antibodies from mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284(1979).
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PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; S:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=79195438; PubMed=109536;
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STRAIN=A/J;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region (Anti-arsonate antibody).
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l Similarity 59.4%;
76; Conservative 1
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                                             114 AA;
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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Pred. No. 6
  Score 369;
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  Length 114;
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                                             CRC64;
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RESULT 3
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HV1B_HUMAN
    33388
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Best Local S
Matches 76
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PIR; A02024; HVHHHG.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NA.
GO; GO:00008955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
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21-JUL-1986 (Rel. (
15-SEP-2003 (Rel. 4
1g heavy chain V-I
 -HV48 MOUSE
P03980;
23-OCT-1986
23-OCT-1986
15-JUL-1999
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NCBI_TaxID=9606;
[1]
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P01743;
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Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene subgroups.";
.Natl Acad Sci. U.S.A. 80:855-859(1983).
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                                                                                                                                    AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC 96
                                                                                                                      AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC 115
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(Rel. 02, Created)
(Rel. 02, Last sequence update)
(Rel. 38, Last annotation updat
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el. 01, Last sequence update)
el. 42, Last annotation update)
V-I region HG3 precursor.
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                                                    STANDARD;
                                                                                                                                                                                                                                                                                12946 MW;
                                                                                                                                                                                                                                         64.5%;
79.2%;
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                                                                                                                                                                                                                                       Score 385; DB 1;
Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V-I REGION HG3 IG-LIKE.
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RESULT 4
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Best Local
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NON TER
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P23083;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., S.
Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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DOMAIN
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DOMAIN
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; ig; 1.
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MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaborati
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on i
                                                                                                                            "Dispersed localization of D segments in the human imm heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain
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Immunoglobulin V region; Signal.
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138 AA;
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Pred. No. 3.1e-31;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                 Kodaira M.,
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C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Caccession: B33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expt
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: B33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-126 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bridence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.6%;
79.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 493; DB 2;
Pred. No. 1.5e-37;
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Pred. No. 8.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 12;
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F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Search completed: December 30, Job time : 11.9277 secs
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Best Local Sin
Matches 100;
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                                                                               121 YGMDVWGQGTTVTVSS 136
                                                                                                                  102 Y---IWGQGTMVTVSS
                                                                                                                                                         61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120
                                                                                                                                                                                               61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----
                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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                  2003,
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Pred. No. 1.6e-37;
6; Mismatches 8
                    11:03:20
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Ig heavy chain V region (G6+ CLI-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: pH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: pH0952; MUID:92202880; PMID:1552291
A;Accession: pH0954
A;Accession: pH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-30/Region: framework 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (G6+ T-L42) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0962
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
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PH0962
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A; Residues: 1-120 <M
C; Superfamily: immun
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                                                                                                                                    F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
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Best Local (
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                                                                   51-67/Region: complementarity-determining 2 68-98/Region: framework 3
  Query
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                                                                                                                   framework 2
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                                             complementarity-determining
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  Score 501;
  BB
2
Length 132;
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural a A;Reference number: PH0952; MUID:92202880; PMID:1552
A;Accession: PH0958
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
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                                                                                                                                                                                          Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
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r;51-67/Region: complementarity-determining 2
r;68-98/Region: framework 3
r;99-110/Region: complementarity-determining 3
                                    A; Molecule type: DNA
A; Residues: 1-127 < MAR>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                             A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Local Similarity 80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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Pred. No. 5e-38;
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PMID:1552291
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A;ACCEBBACH.
A;MOLECULE type: mRNA
A;Residues: 1-627 <FRI>
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change
C;Accession: S14683; S08047
R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of th
A;Reference number: S14683; MUID:90332450; PMID:2115996
A;Accession: S14683;
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A;Residues: 1-133 <KIP>
A;Reperimental source: the sequence was determined from C;Superfamily: immunoglobulin V region; immunoglobulin h C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expra;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: C33548
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C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: C33548
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                   AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC----
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Pred. No. 6.8e-38;
5; Mismatches 7;
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Pred. No. 1.4
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0953
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0953
                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-132 <FIG>
A;Residues: 1-132 <FIG>
A;Cross-references: EMBL: Z31681; NID:g509788; PIDN:CAA83486.1; PID:g1335147
A;Cross-references: EMBL: Z31681; V region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S46394
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
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F;31-35/Region: complementarity-determining
F;36-50/Region: framework 2</pre>
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                                                                                Score 502; DB 2;
Pred. No. 2.4e-38;
7; Mismatches 5
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Pred. No. 1.8e-38;
2; Mismatches 7
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C;Keywords: heterouser 1
F;130/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;15-98/Region: complementarity-determining 1
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. Exp. Med. 175, 983-991, 1992
A;Title: Bvidence for somatic selection of natural a A;Reference number: PH0952; MUID:92202880; PMID:1552 A;Accession: PH0957
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F;51-67/Region: complementar
F;68-98/Region: framework 3
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                                                                                                                                                                                                                                                                                                            AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD------WFYIWGQGTM 109
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Pred. No. 3.8e-39;
5; Mismatches 8
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Pred. No. 1.9e-39;
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PMID:1552291
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R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0952
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A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
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F;68-98/Region: framework 3
F;99-117/Region: complementarity-determining
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F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
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A;Molecule type: DNA
A;Residues: 1-128 <M
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A; Residues: 1-129 < MAR>
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Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
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Similarity 79.8%;
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AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC---
                                                                              QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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Pred. No. 8.1e-39;
3; Mismatches 8
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Pred. No. 6e-
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Maximum Match 100%
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Maximum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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513.5
510.5
508.5
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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    GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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g heavy chain v r
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	PL0105	F49590	S46393	S19665	S49530	A30523	A32483	S36260	D33548	S36271	\$31600	S31667	B49590	GIHUEU	S36265	C49590
	•	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	anti-Sm antibody V	Ig heavy chain V-I		Ig heavy chain V r	heavy		Ig heavy chain V r		heavy	Ig heavy chain V-I	heavy	Ig heavy chain V r

ALIGNMENTS

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RESULT 2
PH0961
                                                                                                                                                                                                            Ig heavy chain V region (G6+ T-L33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0961
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A;Title: Evidence for somatic selection of natural autoantibodies. A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0959
A;Molecule type: DNA
A;Residues: 1-119 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                           R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0961
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F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
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A; Residues: 1-116 <MAR>
A; Residues: 1-116 <MAR>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-30/Region: framework 1
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C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0959
                                                                         A; Status: nucleic acid sequence not
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Best Local Similarity
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87.9%;
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Pred. No. 1.1e-39;
4; Mismatches 8
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APPLICATE: 09-May --
FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
APPLICATION 21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/71
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Paul J. APPLICANT: Leonard
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                           APPLICATION NUMBER: US/08/437,642B
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70.4%; Pred. No. 2.9e-37;
tive 14; Mismatches 18; Indels 5
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                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/146,206C

PILING DATE: 17-NO. 6407213-1993

CLASSIPICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION DATA:

APPLICATION UNMBER: 07/715272

PILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION MINISTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
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08/146206
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PILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 120 amino acids
TYPE: Amino Acid
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
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              REGISTRATION NUMBER: 40,378 REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                          ZIP: 94080
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                       Wendy M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for Making Humanized Antibodies
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                  P0709P1
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US-08-379-057-32
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                       Sequence 32, Application US/08379057 Patent No. 5876950
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches
   GENERAL INFORMATION:
APPLICANT: Siadak
APPLICANT: Holleni
APPLICANT: Gillil
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SILVERMAN, GREGG J.

TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTE
TITLE OF INVENTION: VACCIDATION WITH A B-CELL SUPERANTIGE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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NAME: HOWElls, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD.
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STATE: California
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1880 Century Park East - Suite 500
Siadak, Anthony W.
Hollenbaugh, Diane L.
Gilliland, Lisa K.
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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67.2%; Pred. No. 2.2e-37;
ative 16; Mismatches 25
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; FRAGMENT TYPE: internal
US-08-379-057-32
                                                                                                                                                                                                                                                                     RESULT 13
US-07-934-373C-4
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNBY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REPERENCE/DOCKET NUMBER: 0N0133-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                     GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 727-36
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Aruffo, Alejandro A.
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human 9p39 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
ZIP: 94080
COMPUTER READABLE FORM:
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                                                    CITY: South San
STATE: Californi
                                                                                        STREET:
                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                             106 VIVS 109
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                                                    California
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3005 First Avenue
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                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 727-3670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3) 72.
727-3601
MO: 32:
                                                                       Francisco
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Pred. No. 2.1e-37;
8; Mismatches 11;
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                                                                                                                                                                                                                                    ; OTHER INFORMATION: anti-Rh(D) antibody clone US-09-240-274-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-274-150
                                                                                                                                                        Best Loc
Matches
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SEQ ID NO 150
LENGTH: 126
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APPLICANT: Siegel, Donald L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 150, Apparent No. 62554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: PatentIn Ver. 2.0 SEQ ID NO 144
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                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF FILE REFERENCE: 09596-42U2 CURRENT APPLICATION NUMBER: US/09/240,274 CURRENT FILING DATE: 1999-01-29 EARLIER APPLICATION NUMBER: 60/081,380 EARLIER FILING DATE: 1988-04-10 EARLIER FILING DATE: 1998-04-10 EARLIER FILING DATE: 1998-04-10 EARLIER FILING DATE: 1998-04-10 EARLIER APPLICATION NUMBER: 60/028,550 EARLIER FILING DATE: 1996-10-11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
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TITLE OP INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY
TITLE OP INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
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                        ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAAT
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ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWRVRAFSSG
                                                                              EVQLLESGGGVAQPGRSLRLSCVASGFSLRSYGMHWVRQAPGKGLEWV
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Pred. No. 1.2e-37
.5; Mismatches 2
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LOCATION:
US-08-428-197-1
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Patent No. 5
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                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: PCT/US93/
APPLICATION UNMBER: PCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: FD-2
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (619) 455-5100
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APPLICANT: SILVER
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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California
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1880 Century Park East - Suite 500
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; APPLICANT: REISNER, Yair et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIB
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: REISNER=5
CURRENT APPLICATION NUMBER: US/09/202,181
CURRENT FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: 118625
PRIOR FILING DATE: 1996-06-11
PRIOR APPLICATION NUMBER: IL97/00184
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                                                                                                                                                                  Sequence 4, Application US/09202181
Patent No. 6254867
GENERAL INFORMATION:
APPLICANT: REISNER, Yair et al.
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Best Local Similarity
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APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
PRILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
PRILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD--LGGYSYGY
                                                                                                                                                                                                                                                                                                                                            VIVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                         123
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13-JUN-1996
                                                                                                                                               Yair et al.
HUMAN MONOCLONAL ANTIBODIES TO THE HEPA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.3%; Score 456; DB 4; Length 123
72.0%; Pred. No. 1.7e-38;
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; SEQ ID NO 4
; LENGTH: 121
; TYPE: PRT
; ORGANISM: human
US-09-202-181-4
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APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SCRTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER PILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER: 0F SEO ID NOS: 224

CONTENTANT OF SEO ID NOS: 224
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09240274 Patent No. 6255455
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                       Query Match
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo mapiens
PEATURE:
OTHER INFORMATION: anti-Rh(D) chain D04
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 68.1%; Score 448; DB 3; Length 121; Local Similarity 70.4%; Pred. No. 1e-37; hes 88; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                           68.0%;
Local Similarity 68.3%;
es 86; Conservation
121 MVIVSS 126
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                                    120 MVTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
                                                                                                                                                                               1 EVOLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60
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                                                                                                                                                EVQLLESGGGVAQPGRSLRLSCVASGFSLRSYGMHWVRQAPGKGLEWVADIWFDGSNKDY
                                                                        15; Mismatches
                                                                                                                                                                                                                                      Score 447.5; DB 3
Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                         Length 126;
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US-09-240-274-144

Sequence 144, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER APPLICATION NUMBER: 50/028,550

EARLIER APPLICATION SUMBER: 50/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTING DATE: 2.0

SEQ ID NO 27

TYPE: PRT

TYPE: PRT
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; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
PILE REFERENCE: P0979
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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120
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                                                                   ADAVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDSR-YSNFLRV
                                                                                                                                                             EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWV
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                                                                                                   ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATV
                                                                                                                                          EVOLLESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVS
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GTTVIVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09240274
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72.7%;
                                                                                                                                                                                                                               69.9%;
                                                                                                                                                                                                              11;
                                                                                                                                                                                                              Score 460; DB 3; Length 127
Pred. No. 7e-39;
L1; Mismatches 23; Indels
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Pred. No. 1.4e-38;
B; Mismatches 14
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RESULT

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RESULT 5
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Patent No. 5977322
GENERAL INFORMATION:
                                                                                                            Sequence 30, Application US/09315574 Patent No. 6512097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 90; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/665,202
APPLICATION 1-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
APPLICATION NUMBER: US 60/000,238
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
PILING DATE: 15-JUN-1995
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el i
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            k; Score 456; DB 2; Length 123k; Pred. No. 1.7e-38;14; Mismatches 19; Indels
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to avecore greater than or equal to the score of the result bei {\bf j} and is derived by analysis of the total score distribution
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460.5
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-918-148-78
US-08-918-148-75
US-08-240-274-27
US-08-665-202-30
US-09-315-574-30
US-09-240-274-14
US-09-240-274-15
US-09-240-274-15
US-09-240-274-15
US-08-428-197-1
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US-08-379-057-32
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US-08-191-7898-24
US-09-240-274-24
US-09-240-274-28
US-09-240-274-28
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RESULT 2 US-08-918-148-75

Sequence 75, Application US/08918148A PATENT NO. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: W.

JOCAL SIMILATICY /4.4%; Pred. No. JOCAL NO.	918-148-78 ence 78, Application US/08918148A nt No. 6342220 RAL INFORMATION: LICANT: Adams, Camellia LICANT: W. LICANT: Garter, Paul J. LICANT: Grendly, Brian M. LICANT: MREGIN L. LICANT: Grendly, Brian M. LICANTON MRMBER: US/08/918,148A RERIT FILING DATE: 1997-08-25 BER OF SEQ ID NOS: 79 BER OF SEQ ID NOS: 79 BER OF SEQ ID NOS: 79 BINGTH: 245 PS: PRT GANISM: artificial ATURE: GANISM: artificial ATURE: GANISM: artificial ATURE: GANISM: artificial ATURE: GANISM: GRENDLY COMBONIA ATURE: BRIT GANISM: GRENDLY COMBONIA ATURE: GANISM: GRENDLY COMBONIA ATURE: GANISM: GRENDLY COMBONIA BRIT INFORMATION: unknown amino acid 918-148-78 918-148-78	29 439.5 29 439.5 30 439.5 31 439.5 32 439.5 33 439.5 34 438 36 438 37 438 36 438 37 438 37 438 38 437.5 42 437.5 43 434.5 43 434.5
Indels 7; Gaps 2; TPGKGLEWVSSISSGGNYIDY 60 62 APGKGLEWVSSISSSSYIYY 62 GTIFGSAATWRAFDIWGRGTM 120 RGSTGMDVWGRGTL 115	Length 245;	Sequence 49, Appl Sequence 96, Appl Sequence 96, Appl Sequence 51, Appl Sequence 76, Appl Sequence 76, Appl Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 99, Appli Sequence 54, Appli Sequence 54, Appli Sequence 54, Appli

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PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1937

LENGTH: 241

TYPE: PRT

OCGANISM: Homo sapiens
US-09-880-748-1937
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US-09-880-748-1937
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; ORGANISM: Homo sapiens
US-09-880-748-1179
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1179
LENGTH: 250
                                                                                                           Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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CURRENT FILING DATE: 2001-06-15
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PRIOR FILING DATE: 2000-10-17
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                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCTTDGYYDILTGYSVYYGMDVWGRG 120
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                    2 VQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDYA 61
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VQLVQSGGGLVKSGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYA
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71.7%; Pred. No. 3.5e-36;
vative 12; Mismatches 22;
                                                                                                           70.4%;
75.0%;
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                                                                                      Score 463; DB 11;
Pred. No. 5.1e-36;
8; Mismatches 15;
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Sequence 2040, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212.210
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-10-17
PRIOR PELING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
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US-09-880-748-2019
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US-09-880-748-2019
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SEQ ID NO 2019
LENGTH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.3%;
Best Local Similarity 73.6%;
Matches 92; Conservative
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/279,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                      APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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SEQ ID NO 883
LENGTH: 250
TYPE: PRT
                  FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 270
LENGTH: 126
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Best Local Similarity 75.8%;
Matches 94; Conservative
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NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                               APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO
TITLE OF INVENTION: THEREOF
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TYPE: PRT
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5. US20030059937A1
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PRIOR PELLICATION NUMBER: 60/293,499
PRIOR FILLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1764
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-880-748-1179
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
Sequence 1179, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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Best Local Similarity
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Best Local Similarity
Matches 93; Conserv
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PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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74.6%; Pred. No. 9.7e-37;
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71.0%; Pred. No. 2e-;
tive 11; Mismatches
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CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13

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APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 126
TYPE: PRT
US-10-091-300-31
; Sequence 31, Application US/10091300
; Publication No. US20030108545A1
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Best Local S
Matches 95
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Best Local Similarity
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10-041-860-208
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1 Similarity 75.4%;
95; Conservative
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Similarity 75.4%;
95; Conservative
                                                                                                                 LVTVSS 126
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                                                                                                                                                                                                                                                                                                                                    Score 471.5; DB 12; Length 126;
Pred. No. 4.1e-37;
9; Mismatches 21; Indels 1;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1318
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-880-748-1318
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3239
SOPTMARE: Patentin Ver. 2.0
SEQ ID NO 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1318, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 31
LENGTH: 116
                                                                                                                                                                            Query Match
Best Local (
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rockwell, Patricia APPLICANT: Goldstein, Neil I
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Local Similarity 75.2%;
nes 94; Conservative
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61
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93; Conservative
                    ADSVKGRFTISRDNANNVVYLQMNSLRAEDWAVYFCARD-GTIFGSAATWR----AFDIW 115
                                                                                                   EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60
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ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLGSFYDILTALRLENYGMDVW
                                                                            EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY
                                                                                                                                                       71.4%; Score 469.5; DB 1
72.1%; Pred. No. 1.3e-36;
htive 11; Mismatches 20
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Pred. No. 4.6e-37;
8; Mismatches 14; Indels 9;
                                                                                                                                                                                                 DB 11;
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Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10150475A Publication No. US20030103985A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 444
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CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                     APPLICANT: Adolf, G. et al.

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1211

CURRENT APPLICATION NUMBER: US/10/150,475A

CURRENT FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: US 60/307,451

PRIOR APPLICATION DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 9
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ORGANISM: Human
                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain:
                                                                                                                                                                                                                                            TYPE: PRT
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                                                              l Similarity
92; Conserv
1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60
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                                                            71.8%;
nilarity 73.6%;
Conservative
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                                                            Score 472.5; DB 15; Length Pred. No. 1.3e-36; B; Mismatches 14; Indels
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Pred. No. 1.6
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: 60/05-15
PRIOR APPLICATION NUMBER: 60/210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-01-01-01
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
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US-10-041-860-13
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
             APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OP INVENTION: ANTIBODIES DIRECTED
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
                                                                                                                                                                                                        APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                    APPLICANT:
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ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/10/041,860
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                                                                                                                                        Yang, Xiao-Dong
Chen, Francine
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o. US20030059937A1
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                                                             PDGFD AND USES
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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Gapop 10.0 , Gapext 0.5
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658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLVKSGEGLVKPGGSLRL.....AATWRAFDIWGRGTMVTVSS 125
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            72.6
72.3
71.8
71.7
71.7
71.7
71.7
71.5
71.5
71.6
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71.0
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/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length DB
            244
126
126
116
116
256
250
250
247
247
237
               US-09-880-748-1362
US-10-1091-300-24
US-10-150-475A-6
US-09-880-748-913
US-10-041-860-13
US-10-041-860-208
US-10-091-300-31
US-09-880-748-1318
US-09-880-748-1318
US-09-880-748-1764
US-09-880-748-1179
US-09-880-748-1179
US-09-880-748-2019
US-09-880-748-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
Sequence 1362 Apple Sequence 24, Appl Sequence 913, Apple Sequence 913, Apple Sequence 31, Apple Sequence 31, Apple Sequence 1318, Apple Sequence 270, Apple Sequence 1764, Apple Sequence 1764, Apple Sequence 1779, Apple Sequence 1179, Apple Sequence 1179, Apple Sequence 2019, Apple
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45	44	43	42	41	40	39	38	37	36	35	34	IJ IJ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
•		•		455.5	455.5	456	456	456.5	an.	456.5	456.5	457.5	457.5	458.5	458.5	458.5	458.5	458.5	458.5	458.5	u	459.5	460	460.5	461	461.5	•	•	
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238	237	237	237	237	237	255	250	254	240	240	237	248	237	240	240	239	237	237	237	237	236	240	127	247	255	249	124	248	240
11	11	11	11	H	H	11	12	H	H	#	11	H	11	1	11	1	11	11	11	11	11	11	11	H	11	11	15	H	11
-09-880-748-	-880-748-	-880-748-	US-09-880-748-2111	US-09-880-748-2110	-748-	-748-	US-10-120-414-72	US-09-880-748-1428	-09-880-748-	US-09-880-748-2029	æ	US-09-880-748-1965	ä	*	US-09-880-748-2030	-748	US-09-880-748-2114	-09-880	US-09-880-748-2020	US-09-880-748-2006	US-09-880-748-2010	US-09-880-748-2025	-798	US-09-880-748-1703	US-09-880-748-1608	US-09-880-748-1856	US-10-040-244-16	US-09-880-748-1974	-09-880
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2024,	118,	2115,	?111,	2110,	2005,		72, Ap	1428,	2045,	2029,	2003,	1965,	2039,	2044,	2030,	2034,	?114,	2036,	2020,	2006,	2010,	2025,	27, Ag	1703,	1608,	1856,	l6, Ąį	1974,	7007,
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ALIGNMENTS

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RESULT 1
US-09-880-748-1362
| Sequence 1362, Application US/09880748
| Publication No. US20030059937A1
| GENERAL IMFORMATION:
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
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| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS |
| TITLE OF INVENTION NUMBER: 60/201-06-15 |
| PRIOR APPLICATION NUMBER: 60/2740,816 |
| PRIOR APPLICATION NUMBER: 60/277,379 ```

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В
Search completed: December 30, 2003, 10:54:36 Job time: 41.2945 secs
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 8 B
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 Query Match 70.9%; Score 466.5; DB 22; Length 119; Best Local Similarity 70.3%; Pred. No. 1e-35; Matches 90; Conservative 12; Mismatches 13; Indels 13;
 The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries.
 Producing gene libraries and antibody libraries, involves selecting a light chain that binds to a heavy chain product to produce a functional formation, and producing a gene library of the light chain variable
 Sequence
 Examples; p 168-169; 181pp; Japanese.
 WPI; 2001-565420/63.
N-PSDB; AAH47732.
 Kurosawa Y, Akahori Y, Iba Y, Okuno Y, Shiraki K;
 regions -
 22-FEB-2000; 2000JP-0050543.
 22-FEB-2001; 2001WO-JP01298.
 (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 112
 117
 7 RGTMVTVS 124
:||:||||
2 QGTLVTVS 119
 119 AA;
 Morino K,
 Shinohara M,
 Indels 13;
 Takahashi M;
 Gaps
 60
 60
```

```
RESULT 14
ABP4573
ID ABP4573
XX ABP4573
AC ABP45
XX BLY8;
CHUMAN
XX BLY8;
KW LUMON
KW LUMON
KW LUMON
KW ANTIA
KW SYSTE
KW GOMMO
XX COMMO
XX HOMO
XX HOMO
XX HOMO
XX HOMO
XX HOMO
XX 10-JA
XX 15-JU
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 CC megakaryocytes. They may also be able to stimulate megakaryocytes to come increase platelet production. They can be used for treating communological or hematopoietic disorders, especially thrombocytopenia. CC finmunological or hematopoietic disorders, especially thrombocytopenia. CC following chemotherapy or bone marrow hypoplasia (e.g. aplastic anemia community community or bone marrow transplant) may be effectively community or bone marrow transplant) may be effectively community or compounds as well as disorders such as community or compounds as well as disorders such as community or community or compounds as the community of the communit
 Query Match
Best Local :
 Matches
 The invention relates to an agonist antibody (Ab) which binds to a thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can be used in the same way and for the same indications as thrombopoietin (TPO). They can stimulate proliferation, differentiation or growth of
 New thrombopoietin receptor agonist antibodies - useful treating immunological or hematological disorders
 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 various antibodies.
 Disclosure; Fig 1; 86pp; English.
 19-AUG-2002 (first entry)
 ABP45753;
 ABP45753 standard; Protein; 247 AA.
 Human
15-JUN-2001; 2001WO-US19110
 10-JAN-2002
 Homo sapiens.
 common variable
 WO200202641-A1
 116
 121
 BLyS binding scFv SEQ ID 1764.
 63
 5
 93,
 ω
 μ
 Similarity
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVSS 120
 VIVSS 125
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDR---GST----GMDVWGRGTL
 QVQLVESGGGLVKPGGSLRLSCAASGFTFSSHNMNWVRQAPGKGLEWVSSISSSSYIYY
 245 AA;
 Conservative
 immunodeficiency; acquired
 71.0%;
 11;
 Score 467.5; DB 2
Pred. No. 1.8e-35;
 Mismatches
 DB 20;
 immunodeficiency syndrome
 14;
 Indels
 Length
 7;
 Gaps
 115
 62
 60
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RESULT 15
AAG65568
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 S
 This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TMF) super family and induces B cell the CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antitheumatic and antiAIDS activity and can be used in vaccines to CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC discasses, seek to treat diseases associated with aberrant Expression of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC cquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC of the antibodies and fragments of the antibodies described in the method CC of the invention
 문
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Matches
 Best
 Query Match
 16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
 Claim 1; Page 2507-2508; 3148pp; English
 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
 WPI; 2002-114799/15.
 Sequence
 Ruben SM,
 (HUMA-)
 Amino acid sequence of protein seq Id No. 93
 30-NOV-2001
 AAG65568 standard; protein; 119 AA
 (CAMB-)
 Local
 the invention.
 sapiens.
 library;
 114
 115
 13
 13
 ۲
 93;
 HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
 Similarity
 WGKGTLVTVSS 124
 WGRGTMVTVSS 125
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARD-----GTIFGSAATWRAFDI 114
 EVQLVXSGEGLVXPGGSLRLSCAASGPTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCARDEYDILTGLLQG------MDV 113
 Barash SC,
 247
 Conservative
 (first entry)
 immunoglobulin; antibody library;
 ξ
 71.0%; Score 467.5; DB 2
71.0%; Pred. No. 1.8e-35;
tive 11; Mismatches 14
 Choi GH, Vaughan
 'n
 DB 23;
 14;
 Hilbert
 Indels
 Length 247;
 Ö
 13;
 60
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30-AUG-2001

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RESULT 12
ABP44872
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 Query Match
Best Local
 Matches
 inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
 BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
 16-JUN-2000; 2000US-212210P.
16-MAR-2000; 2000US-240816F.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
 Claim
 Ruben
 (CAMB-)
 10-JAN-2002
 WO200202641-A1
 Homo sapiens.
 Human BLyS binding scFv SEQ ID 883.
 19-AUG-2002
 ABP44872;
 ABP44872 standard; Protein;
 Sequence
 of the invention.
 15-JUN-2001; 2001WO-US19110
 121
 116
 ۲.
 ž,
 61
 13
 93;
 variable immunodeficiency; acquired immunodeficiency syndrome
 ᆫ
 HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TI
 Similarity
Page 1455-1456; 3148pp; English
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARD-GTIFGSAATWR----AFDIW
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 GKGTLVTVS 129
 GRGTMVTVS
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLGSFYDILTALRLENYGMDVW
 EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYY
 Barash SC,
 256 AA;
 Conservative
 (first entry)
 124
 71.4%; Score 469.5; DB 2
72.1%; Pred. No. 1.3e-35;
 Choi GH,
 TECHNOLOGY.
 250 AA.
 Mismatches
 Vaughan T,
 DB 23;
 Hilbert
 20;
 Indels
 Length 256;
 Ģ
 Gaps
 BLyS
 115
 120
 60
 60
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RESULT 13
AAYO6717
ID AAYO6
AC AAYO6
AA
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 문
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 S
 CC This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNF) super family and induces B cell CC proliferation and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiAIDS activity and can be used in vaccines to CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS cand so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease CC associated with aberrant expression of BLyS. They may also be CC administered to treat diseases associated with aberrant appression of BLyS. They may also be compared to treat disease associated with aberrant BLyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and confirm the mothod confirmed immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent CC for the antibodies and fragments of the antibodies described in the method
 Best Loc
Matches
 Query Match
 Agonist antibody; thrombopoletin receptor; TPO-R; thrombopoletin; DIC; megakaryocyte; platelet; immunological; hematopoletic; thrombocytopenia; bone marrow hypoplasia; disseminated intravascular coagulation; anemia; myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR; neuromuscular; muscular dystrophy; complementarity determining region.
 WPI; 1999-204666/17
 25-AUG-1997;
 21-AUG-1998;
 04-MAR-1999
 WO9910494-A2
 Misc-difference
 Homo sapiens.
 Antibody 12B5 single chain Fv (scFv) fragment.
 17-JUN-1999
 AAY06717;
 AAY06717 standard; Protein; 245 AA.
 Sequence
 of the invention.
 (GETH) GENENTECH INC
 госат
 121
 122
 Š
 61
 62
 94;
 N
 N
 Similarity
 TVSS 124
 DSVRGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCARDSYDILTGYRGYYFDYWGKGTLV
 DSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTMV 121
 TVSS 125
 VQLVQSGGGLVQPGGSLRLSCAASGFTFRSYSMNWVRQAPGKGLEWVSSISSGGN-IYYA
 VQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDYA 61
 Carter PJ,
 250 AA;
 71.2%;
ilarity 75.8%;
Conservative
 (first entry)
 97US-0918148
 98WO-US17364
 Location/Qualifiers 208
 /note= "unspecified"
 Fendly
 ; Score 468.5; 1; Pred. No. 1.5e. 9; Mismatches
 묤,
 Gurney AL;
 1.5e-35;
 DB 23;
 20;
 Indels
 Length
 1;
 Gaps
 60
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RESULT 10
ABJ26766
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 Matches
 Query Match
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 expresses VEGFR. It is also useful for inhibiting growth of colon tumou or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR It is preferably useful for treating subjects with both solid tumours preferably high vascular tumours and non-solid tumours. The inhibition or reduction of tumour growth includes prevention or inhibition of the progression of tumour, including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody heavy chain protein.
 Sequence
 Cytostatic; antibody; antigen binding site; leukaemia cell; vascular endothelial growth
 01-MAY-2003
 ABJ26766;
 ABJ26766 standard;
The invention relates to a novel antibody having a first antigen bindi site specific for a first vascular endothelial growth factor (VEGP) receptor and a second antigen-binding site specific as second VEGP receptor. The bispecific antigen-binding proteins block activation of VEGP receptor and are useful for reducing or inhibiting VEGP-induced cellular functions such as mitogenesis of vascular endothelial cells
 New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
 Zhu
 WO2003002144-A1
 Homo
 bispecific
 N-PSDB; ABT23330
 26-JUN-2001;
 26-JUN-2002; 2002WO-US20332
 (IMCL-)
 sapiens
 112
 121
 2003-201468/19.
 61
 61
 94;
 ш
 سر
 Similarity
 IMCLONE SYSTEMS INC
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVSS
 VTVSS 125
 EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY
 ADSVKGRFTISRDNAKDSLYLQMNSLRAEDTAVYYCAR-----VTDAFDIWGQGTM
 Page 74; 98pp;
 116 AA;
 antigen-binding
 Conservative
 2001US-301299P.
 related
 (first
 Protein;
 entry)
 71.5%;
75.2%;
 protein
 ••
 English.
 8
 SEQ
 Score 470.5; DB 2
Pred. No. 4.3e-36;
 Mismatches
 ζ
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 83
 VEGF receptor; mitogenesis;
factor; tumour;
 14;
 23;
 Indels
 Length
 9;
 Gaps
 e tumour
 binding
 111
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 60
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 ABP45307
 RESULT 11
 Matches
 16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
 tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a human protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to
 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 Sequence
 and migration of leukaemia cells. The antibodies are useful
 WO200202641-A1
 Human BLyS binding scFv SEQ
 ABP45307;
 ABP45307
 Antibodies against B Lymphocyte Stimulating polypeptides, untibodies and treatment of cancers and immune disorders
 15-JUN-2001; 2001WO-US19110
 10-JAN-2002.
 Homo
 Claim
 (CAMB-)
 HUMA-)
 COCAL
 Match
 sapiens.
 121
 2002-114799/15
 61
 61
 £
 94;
 Similarity
 CAMBRIDGE
 HUMAN
 SSALA
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 BVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYY
 BVQLVKSGBGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 standard; Protein; 256
 SSAIA
 Page 1975-1976; 3148pp; English.
 71.5%;
nilarity 75.2%;
Conservative
 116 AA;
 Barash SC,
 2000US-212210P.
2000US-240816P.
2001US-276248P.
2001US-277379P.
2001US-293499P.
 (first
 GENOME SCI INC
 116
 125
 ANTIBODY TECHNOLOGY.
 ent ry
 Choi GH,
 ID 1318.
 8;
 Score 470.5;
Pred. No. 4.
 Mismatches
 Vaughan T,
 4.3e-36;
 멂
 14;
 Hilbert
 24;
 Indels
 Length
 Ö
 116;
 useful
 9
 for treating
 Gaps
 120
 111
 60
 60
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RESULT 8
ABP44902
ID ABP4
XX BLys
KW BLys
KW Inmm
KW Syst
KW Comm
XX Homo
XX L15-L
PD 11-L
XX Homo
XX Clail
XX Cla
 5
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 SX
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 Query Match
Best Local S
Matches 92
 16-JUN-2000;
17-OCT-2000;
16-MAR-2001;
 Homo
This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLy and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
 Blys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomdulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritts; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 Sequence
 10-JAN-2002
 Ruben
 WO200202641-A1
 19-AUG-2002
 ABP44902
 Claim
 WPI;
 21-MAR-2001;
 15-JUN-2001;
 ABP44902 standard;
 (CAMB-)
 (HUMA-)
 ibodies against B Lymphocyte Stimulating diagnosis and treatment of cancers and i
 2002-114799/15.
 sapiens.
 110
 121
 33
 61
 BLyS binding scrv SEQ
 13
 μ.
 HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TI
 Similarity
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 VIVSS 125
 LDSIKGRPTISRDNAKNSLYLOMNSLRAEDTAVYYCAROG-----
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY
 Page 1491-1492; 3148pp; English.
 SSALA
 444
 Barash SC,
 ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
 Conservative
 2001WO-US19110
 (first
 114
 8
 Protein;
 entry
 . 6%;
 Choi GH,
 TECHNOLOGY.
 IJ
 8
 248
 Score 472.5; DB 2
Pred. No. 1.2e-35;
B; Mismatches 14
 913.
 ₹
 Vaughan
 H
 polypeptides, useful immune disorders -
 14;
 Hilbert
 24;
 Indels
 Length
 444
 11;
 -LDYWGRGTL
 Gaps
 have
 120
 60
 109
 60
 G
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```
RESULT 9
AAE28873
ID AAE2
 និនិនិនិនិនិនិ<mark>ន</mark>ិ
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 S
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 吊
 Query Match
Best Local S
Matches 90
 Inhibiting tumor growth in numame at endothelial growth factor receptor a radiation, chemotherapeutic agents,
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method
 administered to treat diseases associated with aberrant BLyS and activity such as cancer, immune, and autoimmune disorders
 WPI; 2002-691738/74.
N-PSDB; AAD46294.
 Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 Human
 AAE28873
 Sequence
 Example 12; Page 127; 151pp; English.
 02-MAR-2001; 2001US-0798689
 04-MAR-2002; 2002WO-US06762
 WO200270008-A1
 27-DEC-2002
 AAE28873;
 of the invention.
 antagonists
 12-SEP-2002.
 Homo sapiens.
 breast; VEGFR;
 (GOLD/)
 (IMCL-)
 121
 121
 KDR (VEGFR-2) Fab
 61
 61
 90;
 ROCKWELL P. GOLDSTEIN N
 Similarity
 IMCLONE SYSTEMS
 VIVSS
 standard;
 VIVSS 125
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAREGRDILTGVYYYGLDVWGQGTL
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVESGGGLVQPGGSLRLSCAAFGFTFSSYSMNWVRQAPGKGLEWVSSISNRGSYIYY
 tumor growth in humans involves administering vascular l growth factor receptor antagonists in combination with chemotherapeutic agents, or epidermal growth factor receptor
 248 AA;
 Conservative
 (first
 125
 heart;
 Protein;
 entry
 71.7%;
 EGFR; therapy; invasiveness; heavy chain;
 heavy chain
 14;
 116
 Score 472;
Pred. No. 7.
 Mismatches
 ₹
 Œ
 DB 23;
 protein
 from
 Length
 Indels
 disorders and
 D2H2
 clone
 0;
 expression
 Gaps
 60
 60
 120
```

The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over

The method

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RRESULT 6
AAB3 4873
AXX
AAB3 4873
AX
AB3 4873
AX
AB3 4873
AX
AB3 4873
AAB3 Query Match
 The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a human protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention.
 Sequence
 BIWA8 antibody;
VH; VL; CD44v6;
 BIWA8 antibody heavy chain variable region.
 AAE34873
 New antibodies specific for an epitope coded by the variant exon CD44 gene, useful for treating cancer, including non-small cell l breast, head and neck, ovarian and lung cancer -
 WO200294879-A1
 18-MAY-2001; 2001EP-0112237.
26-SEP-2001; 2001US-325147P.
 17-MAY-2002; 2002WO-BP05467.
 Van Dongen
 HBOEH
HBOEH
 Adolf G,
 Local
 2003-129413/12.
DB; AAD53209.
 112
 121
 61
 61
 -
 95; Conser
 BOEHR INGER
BOEHR INGER
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----VTDAFDIWGQGTM
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 VIVSS 116
 VIVSS 125
 EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYY
 Ostermann
 116 AA;
 Conservative
 (first
 heavy chain variable region; light che medicament; cancer; antibody therapy.
 INGELHEIM
 Protein; 114
 M
 72.3%;
 Patzelt E,
 INT GMBH.
 Score 475.5; DB 2
Pred. No. 1.5e-36;
7; Mismatches 14
 Sproll M,
 DB 24;
 14;
 light chain variable region;
 Heider
 Indels
 Length 116;
 ζ,
 Miglietta
 9
 Gaps
 111
 120
 60
```

The present invention relates to novel antibody molecules comprising variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating

Claim

1; Column 43; 78pp; English.

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RESULT 7
AAB3487
ID AAB37
XX AAB38
XX AAB32
XX AAB32
XX AAB32
XX BIW
DI 28-P
DI 28-P
DI 28-P
DI 28-P
DI 18-P
PR 18-P
P
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 문
 Query Match
Best Local
 Matches
 cancer including colorectum, non-small cell lung, breast, head and necovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIMA8 antibody heavy chain variable region. This sequence is used in the exemplification of the invention.
The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWAA/8 antibody heavy chain mature protein. This sequence is used in the exemplification of the invention.
 BIWA8 antibody; heavy chain VH; VL; CD44v6; medicament;
 WO200294879-A1
 Unidentified
 BIWA4/8 antibody heavy chain mature protein
 28-MAY-2003
 AAB34876;
 AAE34876
 Sequence
 New antibodies specific for an epitope coded by the variant exon of t CD44 gene, useful for treating cancer, including non-small cell lung, breast, head and neck, ovarian and lung cancer
 18-MAY-2001; 2001BP-0112237.
26-SEP-2001; 2001US-325147P.
 17-MAY-2002; 2002WO-EP05467
 Claim 24; Column 44; 78pp;
 Adolf G,
 (BOEH)
 110
 121
 13
 61 ADSVKGRETISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 Similarity
 BOEHRINGER INGELHEIM BOEHRINGER INGELHEIM
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 standard; Protein;
 SSAIA
 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY
 Ostermann
 Conservative
 (first
 114
 AAD53215
 71.8%;
73.6%;
 ά
 entry
 Patzelt
 444
 variable region; light chain variable region; cancer; antibody therapy.
 8
 Score 472.5; DB 2
Pred. No. 2.7e-36;
 PHARM
 INT GMBH.
 Mismatches
 Sproll
 Σ,
 14;
 24;
 Heider
 Indels
 Length
 11;
 -LDYWGRGTL
 and neck,
 Gaps
 60
 60
 109
```

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RRSULT 4
AAAE280 TA
AAE280 TA
AAAE280 TA
AAE280 TA
AAE280 TA
AAE280 TA
AAAE280 TA
AAE280 TA
AAE2
 និនិត្តនិង្គិនិត្តនិង្គិនិង្គិនិង
 문
 ঠ
 밁
 ঠ
 밁
 ঠ
 Query Match
Best Local S
Matches 97
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
 Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
 Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
 02-MAR-2001; 2001US-0798689
 04-MAR-2002; 2002WO-US06762.
 12-SEP-2002.
 WO200270008-A1
 Homo sapiens.
 Human KDR (VEGFR-2) Fab heavy chain protein from D2C6 and D1H4 clone.
 27-DEC-2002
 AAE28870 standard; Protein; 116
 2002-691738/74.
 13
 13
 invention.
 l Similarity
97; Conserv
 _
 -
 IMCLONE SYSTEMS INC. ROCKWELL P.
 GOLDSTEIN N I.
 AAD46290, AAD46292.
 WGRGTLVTVSS 124
 WGRGTMVTVSS
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGHYDILTGYYFG-----
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCAR-----DGTIFGSAATWRAFDI 114
 EVOLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 252 AA;
 Conservative
 (first entry)
 125
 72.6%;
 Score 477.5; DB 2
Pred. No. 2.2e-36;
6; Mismatches 15
 DB 23; Length 252;
 15;
 Indels 13;
 Gaps
 BLyS
 60
 60
```

The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor

Example 9; Page 123; 151pp; English

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 밁
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic cagent, or epidermal growth factor receptor (EGFR) antagonist. The method cc is useful for inhibiting tumour growth in a human, where the tumour (e.g. ctumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, colone marrow, blood, thymus, uterus, testicles, cervix or liver) over cc expresses VEGFR. It is also useful for inhibiting growth of colon tumour cor non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, cc preferably high vascular tumours and non-solid tumours. The inhibition cor reduction of tumour growth includes prevention or inhibition of the progression of tumour, including cancerous and non-cancerous tumours, cc where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is cc human KDR (VEGFR-2) Fab antibody heavy chain protein.
 Matches
 Query Match
Best Local
 New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGP) receptor and for a second VEGP receptor, useful for inhibiting migration of leukemia cells, or for treating tumors -
 Cytostatic; antibody; antigen binding site; leukaemia cell; vascular endothelial growth bispecific antigen-binding protein; human.
 Claim 15; Page 70-71; 98pp; English
 WPI;
 26-JUN-2001; 2001US-301299P
 26-JUN-2002; 2002WO-US20332
 09-JAN-2003.
 Homo sapiens.
 VEGF binding
 01-MAY-2003
 ABJ26763;
 ABJ26763 standard; Protein; 116
 Sequence
 N-PSDB;
 (IMCL-)
 WO2003002144-A1
 2003-201468/19.
DB; ABT23325.
 112
 121 YTVSS 125
 52
 5
 1 EVOLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 95
 IMCLONE SYSTEMS INC
 Similarity
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-----VTDAFDIWGQGTM
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY
 116 AA;
 Conservative
 related
 (first entry)
 72.3%;
76.0%;
 protein
 Score 475.5; 1
Pred. No. 1.5e
7; Mismatches
 7;
 SEQ
 ij
 ö
 1.5e-36;
 76.
 DB 23;
 factor; tumour;
 VEGF receptor; mitogenesis;
 14;
 Indels
 Length 116;
 9
 Gaps
 60
 60
```

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밁
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 Matches
 Query Match
 This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a fragment of the human factor VIII antibody heavy chain variable region protein B04 which is used in the method of the invention.
 Human; heavy hemophilia A;
 Human FVIII antibody A3-C1 scFv heavy chain protein B04
 AAY50965;
 Sequence
This invention describes a novel polynucleotide (I) (and comple hybridizable polynucleotides) comprising a contiguous nucleotic coding for a human antibody with factor VIII specificity which hemostatic activity. (I) is useful a primer or probe for detect
 New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
 08-MAY-1998;
 07-MAY-1999;
 18-NOV-1999.
 WO9958680-A2
 Homo sapiens
 23-MAR-2000
 AAY50965 standard; Protein; 126
 WPI; 2000-053102/04
 (SANQ-)
 Local
 121
 121
 125;
 61
 61
 Similarity
 8; Fig
 8
 STICHTING
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVSS 125
 VIVSS 125
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 'n
 of hemophilia A patients with these antibodies
 Fig
 125 AA;
 Conservative
 chain;; scrv;
 (first entry)
 Van
 9A; 61pp;
 98EP-0201543
 99WO-NL00285
 Den
 SANQUIN BLOEDVOORZIENING
 antibody;
A3-C1.
 100.0%;
 Brink
 English.
 English
 EN,
 0
 Score 658; DB 21;
Pred. No. 2.1e-53;
 factor VIII; hemostatic;
 Mismatches
 Turenhout EAM;
 0;
 Length
 Indels
 125;
 complements and
 0
 120
 120
 60
 60
 0
```

detecting

sequence

This invention describes novel antibodies that immunospecifically bir B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWP) super family and induces B cell proliferation and differentiation. The antibodies of the invention has

bind to

have

Page

2028-2029; 3148pp; English.

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RRSULT 3
ABP453511
ABP453511
ABP45351
ABP465351
ABP46531
ABP465351
ABP465351
ABP465351
ABP465351
ABP465351
ABP465351
ABP465351
ABP465351
ABP46531
ABP465351
ABP46531
ABP466531
ABP466531
ABP466531
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ABP46667
ABP46667
ABP46667
ABP46667
ABP46667
ABP46667
ABP46667
ABP4
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 Query Match
Best Local Simi
Matches 125;
 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from the are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the factor VIII antibody A3-C1 specific scrv protein B04 which is used in the method of the invention.
 16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
 Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
 Human
 19-AUG-2002
 ABP45351
 Sequence
 15-JUN-2001; 2001WO-US19110
 WO200202641-A1
 Homo sapiens.
 (CAMB-)
 10-JAN-2002
 2002-114799/15
 121
 121
 Z.
 BLyS binding
 61
 61
 -
 HUMAN GENOME SCI II
CAMBRIDGE ANTIBODY
 Similarity 100
25; Conservative
 standard;
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VTVSS
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 SSAIA
 Barash SC,
 126
 (first
 125
 125
 ξ
 BCFV SEQ
 Protein;
 entry)
 100.0%;
 Choi GH,
 INC.
DY TECHNOLOGY
 252
 0;
 ID 1362
 Score 658; DB 21;
Pred. No. 2.1e-53;
Mismatches 0;
 $
 Vaughan
 ,
 Hilbert
 Indels
 Length
 0
 The
 Gaps
 human
 120
 120
 60
 60
 0
```

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Regult
No.
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Database
 Total number of hits satisfying chosen parameters:
 Post-processing: Minimum Match 0%
Maximum Match 100%
 Scoring table:
 Perfect score:
 Title:
 protein -
 95
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 658
477.5
475.5
475.5
472.5
472.5
 Score
 658
 protein search, using sw model
 A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
 Query
Match
 100.0
100.0
72.6
72.3
72.3
71.8
71.8
71.7
 December 30, 2003, 10:42:39; Search time 40.2112 Seconds (without alignments) 493.415 Million cell updates/sec
 US-09-674-752-49
658
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 1107863 seqs, 158726573 residues
 Listing first 45 summaries
 EVQLVKSGEGLVKPGGSLRL.....AATWRAFDIWGRGTMVTVSS 125
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Length
 125
126
252
116
116
444
 89
 딤
 AAY50969
AAY50965
ABP245351
AAE26763
ABJ26763
AAE34873
AAE34873
AAE34876
ABP44902
AAE28873
 SUMMARIES
 1107863
Human FVIII antibo
Human FVIII antibo
Human BLYS binding
Human KCR (VEGFR-2
VEGF binding relat
BIWA# antibody hea
BIWA#/ antibody h
Human BLYS binding
Human KDR (VEGFR-2
 Description
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| 45                 | 44                 | 43                 | 42       | 41       | 40   | 39       | 38       | 37       | 36       | ω<br>S   | 34       | 33       | 32                 | 31                 | 30                 | 29                 | 28                 | 27                 | 26                 | 25                 | 24                 | 23                 | 22       | 21       | 20       | 19       | 18       | 17       | 16       | 15                 | 14       | 13       | 12       | 11       | 10                 |
|--------------------|--------------------|--------------------|----------|----------|------|----------|----------|----------|----------|----------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|----------|----------|----------|----------|--------------------|----------|----------|----------|----------|--------------------|
| 457                | 457.5              | .7                 | ம        | 458.5    |      |          |          |          |          | 458.5    |          |          |                    |                    | 8                  |                    | 460                | 460.5              | 60.                | σ                  |                    | •                  | 462.5    | •        | •        | •        | 463      | σ        | ٥,       | 66.                | 67.      | .7       | 468.5    | 469.5    | 70.                |
|                    | 69.5               | •                  | •        | •        | •    | ٠        | •        | •        | 69.7     | 69.7     | 69.7     | 69.7     | 69.7               | 69.7               | •                  | 69.8               | •                  | •                  | •                  | 70.1               |                    | •                  | 70.3     |          | ٠        | •        | 70.4     |          | •        | •                  | •        |          | •        | 71.4     | •                  |
| 127                | 248                | 237                | 138      | 240      | 240  | 239      | 237      | 237      | 237      | 237      | 236      | 152      | 126                | 118                | 118                | 240                | 127                | 247                | 245                | 255                | 249                | 177                | 248      | 240      | 237      | 237      | 241      | 250      | 240      | 119                | 247      | 245      | 250      | 256      | 116                |
| 22                 | 23                 | 23                 | 21       | 23       | 23   | 23       | 23       | 23       | 23       | 23       | 23       | 22       | 22                 | 22                 | 21                 | 23                 | 22                 | 23                 | 20                 | 23                 | 23                 | 24                 | 23       | 23       | 23       | 23       | 23       | 23       | 22       | 22                 | 23       | 20       | 23       | 23       | 24                 |
| AAU02616           | ABP45954           | ABP46028           | AAY32406 | ABP46033 | 2    | ABP46023 | ABP46103 | ABP46025 | ABP46009 | ABP45995 | ABP45999 | AAB99111 | AAG62934           | AAU02570           | AAB52191           | ABP46014           | AAG93584           | ABP45692           | AAY06714           | ABP45597           | ABP45845           | ABJ36939           | ABP45963 | ABP45996 | ABP46029 | ABP46008 | ABP45926 | ABP45168 | AAB46007 | AAG65568           | ABP45753 | AAY06717 | ABP44872 | ABP45307 | ABJ26766           |
| Anti-adipocyte mon | Human BLyS binding | Human BLyS binding | anti-    |          | BLyS |          |          |          |          |          | BLyS     | æ        | Amino acid sequenc | Anti-adipocyte mon | Human anti-HBs ant | Human BLyS binding | Human anti-Rh(D) c | Human BLyS binding | Antibody 5E5 singl | Human BLyS binding | Human BLyS binding | Anti-CD40 monoclon | CO.      |          |          | BLyS     | BLyS     | BLyS     |          | Amino acid sequenc | Į,       | ĕ        | Ď.       | σ        | VEGF binding relat |

## ALIGNMENTS

| XX                                                                                                                                                                                      | (SANQ-) STICHTI      | XX PF 07-MAY-1999; 99WO-NL00285 XX DB 08-MAY-1998: 98ED-0201543 | PD 18-NOV-1999. | XX<br>PN WO9958680-A2. | OS Homo sapiens. |                                                                                       |                                                                        | DT 23-MAR-2000 (first entry) | XX<br>AC AAY50969;<br>XX | RESULT 1 AAY50969 ID AAY50969 standard; Protein; 125 AA. |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|-----------------------------------------------------------------|-----------------|------------------------|------------------|---------------------------------------------------------------------------------------|------------------------------------------------------------------------|------------------------------|--------------------------|----------------------------------------------------------|
| Voorberg JJ, Van Den Brink EN, Turenhout EAM; WPI; 2000-053102/04. N-PSDB; AAZ43866. New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for | IN BLOEDVOORZIENING. | 0285.<br>11543                                                  |                 |                        |                  | Human; heavy chain; antibody; factor VIII; hemostatic; variable region; hemophilia A. | Human FVIII antibody heavy chain variable region B04 protein fragment. | ry)                          |                          | ein; 125 AA.                                             |

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 Q9HCC1 PRELIMINARY;
Q9HCC1;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 16, Li
01-MAR-2003 (TrEMBLrel. 23, Li
Single chain Fy (Fragment).
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_IKE; 1.
 11
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
Wan der Merwe P.L.,
 NON_TER
NON_TER
SEQUENCE
 Q9UL93; PRELIMINARY; PRT; 116 AA.
Q9UL93; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
(Fragment).
 SEQUENCE FROM N.A.

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

"An antibody fragment2A3 specific for native lysozyme :Isolaion

"An antibody fragment2A3 specific for native lysozyme :Isolaion

human synthetic phage display library and characterization.";

submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB049915; BAB16829.1; -.

HSSP; P01772; 2FB4.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
 Homo sapiens (Human)
 InterPro;
InterPro;
 EMBL; AP035021; AAI
HSSP; P01772; 2FB4.
 Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AP035021; AAD56257.1; -.
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis
 Homo sapiens (Human)
 fetus."
 112
 121
 13
 13
 81;
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 Similarity
; IPR007110; Ig-like.; IPR003006; Ig_MHC.; IPR003596; Ig_v.; IPR003596; Ig_v. 00047; Ig; 1.
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
|||||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
 <
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 V 112
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCAR-----RRYALDYWGQGTL
 121
 112
112 AA;
 62.1%; Score 408.5; DB 4 llarity 66.9%; Pred. No. 1.1e-34; Conservative 10; Mismatches 21
 112
; 12243 MW;
 Last sequence update)
Last annotation updat
 Created)
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 24F1A45EC3B84788 CRC64;
 Kalis N.N., Berney S.M
 112
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 DB 4; Length 112;
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 TVSS 125
 PS50835; IG_LIKE;
 DSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTMV 121
TVSS 116
 DSVKGRFTI
 116 116
116 AA; 12434 MW; ODA0348154DD6061 CRC64;
 Conservative
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|SRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGL----
 62.0%; Score 408; DB 4; Length 116; 65.3%; Pred. No. 1.3e-34;
 13; Mismatches
 Indels
 -GLGYWGQGTLV 112
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Search completed: December 30, 2003, 11:01:09 Job time : 31.463 secs

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RESULT 12
Q91Z05
ID Q91Z0
AC Q91Z0
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 Strausberg R.;
Stbmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -.
MGD; MGI:2144967; AU044919.
InterPro; IPR000345; CytC heme_bind.
InterPro; IPR007110; Ig_like.
InterPro; IPR007106; Ig_wHC.
InterPro; IPR003906; Ig_wHC.
InterPro; IPR003906; Ig_wHC.
 NON_TER
 Q9UL84 PRELIMINARY; PRT; 122 AA.
Q9UL84;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
 O91Z05; PRELIMINARY; PRT; 473 AA.
Q91Z05;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.9 kDa protein.
AU044919.
 SEQUENCE FROM N.A.

MEDLINE-98277139; PubMed-9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;

"Myosin-reactive autoantibodies in rheumatic carditis and normal
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 EMBL; AF035030; AAI
HSSP; P01772; 2FB4.
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Homo sapiens (Human)
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 (Fragment).
 etus."
 119
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 61
 Immunol. Immunopathol. 87:184-192(1998).
 84;
 Similarity
 ADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDERGRLVGT----YFDYWGQG 115
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARD--GTIFGSAATWRAFDIWGRG 118
 SSALAML
 EVQLVESGGGVVQPGRSLRLSCAASRFTFSNYGMMVRQAPGKGLEWVAAISNDGSNKFY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 TLVTVSS
 1
122
122 AA;
 Conservative
 AAD56266.1; -.
 122
 125
 122
13579 MW; 36054D41366545B8 CRC64;
 Chordata;
 63.9%; Score 420.5; DB 4
66.1%; Pred. No. 7.1e-36;
tive 17; Mismatches 19
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 DB 4; Length 122;
 19;
 Indels
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 7;
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RESULT 13
202087
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 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 NON TER
 Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Exprin Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP307937; AAL094211; -.
 Q920E7 PRELIMINARY; PRT; 119 AA. Q920E7; Q920E7; Q920E7; Q1-DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update) Pterin-mimicking anti-idiotope heavy chain variable
 SEQUENCE
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 SMART; SM00406; IGv; 1.
PROSITE; PS00190; CYTOCHROME C;
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW;
 SEQUENCE FROM N.A.
 (Fragment)
111
 117
 132 TITVSS 137
 120 MVTVSS 125
 61
 5
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 Similarity
 h 63.6%;
Similarity 65.1%;
82; Conservative 14
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDI----WG
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATW-RAFDIWGRGT
OGTLVIVSA
 RGTMVTVSS
 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHGD
 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCARE-----LWLRRIDYWGQGT
 119 AA; 13025 MW;
 119
 Conservative
 125
 63.5%; Score 418; DB 11; 63.6%; Pred. No. 1.2e-35; tive 17; Mismatches 16;
 14;
 Score 418.5; DB 11; Length
Pred. No. 6.4e-35;
4; Mismatches 21; Indels
 F6E904044381CA7C
 CF625F008932AF12 CRC64;
 16;
 CRC64;
 Length 119;
 Indels
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RESULT
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 Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat
Submitted (JUN-2002); to the EMBL/GenBank/DDBJ dat
EMBL; BC032249; AAH32249.1; -.

InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003006; Ig_W.
RINTERPO; IPR003596; Ig_W.
RINTERPO; IPR003596; Ig_W.
REART; SM00407; IG; 4.
SMART; SM00409; IG; 4.
SMART; SM00406; IGV; 1.
ROSITE; PS05035; IG_LIKE; 4.
RPOSITE; PS05035; IG
 099KA4 PRELIMINARY; PRT; 487 AA.
099KA4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
 Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Q8N5K4;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Q8N5K4
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
 EMBL; BC004786; AAH04786.1; HSSP; P01810; 2FBJ.
 Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
 TISSUE=Blood;
 SEQUENCE FROM N.A.
 8
 Local Similarity
 119
 140
 8
 61
 20
 85;
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAF--DIWGRG 118
 TTVIVSS
 ADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPTKYCSGGSCLGYYMDVWGKG
 EVOLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY
 TMVTVSS 125
 Conservative
 PRELIMINARY;
 146
 66.9%;
 ; Score 429; DB 4;
; Pred. No. 5.6e-36;
13; Mismatches 27
 Created)
Last sequence update)
Last annotation update)
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 93A5C89582054F32 CRC64;
 ₽
 4; Length 499;
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 Indels
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RESULT 10
Q9UL9
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 Q9UL90;
Q9UL90;
01-MAY-2000 (
 NON_TER
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SEQUENCE
 PROSITE; P850835; IG_LIKE; 4.
PROSITE; P800290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 487 AA; 52554 MW;
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 EMBL; AF035024; AAD56260.1; HSSP; P01772; 2FB4.
 Wu X., Liu B., Van der Young D.C.;
 SEQUENCE FROM N.A. MEDLINE=98277139;
 NCBI_TaxID=9606;
 (Fragment).
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 Myosin-reactive autoantibodies in rheumatic carditis and normal
 119
109
 121
 137
 Immunol. Immunopathol. 87:184-192(1998).
 80
 61
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 61
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 83;
 83;
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 Similarity
 Similarity
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVVFCARD--GTIFGSÅATWRAFDIWGRG
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
|||||:|| |||||||||||||| | : ||||||| | ||||::|| ||||:||
EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAWSWVRQTPEKRLEWVATISDGGSYTYY
 PDNVKGRPTISRDNAKNNLYLOMSHLKSEDTAMYYCARDMGGSPYGG---YSRFDYWGOG
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 EVOLVKSGEGLYKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 TTITVSS
 SSALAMI
 SSAIA
 ADSVKGRFTISRDNSKVTLYLQMNSLRAEDTAVYYCAKD
 EVQLVESGGGVVQPGGSLRLSCAASGPTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY
 VTVSS 113
 113
113 AA;
 ll protein.
487 AA; 52554 MW;
 64.6%; Score 425; DB 4; llarity 66.4%; Pred. No. 2.2e-36; Conservative 13; Mismatches 17
 Conservative
 PRELIMINARY;
 125
 125
 143
 PubMed=9614934;
n der Merwe P.L.,
 12437 MW;
 64.7%; Score 425.5; DB 11; Lung-
65.4%; Pred. No. 1.2e-35;
49. Wismatches 21; Indels
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 ED57FDD19086D07F CRC64;
 7DC8E96DB333077B CRC64;
 Kalis N.N.,
 17; Indels
 Length 113;
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 487;
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 Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
SMART; PS50835; IG_LIKE; 5.
PROSITE; PS500290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW;
 01-MAR-2002 (TrEMBLrel. 20, 0
01-MAR-2002 (TrEMBLrel. 20, 1
01-MAR-2003 (TrEMBLrel. 23, 1
Hypothetical protein.
Homo sapiens (Human).
Bukaryotei, Metazoa; Chordata,
Mammalia, Butheria; Primates;
 OJUL71;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC020240; AAH20240.1; -. InterPro; IPR007110; Ig-11ke. InterPro; IPR003006; Ig_MHC. InterPro; IPR003006; Ig_WHC.
 SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L.,

Young D.C.;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Q9UL71
 Strausberg R.;
 SEQUENCE FROM N.A.
 "Myosin-reactive autoantibodies in rheumatic carditis
 (Fragment)
 FISSUE=Tonsil;
 NCBI_TaxID=9606;
 v
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 140
 121
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 87;
 Similarity
 ADSVXGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATW----RAFDIWG
 VIVSS 144
 VIVSS
 RGTMVTVSS 125
 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL
 QGTMVTVSS
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD--
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 125
 Immunopathol.
 Chordata;
Primates;
 67296 MW; 60C7F5950671B315 CRC64;
 66.6%;
 12; Mismatches
 Last sequence update)
Last annotation updat
 Created)
 Score 438.5; DB 4;
Pred. No. 7.5e-37;
 87:184-192(1998)
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMB
EMBL; BC021276; AAH21276.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; Ig; 4.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 573 AA; 62967 MW;
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Q8WU38
Q8WU38;
Q1-MAR-2002 (TTEMBLrel. 20,
01-MAR-2002 (TTEMBLrel. 20,
01-MAR-2003 (TTEMBLrel. 23,
 NON_TER
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 Hypothetical protein. Homo sapiens (Human)
 EMBL; AF035043; AAD56279.1;
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-lik
 SEQUENCE
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 138
 120 MYTYSS 125
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 98;
 Similarity
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 121
121 AA;
 Conservative
 143
 13154 MW;
 66.0%;
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 EMBL/GenBank/DDBJ
 Created)
 Score 434.5; DB 4
Pred. No. 1.8e-36;
 Mismatches
 573
 8
 DB 4;
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2F045CCFA5D50736 CRC64;
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| 120 MV<br>116 MV                           | 61 AI<br> -<br>61 AD                                                | 1 BV<br>1 EV                                                    | Y Macch<br>Local Sim                                                                                                                         |
|--------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| 120 MVTVSS 125<br>      <br>116 MVTVSS 121 | 61 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAAT-WRAFDIWGRGT 119 | EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60 | ob.of; Score 436; UB 4; Length 121;<br>Local Similarity 69.8%; Pred. No. 1.1e-37;<br>Thes 88; Conservative 11; Mismatches 21; Indels 6; Gaps |
|                                            | 19<br>15                                                            | 0 0                                                             | 2;                                                                                                                                           |

Last sequence update)
Last annotation update)

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

FD072344033AC530 CRC64;

EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGS-AATWRAFDIWGRGT EVOLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY Indels ω •• Gaps 119 79

Length 573;

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121

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295K8
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Matches 92
 Q96K68 PRELIMINARY; PRT; 494 AA.
Q96K88;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Hunan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
 NON TER
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SEQUENCE
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
 (1)
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (Fragment).
Homo sapiens (Human)
TISSUE=Mammary gland;
Isogai T., Ota T., Hayashi K.,
Nishikawa T., Nagai K., Sugano
 fetus.
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 137
 121
 114 VIVS 117
 61
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 92;
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 Similarity
 VIVS 124
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAEDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR----GDSS--BAFDIWGQGTM
 EVQLVESGGGLVQPGGSLRLSCAASGPTFSSYSMNWVRQAPGKGLEWVSYISSTITTIYY
 VIVSS
 118 AA;
 118
 Conservative
 141
 118
12843 MW; D0633949F2AC149D CRC64;
 67.7%; Score 445.5; DB 4; Length 74.2%; Pred. No. 1.7e-38; tive 9; Mismatches 16; Indels
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Sugiyama T., Otsuki T.,
S., Shiratori A., Sudo I
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 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamateu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
"URDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
"BUBLI AKO27379; BAB55072.1; --.
DR InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
RI InterPro; IPR003056; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PP00047; 1g; 4.
DR PROSITE; P800290; IG_MIK; 1.
RMART; SM00406; IGv; 1.
RMART; P800290; IG_MIK; 1.
RMART; P800290; IG_MIK; 1.
RMART; P800290; IG_MIK; 1.
RMART; SM00406; IGv; 1.
RM Hypothetical protein.
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Matches
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Matches 83; Conserv
 Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
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PROSITE; PS05093; IG-MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
 Query Match
 Hypothetical protein. Homo sapiens (Human).
 Q96BB9 PRELIMINARY;
Q96BB9; TremBLrel 19,
01-DEC-2001 (TremBLrel 19,
01-DEC-2001 (TremBLrel 23,
01-MAR-2003 (TremBLrel 23,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM
 NCBI_TaxID=9606;
 rissum=B-cell;
 Local
 137
 121 VTVSS 125
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 88;
 ADSYKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 Similarity
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60
ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 VIVSS
 RDSVKGRPTISRDNAKNSLYLQMNSLRVDDTAVYYCARDSC---NGAICYGFSPWGQGTL 136
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 66.7%; Score 439; DB 4; ilarity 66.4%; Pred. No. 6.5e-37; Conservative 18; Mismatches 24
 Conservative
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 141
 67.1%; Score 441.5; DB 4 70.4%; Pred. No. 2.8e-37;
 11; Mismatches
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Maximum Match 100%
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 Minimum DB seq length: 0
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 Database :
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1 EVQLVKSGEGLVKPC
 December 30, 2003, 10:46:19 ; Search time 30.463 Seconds (without alignments) 1058.876 Million cell updates/sec
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
 830525 segs, 258052604 residues
 EVQLVKSGEGLVKPGGSLRL.....AATWRAFDIWGRGTMVTVSS 125
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
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sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 sp_human: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Q8TC77 Q8TC77 Q9UL91 Q9GK68 Q96B89 Q96B89 Q96WUX1 Q9UL71 Q9UL71 Q9UL71 Q9UL71 Q9WU38 Q8W038 Q98SK4 Q99KA4 |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OBtc77 homo sapien O9u191 homo sapien O9u191 homo sapien O96k68 homo sapien O96kb9 homo sapien O9u171 homo sapien O9u171 homo sapien O9u171 homo sapien O9u184 homo sapien O9u5k4 homo sapien O9u5k4 homo sapien O9u190 homo sapien O9u190 homo sapien O9u180 homo sapien O9u180 homo sapien O9u180 homo sapien O9u180 musculu                                                                                                                                                                                                                                                                                                                                       |

| 5      | 44     | ů      | 42                 | 41     | 40     | 39     | 38     | 37     | 36     | 35     | 34     | y<br>Y             | 32     | 31     | 30     | 29     | 28     | 27     | 26     | 25                 | 24                 | 23     | 22     | 21     | 20     | 19                 | 18     | 17                 |
|--------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------|--------------------|
| 309    | 313    | 313.5  | 314                | 314    | 315    | 316    | 318    | 320    | 324    | 328.5  | 342    | 348.5              | 350    | 352    | 356.5  | 357.5  | 357.5  | 360    | 360.5  | 362                | 363.5              | 379    | 380.5  | 382    | 383    | 392                | 402.5  | 406.5              |
| 47.0   | 47.6   | 47.6   | 47.7               | 47.7   | 47.9   | 48.0   | 48.3   | 48.6   | 49.2   | 49.9   | 52.0   | 53.0               | 53.2   | 53.5   | 54.2   | 54.3   | 54.3   | 54.7   | 54.8   | 55.0               | 55.2               | 57.6   | 57.8   | 58.1   | 58.2   | 59.6               | 61.2   | 61.8               |
| 117    | 168    | 613    | 497                | 147    | 481    | 119    | 614    | 473    | 142    | 159    | 125    | 124                | 112    | 104    | 484    | 298    | 124    | 95     | 124    | 521                | 437                | 480    | 469    | 486    | 131    | 479                | 118    | 147                |
| 11     | H      | 11     | 4                  | 11     | 11     | 4      | 4      | 11     | 11     | 4      | 4      | 4                  | 4      | 4      | 11     | 11     | σ      | 4      | 9      | 4                  | 11                 | 11     | 11     | 1      | 4      | 1                  | 4.     | 4                  |
| Q9QXE9 | OBVDC9 | Q8VCX7 | Q8WY24             | Q925S3 | Q91WT1 | Q9UL94 | Q96GA6 | Q9D8L4 | Q924Q1 | Q96QS0 | Q9UL95 | Q9UL92             | Q9UGP3 | Q9UL87 | Q8VEA0 | Q9QYF0 | Q9N0W6 | Q9ULB6 | Q9NOW4 | Q8N4Y9             | Q9R1A4             | Q91XE1 | Q8R3V9 | Q91Z07 | Q9UL88 | Q91WP5             | Q9UL72 | Q9Y509             |
| Brim   |        |        | Q8wy24 homo sapien |        |        | -      |        | mus    |        |        |        | O9ul92 homo sapien |        | homo   | -      |        | 7      |        |        | Q8n4y9 homo sapien | Q9rla4 mus musculu | Bnw    | Brum ( | Bru    | OWO    | Q91wp5 mus musculu | -      | Q9y509 homo sapien |

## ALIGNMENTS

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|----------------------------------------------------------------|--------|-------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------|---------------------------------------------------|----------------------------------------------------|-----------------------------------------------|------------------------------|------------|--------------|------------|------------|-------------------------------|-----------------|----------------------------------------------------------|---------------|----|--------------------|---|---|----------------------------------|-----|-------------------------------------|-----------------|-------------------------------------------------|----------------------------------|-----|--|
| 80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYMYFDLWGRGTL 1 | WGRGTM | 20 BVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSNSSSSYIYY 79 | 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60 | es 93; Conservative 11; Mismato | Query Match 72.3%; Score 475.5; DB 4; Length 471; | SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64; | U-130-17-17-17-17-17-17-17-17-17-17-17-17-17- | PROSITE: PS00290: IG_MHC: 2. | M00406; IG | 0047; ig; 4. | IPR003596; | IPR003006; | InterPro; IPR007110; Ig-like. | 24289; AAH24289 | Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. | Strangherg R. |    | SEQUENCE FROM N.A. |   |   | Primates: Catarrhini; Hominidae; |     | <br>(TrEMBLrel. 23, Last annotation | (TrEMBLrel. 21, | QBTC77;<br>01-JUN-2002 (TrEMBLrel, 21, Created) | QBTC77 PRELIMINARY; PRT; 471 AA. |     |  |
| 136                                                            | 120    | ø                                                                 | 0                                                                 | 1;                              | -                                                 |                                                    |                                               |                              |            |              |            |            |                               |                 |                                                          |               |    |                    |   |   |                                  |     |                                     |                 |                                                 |                                  |     |  |

| Searc<br>Job t                                                           | дb            | ঠ             | 맑                                                      | Ş                                                                | 망                                                               | ð                                                                 | Que<br>Bes<br>Mat                                                                                                                                             | SOF                                                  |
|--------------------------------------------------------------------------|---------------|---------------|--------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------|
| Search completed: Decem<br>Job time : 7.70187 secs                       | 110           | 121           | 61 /                                                   | 61 /                                                             | 1 1                                                             | <b>1</b>                                                          | ry Match<br>t Local S:<br>ches 77                                                                                                                             | NON TER<br>SEQÜENCE                                  |
| ed: Decemb<br>0187 secs                                                  | 110 VTVSS 114 | 121 VTVSS 125 | DAVKGRETI                                              | ADSVKGRFTI                                                       | SVQLVBSGGDI                                                     | SVQLVKSGEGI                                                       | imilarity<br>Conserv                                                                                                                                          | 114 :                                                |
| er 30, 200:                                                              |               |               | SKONAKOSLYI                                            | SRDNANNVVYI                                                      | VKPGGSLRLS                                                      | VKPGGSLRL                                                         | 57.7%; § 61.6%; § ative 15;                                                                                                                                   | 114<br>12430 MW;                                     |
| Search completed: December 30, 2003, 10:55:54<br>Job time : 7.70187 secs |               |               | ADAVKGRETISKDNAKDSLYLQMNSLRAEDTAVYYCAPWQ-FEYMGQGTL 109 | ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120 | EVQLVESGGDLVKPGGSLRLSCVASGITFSGYDMQWVRQAPGKGLQKVAYFNDALSAQGY 60 | 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY 60 | Query Match 57.7%; Score 379.5; DB 1; Length 114; Best Local Similarity 61.6%; Pred. No. 1.7e-32; Matches 77; Conservative 15; Mismatches 22; Indels 11; Gaps | 114 114<br>114 AA; 12430 MW; B1D4745D2C4E13C4 CRC64; |
| -                                                                        |               |               | AVYYC                                                  | IAVYFCARDGT                                                      | YDMQWVRQAF                                                      | YDIHWVRQTE                                                        | DB 1;<br>.7e-32;<br>.es 22;                                                                                                                                   | C4E13C4 CR                                           |
|                                                                          |               |               | APWQ                                                   | TIFGSAATWRJ                                                      | GKGLQKVAYI                                                      | GKGLEWVSS                                                         | Length 114 Indels 1                                                                                                                                           | C64;                                                 |
|                                                                          |               |               | FEYWGQGTL                                              | VEDIWGRGTM                                                       | NDALSAOGY                                                       | SSGGNYIDY                                                         | 1;<br>.1; Gaps                                                                                                                                                |                                                      |
|                                                                          |               |               | 109                                                    | 120                                                              | 60                                                              | 60                                                                | N.                                                                                                                                                            |                                                      |

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 P01789;
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p01789;
p01789;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region M603.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DOMAIN
NON TER
SEQUENCE
 MEDLINE=8019926; PubMed=6769593;
Barly P., Huang H., Davis M., Calame K., Hood I
"An immunoglobulin heavy chain variable region
three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
 MOUSE
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
 X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
MEDLINE=75065510; PubMed=4530984;
Segal D.M., Padlan B.A., Cohen G.H., Rudikoff S., Potter M.,
 PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure
SIGNAL 1 19
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure.
DOMAIN 1 121 IG-LIKE.
 "The three-dimensional structure of a phosphorylcholine-binding maximumoglobulin Pab and the nature of the antigen binding site."; Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
 binding myeloma protein.";
Biochemistry 13:4033-4038(1974).
 Rudikoff S., Potter M.;
 MEDLINE=75017346; PubMed=4213527;
 SEQUENCE OF 1-120.
 CHAIN
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
 InterPro; IPR003006;
InterPro; IPR003596;
 Davies D.R.
 "Variable region sequence of the heavy chain from a phosphorylcholine
 SIMILARITY: Contains 1 immunoglobulin-like
 BINDS PHOSPHORYLCHOLINE
 IMCP;
 B90795; AVMS63
 BSDOM
 80
 61 ADSVKGRPTISRDNANNVVYLQMNSLRAEDMAVYFCAR 98
 20
 Similarity
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 117
 Conservative
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 STANDARD;
 >117
 12582 MW; E826733F1A3CB0F1 CRC64;
 58.4%;
74.5%;
 Ig_wHC.
 9
 Pred. No. oc.
 Score 384; DB 1
Pred. No. 6e-33;
 IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
 PRT;
 122
 Hood L.;
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 DB 1; Length 117;
 16;
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 RESULT 15
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 Query Match
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Matches 76
PIR; A02067; AVDGGM.
HSSP; P01772; 2F84.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
IRMUNOG10bulin V region.
Immunog1obulin V region.
IGMAIN
 P01784;
21-JUL-1986
21-JUL-1986
15-SEP-2003
 HELIX
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NON TER
SEQUENCE
 Wasserman R.L., Capra J.D.;
"Primary structure of the variable regions immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
 15-SEP-2003 (Rel. 42, Last a Ig heavy chain V region GOM. Canis familiaris (Dog).
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
 HV01
 -!- MISCELLÂNEOUS: THIS CHAIN WAS ISOLATED FROM A MYB!
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
 NCBI_TaxID=9615;
 SEQUENCE.
 MEDLINE=77242268; PubMed=407924;
 CANFA
 116
 119
 19
 59
 76;
 Similarity
 TTVTVSS 122
 EYSASVKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCARN--YYGS--TW-YFDVWGAG
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIH#VRQTPGKGLE#VSSISSGGN--YI
 TMVIVSS 125
 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKGNKYTT
 Conservative
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 STANDARD;
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42, Last annotation
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 58.1%;
 13626 MW;
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H-BOND WITH THE I PHORYLCHOLINE.
 Score 382.5;
Pred. No. 8.5
 IG-LIKE
 PRT;
 BA2C864438B64F0F CRC64;
 Mismatches
 update)
 114 AA
 update)
 .9e-33;
 DB 1;
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 PHOSPHATE
 A MYBLOMA
 canine
 Indels
 Length
 Euteleostomi;
Canis.
 GROUP
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 Gaps
 PHOS-
 115
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RESULT 12
HV3E HUMAN STANDARD; PRT; 1
AC P01766; BC Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence up
DT 21-JUL-1986 (Rel. 42, Last annotation
DE 19 heavy chain V-III region BRO.
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 Query Match
Best Local Similarity
Matches 78; Conserv
 DOMAIN
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SEQUENCE
 Torano A., Putnam P.W.;

"Complete amino acid sequence of the alpha 2 heavy chai "IgA2 immunoglobulin of the A2m (2) allotype.";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-!- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2)

REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (N-III region BUT.
MEDLINE-77117674; PubMed-65324;
Capra J.D., Hopper J.E.;
Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the vergion of the IgM paraprotein.";
Iregion of the IgM paraprotein.";
Immunochemistry 13:995-999(1976).
--- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
 PIR; A02050; A2HUBU.
HSSP; P01789; 1MCP.
 SEQUENCE
 NCBI_TaxID=9606;
 Homo sapiens (Human).
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 MEDLINE=78137069; PubMed=416441;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
[1]
 Homo sapiens (Human)
 EQUENCE
 111
 121
 60
 61
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 VIVSS 125
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 VTVSS 115
 ADSVKGRFTISRDDSRBTVYLQMBSLRAEDTAVYYCARD------LAAARLFGKGTT
 115 AA;
 Conservative
 12379 MW; 208876A7DF52DCF4 CRC64;
 58.8%;
 16;
 Score 387; DB
Pred. No. 2.9e
16; Mismatches
 IG-LIKE
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 DB 1; Length 115; .9e-33;
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Matches 79
 Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

SMART; SM00406; IG LIKE; 1

PROSITE; PS50835; IG LIKE; 1

Immunoglobulin V region.

DOMAIN

1 111

NON TER 120 120

SEQUENCE 120 AA; 13227 MW
 HSSP; P01772; 3
GO; GO:0005576;
GO; GO:0003823;
GO; GO:0006955;
 PIR; A02049; M3HUBW.
EMBL; J00236; AAA53516.1; -.
EMBL; M35415; AAA59735.1; -.
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
Genew; HGNC:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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 Matthyseens G., Rabbitts T.H.;

"Structure and multiplicity of genes for the human immunoglobulin mattable region.";

Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;)
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region VH26 precursor.
 Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
 MEDLINE=81101090; PubMed=6450418;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding acti
GO:0006955; P:immune response; NAS
 SIMILARITY: Contains 1 immunoglobulin-like
 114 -- VWGQGTL 120
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 79;
 Similarity
 ADSVKGRFTISRNDSKNTLYLNMNSLRAEDTAVYYCARSPVSLVDGWLYYYYGS-----
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCAR-----DGTI---FGSAATWRA 111
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYYNMNWVRQVTGKGLEWVSAIGTAGDQY-Y
 EVQLVKSGEGLYKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 PDIWGRGTM
 Conservative
 2FB4.
 STANDARD;
 120
 13227 MW; D3F0428F7C2E6410 CRC64;
 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 58.8%;
 ; Score 387; DB 1; Length 120; ; Pred. No. 3e-33; 18; Mismatches 14; Indels
 IG-LIKE
 activity; NAS
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 PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
GG: GG::0005576; C:extracellular; NAS.
GG::GO::0003823; F:antigen binding activity; NAS.
GG::GO::0006955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SEQUENCE
 Pfam; PFUUUW:, *5, .
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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 SEQUENCE, AND DISULFIDE BONDS.

MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

"Three-dimensional structure determination of antibodies.

structure of crystallized monoclonal immunoglobulin IgG1;
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 HELIX
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 InterPro; IPR003596;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
 TURN
 PIR; A02055; G1HUKL
 J. Mol. Biol. 141:369-391(1980).
 Marquart M., Deisenhofer J., Huber R., Palm W., "Crystallographic refinement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment
 MEDLINE=81072295; PubMed=7441755;
 and 1
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 0-A resolution
61
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 Similarity
 QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWGRGT
ADSVKGRFTISRDNSKNTLFLOMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT
 45
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1109
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1126
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 Conservative
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 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 13718 MW;
 60.1%;
 17;
 Score 395.5; DB 1
Pred. No. 4.2e-34;
 E4D71B52B16F8776 CRC64;
 Mismatches
 DB 1;
 Length 126;
 Indels
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 Gaps
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RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN
AC P01767;
 RESULT
HV3U_HC
 Query Match
Best Local S
Matches 79
 InterPro; IPRO07110; Ig-like, InterPro; IPRO03006; Ig-MHC. InterPro; IPR003006; Ig-V. Pfam; PP00047; Ig; 1.

SMART; SM00406; IGv; 1.

SMOSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.
DOMAIN 112 12

NON TER 120 120

SEQUENCE 120 AA; 13440 MW;
 MEDLINE=80020921; PubMed=114209;
Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region DOB.
Homo sapiens (Human).
 HUMAN
HV3U_HUMAN
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
 Biochemistry 18:4054-4067 (1979).

-I- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
 "The crystallizable human myeloma
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 PIR; A90431; G1HUDB.
HSSP; P01772; 2FB4.
 P01782;
 -1- SIMILARITY:
 MEDLINE=80020920; PubMed=114208;
 CRYSTALLIZATION.
 SEQUENCE
 NCBI_TaxID=9606;
 116
 121
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 120 MYTYSS
 61
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 Similarity 63.:
79; Conservative
 SSALA
 SSALA
 ADSVKGRFAISRDNAQKTLYLQLNILRPEDTAFYYCAK-GYIWN--GNW--FDSWGQGTL
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 EVQLVESGGDLVQPGRSLRLSCAASGENEHEYNMHWLRQGPGKGPEWVSTITMNGGSVLY
 EVQLVKSGEGLVKPGGSLRLSCAASGPTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 PVIVSS
 120
120
 125
 120
 STANDARD;
 Contains 1 immunoglobulin-like domain
 126
 125
 120
13440 MW;
 59.7%; Score 392.5; 63.2%; Pred. No. 8.1
 15;
 IG-LIKE
 PRT;
 880DDE307C4B2627 CRC64;
 Mismatches
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SEQUENCE
 PROSOTE; 19; 1.

Team; PRO0047; 19; 1.

SMART; SM00466; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Teamunoglobulin V region; Pyrrolidone carboxylic acid.

Teamunoglobulin V region; Pyrrolidone Carboxylic ACC
 structure of the complete IgA-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
--- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN
---- SIMILARITY: Contains 1 immunoglobulin-like domain.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region TRO.
 HUMAN
 SEQUENCE (MYELOMA PROTEIN TRO)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens (Human)
 HSSP;
 PIR; A02045; A1HUTR.

 The amino acid sequence of the H-chain,

 Hilschmann N.;
 Kratzin H.,
 MEDLINE=76023781; PubMed=809331;
 NCBI_TaxID=9606;
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
 117
 121
 P01772; 2FB4.
 61
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 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 Similarity
 Similarity
 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDIL----TAFSFDYWGQGVL 116
 SSALA
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVOLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 SSALA
 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAF--DIWGRG
 ADSVKGRFTISRDNAQKSLYLZMBSLRTZBTAVYYCAATBBF-----BWSTFSLBYWGZG
 121
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122
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 Altevogt P., Ruban B.,
 Conservative
 125
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 STANDARD;
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13566 MW;
 13472 MW;
 60.6%;
 17;
 18;
 Score 400; DB 1; Length 121; Pred. No. 1.4e-34; Indels 17; Mismatches 27; Indels
 Score 398.5; DB Pred. No. 2e-34; 8; Mismatches
 PYRROLIDONE CARBOXYLIC ACID
 480FC53610EF5DAB
 2E21A11DA04D80F9 CRC64;
 Kortt A., Staroscik K.,
 122
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 DB 1;
 27;
 CRC64;
 Length
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HV3K_HUMAN
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 HV3T_HUMAN
P01781;
 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-III region GAL. Homo sapiens (Human).
 Hilschmann N.;
Submitted (JUN-1975) to
-!- MISCELLANEOUS: THIS
MACROSLOBULIN.
 Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 HUMAN
P01772;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region KOL.
Homo sapiens (Human).
 SEQUENCE
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
 PIR; A02064; M3HUGL.
 SEQUENCE.
MEDLINE=75059123; PubMed=4803843;
 NCBI_TaxID=9606;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS:
GO; GO:0003823; F:antigen binding activity;
GO; GO:0003823; F:immune response; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0071110; Ig_HC.
InterPro; IPR003006; Ig_MC.
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 NON TER
 DOMAIN
 HV3K HUMAN
 REVISION TO 28-33.
 Local
 116
 112
 121 YTVSS 125
 61
 61
 Similarity
 BLVTVSS
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVST 116
 VDSVKGRFT1
 116 116
116 AA; 12730 MW;
 (Rel. 01, Created) (Rel. 01, Last seq
 Conservative
 STANDARD;
 STANDARD;
 122
 60.4%; Score 397.5; DB 1 62.4%; Pred. No. 2.4e-34;
 the PIR data
 13; Mismatches
 IG-LIKE
 PRT;
 2C67CA9AAAAA1282
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ISOLATED FROM A WALDENSTROM'S
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RESULTI
HV3 HVU
ID HV0
AC PO
DT 211
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DT 115
DT 15
DT 21
DT 2
 PIR; A91600; CHR.

(GG) GG0:0005576; C:extracellular; NAS.

(GO) GG0:0005576; C:extracellular; NAS.

(GO) GG0:0005655; P:immune response; NAS.

(R) InterPro; IPR007110; Ig-11ke.

(R) InterPro; IPR003106; Ig_MHC.

(R) InterPro; IPR003596; Ig_V.

(R) InterPro; IPR003596; Ig_V.

(DR) Ffam; PP00047; ig; 1.

(DR) SMART; SM00406; IGv; 1.

(DR) ROSITE; PS00407; ig; 1.

(DR) FR0SITE; PS00406; IGv; 1.

(DR) ITMUNDOGlobulin V region; Pyrrolidone carboxy; IMMAIN

(M) ITMUNDOGLOBULIN V region; Pyrrolidone CAR
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Goni F., Frangione B.;

"Amino acid sequence of the Pv region of a human monoclonal 1
(protein WEA) with antibody activity against 3,4-pyruvylated
(palactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL
 P01763;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation updat
Ig heavy chain V-III region WEA.
Homo sapiens (Human).
 HUMAN
 MOD_RES
DISULFID
NON_TER
 MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 SEQUENCE
 SEQUENCE
 MEDLINE=83273707; PubMed=6410398;
 NCBI_TaxID=9606;
 HV3B
 DISULFIDE BOND
 SIMILARITY: Contains 1 immunoglobulin-like domain.
 HUMAN
 113
 119
 61
 51
 81;
 Similarity
 TLVTVSS
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCA--RDGTIFGSAATWRAFDIWGRG 118
 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCARIRDTAMF-----
 IMVIVSS
 119 AA;
 1
1
22
119
 Conservative
 STANDARD;
 119
 125
 Chordata; (Primates;
 119
 13242 MW; C96935A6E55E165B CRC64;
 61.2%;
 15;
 Score 403;
Pred. No.
 PYRROLIDONE CARBOXYLIC ACID
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 PRT;
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P01771;
21-JUL-1986
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SEQUENCE
Pfam; PF00047; ig; i. SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
1 12
PYRROLIDONE CARBOXYLIC A
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC A
 PIR; A02054; G1HUHL.
HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activity; NAS.
G0; G0:00008955; P:immune response; NAS.
 Biochemistry 18:553-560(1979)
 "Amino acid sequence of the V
cryoimmunoglobulin IgG Hil.";
 SEQUENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 HUMAN
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrry
DOMAIN
 HSSP; P01772; 2FB4.
HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activity;
G0; G0:00036955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_w.
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02046; M3HUWE.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 -
 MEDLINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A.,
 Homo sapiens (Human)
 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation Ig heavy chain V-III region HIL.

 -!- SIMILARITY: Contains 1 immunoglobulin-like domain

 MISCELLÂNEOUS: THIS CHAIN WAS
 110
 121
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 Similarity
 ADSVKGRFTISRNBSKNSLYLQMSSLRAEDTAVYYCAR-GWLLN---
 VIVSS 125
 ADSVXGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 SSAIA
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114 AA;
 Conservative
 Lopez de Castro J.A., Por equence of the VH region
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 STANDARD;
 12256 MW;
 64.0%;
 Pyrrolidone carboxylic acid
 16;
 Score 400.5; Pred. No. 1.1e
 PYRROLIDONE CARBOXYLIC ACID
 IG-LIKE
 D88294FB418A07B7
 ISOLATED FROM
 Poljak R.J.;
on of human myeloma
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 CARBOXYLIC ACID
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 DB 1;
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 CRC64;
 Indels
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 WGQGTL 109
 Gaps
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P01783;
 Immunoglobulin
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SEQUENCE
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 21 precursor (Fragment).
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 "Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
 CHAIN
DOMAIN
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKB; 1.
 EMBL; J00522; AAD15290.1; -. PIR; E90809; G1MS21.
 MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
 NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 PDB; 1IGC; 03-JUN-95.
 "Molecular analysis of spontaneous somatic mutants."; Nature 265:299-304(1977).
 MEDLINE=77100368; PubMed=401950;
 SEQUENCE OF 17-136.
 Baltimore D.;
 SEQUENCE FROM N.A.
 Mus musculus (Mouse)
 Adetugbo K., Milstein
 [nterPro;
 interPro;
 nterPro;
 MOUSE
 132
 121
 17
 77
 61 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 Similarity
VIVSS 136
 VIVSS 125
 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNY-----PYYAMDYWGQGTS
 IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
 115
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 Conservative
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 STANDARD;
 region;
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 15071 MW;
 62.1%;
63.2%;
 Signal; 3D-structure
 Secher D.S.;
 ; Score 408.5; ; Pred. No. 2.16 17; Mismatches
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 contribution to the NPb family of evident in a gamma 2a variable region.";
 HYAD -> DYAH (IN REF. 2)
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
 IG HEAVY CHAIN V
D SEGMENT.
 JH4 SEGMENT
 2276A98DBDBF7016 CRC64;
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 Imanishi-Kari T.,
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 DB 1;
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 REGION MOPC
 Length 136;
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RESULT 3
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Matches 77
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; P850835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic iDOMAIN
1 112 IG-LIKE.
 MOD_RES
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SEQUENCE
 HV3I HUN
P01770;
 HSSP, P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS
 Florent G., Lehman D., Putnam F.W.;
"The switch point in mu heavy chains of human IgM Biochemistry 13:2482-2498(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GA.
Ig heavy chain V-III region GA.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 21-JUL-1986 (Rel. 01, Created)
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1g heavy chain V-III region NI
Homo sapiens (Human).
 NAMUH
 PIR; A02052; M3HUGA.
 HV3H_HUMAN
 MEDLINE=74175307; PubMed=4208843;
 SEQUENCE
 NCBI_TaxID=9606;
 SEQUENCE.
MEDLINE=77070269; PubMed=826475;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain
 Ponstingl H., Hilschmann N.;
 MACROGLOBULIN.
 HUMAN
 118
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 Similarity
77; Conserv
 SSAIA
 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVA---GTDYWGZGTL
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VTISS 122
 122
122 AA;
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 STANDARD;
 STANDARD;
 13166 MW; 74E5B6959E84100A CRC64;
 61.8%; Score 406.5; DB 1
61.6%; Pred. No. 2.9e-35;
 Last sequence update)
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region NIE.
 19; Mismatches
 PYRROLIDONE CARBOXYLIC ACID
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.

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Result
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| 351.5      | 353        | 355      | 355         | 355        | 356        | 356        | 358        | 358.5      | 359        | 359.5      | 360.5       |
| 53.4       | 53.6       | 54.0     | 54.0        | 54.0       | 54.1       | 54.1       | 54.4       | 54.5       | 54.6       | 54.6       | 54.8        |
| 111        | 113        | 142      | 117         | 115        | 118        | 117        | 116        | 119        | 119        | 119        | 119         |
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| HV35_MOUSE | HV30_MOUSE | HV01_RAT | HV59_MOUSE  | HV32_MOUSE | HV39_MOUSE | HV54_MOUSE | HV3R_HUMAN | HV3M_HUMAN | HV3L_HUMAN | HV3P_HUMAN | HV3N_HUMAN  |
| P01804     |            |          |             |            |            |            |            |            |            |            | P01775      |
|            | =          | Ħ        | mus musculu | ᆵ          | Bull       | mus        | hom        | homo       | homo       | homo       | homo sapien |

#### RESULT 1 HV3G HUMAN ID HV3G H HASG HO1768 AC P01768 AC P1768 AC P176 Query Match 66.6%; Score 438.5; DB 1 Best Local Similarity 65.6%; Pred. No. 1.4e-38; Matches 82; Conservative 21; Mismatches 19 -!- SIMILARITY: Contains 1 immunoglobulin-like domain. HSSP; P01772; 2FB4. GO; GO:0005576; C:extracellular; NAS. GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding activity; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig\_MHC. InterPro; IPR003596; Ig\_W. Lehman D.W., Putnam F.W.; "Amino acid sequence of the variable region of a human mu chai location of a possible JH segment."; Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980). -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA PATIENT WITH MACROGLOBULINGNIA. HV3G HUMAN STANDARD; PRT; 122 AA. P01768; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 19 heavy chain V-III region CAM. Homo sapiens (Human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MEDLINE=81013859; PubMed=6774332; Lehman D.W., Putnam F.W.; SEQUENCE NCBI\_TaxID=9606; 121 61 61 1 BVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY VTV8S 125 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120 QVELVESGGGVVZPGRSLRLSCAASGPTPSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 122 122 13668 MW; A42D0F17D252F1C2 CRC64; PYRROLIDONE CARBOXYLIC ACID DB 1; 19; Indels Length 122; chain: <u>ب</u> 60

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Ig heavy chain V region (30p1) - human
(;Species: Homo sapiens (man))
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
 RESULT 15
C36005
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 C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Search completed: December 30, 2003, 11:03:19 Job time: 11.9821 secs
 Query Match 67.6%; Score 445; DB 2; Length 119; Best Local Similarity 69.8%; Pred. No. 1.9e-34; Matches 88; Conservative 11; Mismatches 19; Indels
 Query Match 67.8%; Score 446; DB 2; Length 121; Best Local Similarity 69.6%; Pred. No. 1.6e-34; Matches 87; Conservative 13; Mismatches 21; Indels
 117 VTVSS 121
 121 VTVSS 125
 114 LVTVSS 119
 120 MVTVSS 125
 8
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 Gaps
 Gaps
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Bubmitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Recession: S30532
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 cMAR>
A;Cross-references: EMBL: Z18318
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #text_change 16-Aug-1996 C;Accession: S30532 R;Mariette, X.
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Residues: 1-118 Residues: mRNA A;Residues: 1-118 Residues: 1-118 Residues: 1-118 Residues: ncb/main.cb/4
A;Cross-references: EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991 C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
 C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
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 Ig heavy chain - human
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Best Local S
Matches 87
 Species: Homo sapiens (man)
 Local
 121
 115
 121 VTVSS 125
 61
 61
 13
 13
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 90,
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87; Conserva
 Similarity
 SSALA
 SSALA
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCATDG---GKA---
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY
 VIVSS 119
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRLTGT-----
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVOLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 Conservative
 Conservative
 118
 68.1%;
69.6%;
 68.0%; Score 447.5; DB 2 72.0%; Pred. No. 1.1e-34;
 11; Mismatches
 13; Mismatches
 Score 448; DB 2
Pred. No. 1e-34;
 DB 2;
 DB 2;
 17;
 19; Indels
 Length 119;
 Indels
 Length
 7;
 6
 Gaps
 113
 60
 60
 60
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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; imm
 C;Accession: G36005

R;Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A;Title: Preferential utilization of conserved immunoglobulin heavy

A;Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: G36005

A;Status: preliminary

A;Residues: 1-121 <SCH>
 Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990
 R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Eur. J. Immunol. 22, 241-245, 1992

Bur. J. Immunol. 22, 241-245, 1992

A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam A;Reference number: S26786; MUID:92111632; PMID:1730251

A;Accession: S26786
 Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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 A;Cross-references: EMBL:X61014; NID:g32800; PIDN:CAA43348.1; PID:g1335129 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
 A; Gene: GDB: IGH@; IGHDY1
 A; Molecule type: mRNA
A; Residues: 1-128 < MOR>
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 A;Cross-references: GB:M34031
 A; Status: preliminary
 C; Accession: S26786
 RESULT 13
 Query Match
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Matches 91
 ;Genetics:
 Query Match
 Matches
 Local
 118
 118
 120 MVTVSS 125
 61
 61
 61
 61
 91;
 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 l Similarity
91; Conserv
 h 67.9%; Score 446.5; DB 2 Similarity 69.5%; Pred. No. 1.5e-34;
 ADSVKGRFTISRDNAKNSLYLØMNSLRAEDTAVYYCAR-GLYCSSTSCYIWSNNW--FDP
 WGRGTMVTVSS
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAA-----TWRAFDI 114
 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
 ADSVKGRFAISRDNAKNSLYLOMNSLRAEDTALYYCAKD-TPYSSG--WSNAFDIWGQGT
 MVTVSS 123
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATW-RAFDIWGRGT 119
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 EVOLVESGGGLVOPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGTLGY
 Conservative
 Conservative
 128
 67.9%; Score 447; DB 2; Length 123
72.2%; Pred. No. 1.3e-34;
ive 10; Mismatches 21; Indels
 region; immunoglobulin homology
 11; Mismatches
 DB 2;
 20;
 #text_change
 Indels
 Length 128;
 16-Dec-1998
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Ig heavy chain (subclass IgM) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31104
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse tl
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 «ARA»
A;Cross references: EMBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
A;Cross references: EMBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Octob
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
 A,Cross-references: EMBL:X63081; NID:g32648; PIDN:CAA44803.1; PID:g32649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
 C;Speciés: Homo Bapiens (man)
C;Date: 22-Nov1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.I.Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31105
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 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type; mRNA
A;Residues: 1-118 <RAA>
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 Matches
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 61
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 Similarity
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVSS 125
 ADSVKGRFTISRDNÁKNSLÝLOMNSLRAEDTAVYYCA--GOLGDD----
 ADSVKGRETISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM
 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYY
 VIVSS
 VTVSS 125
 ADSVKGRETISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAEDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSRNYDSSGYYSHYFDYWGQGTL
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWISYISSSSSTIYY
 (subclass IgM) - human (fragment)
 Conservative
 Conservative
 68.3%;
73.6%;
 68.5%;
 Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
 10;
 9
 Score 449.5; DB 2;
Pred. No. 7.4e-35;
9; Mismatches 17;
 26-May-1995 #text_change 23-Jul-1999
 DB 2;
 Length 125;
 Length 118;
 Indels
 Indels
 M.J.D.; Vossen, J.M.;
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C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse thir
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
A;Accession: S31108
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Residues: 1-119 <RAA>
A;Cross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
 RESULT 10
S31108
 C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 RESULT 9
$31595
$31595
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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 A;Cross-references: EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID:g31008 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMM>
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 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
 Ig heavy chain - human
 A; Molecule type: mRNA
A; Residues: 1-128 <CUI>
 A; Status: preliminary
 A; Accession: S31595
 A; Reference number: S31585
 C; Accession: S31595
R; Cuisinier, A.M.;
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 Matches
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 121
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 69
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 90;
 Similarity
 68.2%;
Similarity 72.8%;
 ADSVKGRFTISRDNANNVVYLOMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 VIVSS 125
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 SSALA
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTALYYCAKD-----APGDHDAFDIWGQGTM
 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
 VTVSS 121
 VIVSS 125
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTALYYCAKD-VFWGSG--W-YPDLWGRGTL 116
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
 Conservative
 Conservative
 68.2%;
 10;
 9;
 Score 449; Ub .,
Pred. No. 8.4e-35;
Ches 20; Indels
 Score 448.5; DB
Pred. No. 1e-34;
 Mismatches
 DB 2;
 21;
 Indels
 Length
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 Gaps
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Ig heavy chain V region - human (fragment)
(Species: Homo Bapiens (man)
(Species: Homo Bapiens (man)
(C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
(;Accession: S11239
(;Accession: S11239
R;Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and A;Reference number: S11239; MUID:90370490; PMID:1697678
A;Accession: S11239; MUID:90370490; PMID:1697678
A;Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145 <FEL>
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 R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23624
A;Status: preliminary A;Molecule type: DNA
 Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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 A;Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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 A; Residues: 1-143 <OLE>
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 C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
 C; Accession: S23624
 Best Lo
 Query Match 71.0%;
Best Local Similarity 73.6%;
Matches 95; Conservative
 Local
 121 VIVSS 125
 113
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 117
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 l Similarity
90; Conser
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 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 VIVSS
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARSG-----
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWRAFDIWGRGTM 120
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWVSYISSSSSTIYY
 RGTLVTVSS
 RGTMVTVSS 125
 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDGPGGGLRIAVAGDW-YFDLWG
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFG----SAATWRAFDIWG
 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYY
 immunoglobulin homology <IMM>
 Conservative
 117
 128
 69.0%; Score 454; DB 2; 72.0%; Pred. No. 3.5e-35; tive 10; Mismatches 17
 9,
 Score 467.5; DB 2
Pred. No. 1.7e-36;
9; Mismatches 20
 DB 2;
 17;
 20;
 Length 143
 Indels
 Length 128;
 Indels
 8;
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 of H- and L-chains
 Gaps
 Gaps
 60
 112
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 F;34-117/Domain: immunoglobulin homology <IMM>
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A;Reference number: S30520
A;Reference number: S30520
A;Accession: S30531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-125 <MAR>
A;Residues: 1-125 <MAR>
A;Cross-references: EMBL: Z18317
C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
 Ig heavy chain V region - hum C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence C;Accession: S30531 R;Mariette, X.
 A;Molecule type: mRNA
A;Residues: 1-117 <MAR>
A;Cross-references: EMBL:Z18324
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-95/Domain: immunoglobulin homology <IMM>
 submitted to the EMBL Data A; Reference number: S30520
 C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34012; S30538
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Bux. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human
A;Reference number: S34001; MUID:93209281; PMID:7681398
 RESULT
S34012
 A; Status: preliminary
 A; Accession: S34012
 Ig heavy chain V region
 Query Match
Best Local S
Matches 90
 Query Match
 Matches
 Local Similarity
 112
 120 MVTVSS 125
 120
 140
 58 ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARAGEYSYGFA-----DYWGRGT
 61
 80
 61
 20
 <u>س</u>
 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 94,
 90;
 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHWVRQTPGKGLEWVSSISSGGNYIDY
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWGRGT
 LVTVSS
 BVQLVESGGGLVKPGGSLRLSCAASGFTFSSYNMMVRQAPGKGLEWVSSSSS---YIFY
 SSALAW
 ADSVKGRFTISRDNANNVVYLQMNSLRAEDMAVYFCARDGTIFGSAATWR-AFDIWGRGT
 SSALAW
 EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGY
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYYCVKGRDYYDSGGYFTVAFDIWGQGT
 Conservative
 Conservative
 #sequence_revision
 125
 68.7%;
74.6%;
 human
 68.8%;
 Library,
 ; Score 452.5; DB 2;
; Pred. No. 4.8e-35;
11; Mismatches 24;
 8
 Score 452; DB 2;
Pred. No. 4.3e-35;
 October 1992
 Mismatches
 06-Jan-1995
 14;
 #text_change 16-Aug-1996
 Length 117;
 Indels
 Length
 145;
 of four human monoclona.
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 Gaps
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 119
 57
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Title:
Perfect score:
 Total number of hits satisfying chosen parameters:
 Searched:
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 OM protein -
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 Sequence:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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4449.51
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 December 30, 2003, 10:47:09 ; Search time 11.9821 Seconds (without alignments) 1003.251 Million cell updates/sec
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1: pir1:*
2: pir2:*
3: pir3:*
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658
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Length
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 SUMMARIES
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Description
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| 437.5 66.5 120 2 S48798 Ig heavy 436.5 66.3 122 2 S20772 Ig heavy 436.5 66.3 122 2 S20772 Ig heavy 436.5 66.3 127 2 S20772 Ig heavy 436.6 66.3 127 2 S308489 Ig varia 436.6 66.3 134 2 S308489 Ig heavy 436.6 66.3 134 2 S31699 Ig heavy 436.6 66.1 140 2 S31686 Ig heavy 437.6 66.1 140 2 S31686 Ig heavy 438.6 66.0 140 2 S31588 Ig heavy 439.6 66.0 140 2 S31588 Ig heavy 431.5 65.6 110 2 P137781 Ig varia 431.5 65.6 110 2 P13781 Ig heavy 431.5 65.6 122 2 B36005 Ig heavy 431.6 65.2 135 2 S31598 Ig heavy 431.6 65.2 135 2 S31598 Ig heavy 431.6 65.2 135 2 S31598 Ig heavy 431.6 65.5 110 2 P13781 Ig heavy 431.6 65.6 122 2 B36005 Ig heavy 431.6 65.5 110 2 D36005 Ig heavy | 45     | 44     | 43       | 42       | 41     | 40        | 39       | 38       | 37       | 36       | 35       | 34       | 33       | 32       | <u>,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</u> |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------|--------|----------|----------|--------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------------------------------------------|
| 123 2 \$48798 I9 123 2 \$31114 I9 122 2 \$20772 I9 127 2 \$320780 I9 127 2 \$336489 I9 134 2 \$33699 I9 140 2 \$33696 I9 140 2 \$33588 I9 140 2 \$33588 I9 140 2 \$33588 I9 150 2 \$147781 I9 110 2 \$14781 I9 110 2 \$14695 I9 110 2 \$14781 I9                                                                                                                                                                                                                                                                                                                                                                               | 428.5  | 429    | 431      | 431.5    | 431.5  | 433       | 434      | 435      | 435      | 436      | 436      | 436.5    | 436.5    | 437      | 437.5                                        |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | N      | N      | N        | N        | N      | N         | N        | N        | N        | N        | 2        | N        | N        | N        | N                                            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | S46390 | S31598 | D36005   | E36005   | PH1652 | 137781    | \$31588  | S31686   | S78486   | S31699   | S38489   | I37780   | S20772   | 831114   | S48798                                       |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | _      | _      | Ig heavy | Ig heavy | _      | Ig variab | Ig heavy | Ig varia | Ig heavy | Ig heavy | Ig heavy                                     |

### ALIGNMENTS

| RESULT 2 \$26790 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 13-Jan-195 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C;Accession: \$26790 R;Mortari, F:; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W. Bur. J Immunol. 22, 241-245, 1992 A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam A;Accession: \$26790 A;Accession: \$26790 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-128 -MOR> A;Cross-references: EMBL:X61013; NID:g32798; PIDN:CAA43347.1; PID:g1335128 C;Superfamily: immunoglobulin V region; immunoglobulin homology | 1 EVQLVKSGEGLVKPGGSLRLSCAASGFTFRRYDIHMVRQTPGKGLEWVSSISSGGNYIDY 60 | RESULT 1  \$31669  Ig heavy chain V region - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_ revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: \$31669 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992 A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: \$31585 A;Accession: \$31669 A;Reference mumber: \$31585 A;Accession: \$31669 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-141 <cuii- <imm'="" a;cross-references:="" c;keywords:="" c;superfamily:="" domain:="" embl:z14212;="" heterotetramer;="" homology="" immunoglobulin="" nid:g30959;="" p;34-117="" pid:g30960="" pidn:caa78581.1;="" region;="" v=""> Cuery Match Best Local Similarity 75.3*; Score 475.5; DB 2; Length 141; Best Local Similarity 75.2*; Pred. No. 3.4e-37; Matches 94; Conservative 9; Mismatches 19; Indels 3; Gaps 1;</cuii-> |
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Search completed: December 30, 2003, 11:05:35 Job time : 12.2685 secs

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 RESULT 14
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 US-09-240-274-21
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 ; OTHER INFORMATION: anti-Rh(D) chain D15 US-09-240-274-20
 ; OTHER INFORMATION: anti-Rh(D) chain D16 US-09-240-274-21
Sequence 22, Application US/09240274

PATENT NO. 625455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: CRITING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SCRITING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2
 GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver: 2.0
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 Query Match
Best Local
 SEQ ID NO 21
 Sequence 21, Appli
Patent No. 6255455
 Matches
 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
 ORGANISM: Homo
 LENGTH: 125
 Local Similarity
 118
 113 GTLVTVSS 120
 113 GTLVTVSS 120
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 95;
 μ
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95; Conservative 10; Mismatches 12;
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 Application US/09240274
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 10; Mismatches
 DB 3;
 Length 125;
 Indels
 Indels
 Length 125;
 11;
 11;
 117
 60
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 ; OTHER INFORMATION: anti-Rh(D) chain US-09-240-274-24
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 OTHER INFORMATION: anti-Rh(D) chain US-09-240-274-22
 US-09-240-274-24
 Query Match
Best Local S
Matches 92
 SEQ ID NO 24
LENGTH: 125
TYPB: PRT
ORGANISM: Homo sapiens
 GENERAL INFORMATION:
 Sequence 24, Application US/09240274 Patent No. 6255455
 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 22
 APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-9

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-01-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0
 Query Match
Best Local 8
 CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILLING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILLING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
 LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
 FEATURE:
121
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 118 GTLVTVSS 125
 113
 61
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 61
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 1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
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l Similarity 74.2%; Pred. No. 2.3e-40;
95; Conservative 10; Mismatches 12;
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125
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 76.1%;
73.6%;
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k; Pred. No. 5.6e-40;
11; Mismatches 17;
 D17
 Indels
 Indels
 Length 125;
 Length 125;
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 60
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APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
ITILE OF INVENTION: Specific binding members for
FILE REFERENCE: 2811/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR FILING DATE: 1999-04-30
INUMBER OF SEQ ID NOS: 25
SOFTWARE: PACENTIN VEY: 2.1
SEQ ID NO 4
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 RESULT 10
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 SOFTWARE: Patentin SEQ ID NO 10
 Query Match
Best Local
 3-09-560-198A-10
Sequence 10, Application US/09560198A
 GENERAL
 Patent No.
 Matches
 Query Match
 CURRENT APPLICATION NUMBER: US/09/560,198A CURRENT FILING DATE: 2000-04-28 PRIOR APPLICATION NUMBER: US 60/131,983 PRIOR FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 25
 APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbetal
FILE REFERENCE: 2811/35520A
 ORGANISM: Homo sapiens
09-560-198A-10
 APPLICANT: Thompson, Julia B
APPLICANT: Lennard, Simon N
APPLICANT: Wilton, Alison J
APPLICANT: Braddock, Peta SH
 LENGTH: 12
TYPE: PRT
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 LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
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 h 76.8%;
Similarity 78.0%;
 l Similarity
96; Conserv
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 Thompson, Julia E
Lennard, Simon N
Wilton, Alison J
 Braddock, Peta SH
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 Sarah L
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Pred. No. 2.2e-40;
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Pred. No. 1.8e-40;
5; Mismatches 19
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 19;
 19;
 Length
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 3;
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 Gaps
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 120
 60
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APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

PILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN Ver. 2.0

FYPE: PRT

OPENION: USD 115-11
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 US-09-240-274-20
 ; OTHER INFORMATION: anti-Rh(D) chain D01 US-09-240-274-8
 US-09-240-274-8
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 RESULT 11
SOFTWARE: Patentin Ver.
SEQ ID NO 20
LENGTH: 125
TYPE: PRT
 GENERAL INFORMATION:
 Sequence 20, App...
8 No. 6255455
 Sequence 8, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
 APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER PILING DATE: 1998-10-11

NUMBER: 0958-10-11

NUMBER: 0958-10-11

NUMBER: 0958-10-11

NUMBER: 0958-10-11
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 113
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 95;
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 GTLVIVSS 120
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 Application US/09240274
 123
 Length 125;
 Indels 11;
 Gaps
 117
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US 07/596,289

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APPLICANT: McCafferty, John S
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
APPLICANT: Tempest, Philip R
ITILE OP INVENTION: Specific binding members for TGFbetal
FILE REFERENCE: 2811/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 123
TYPE: PRT
ORGANISM: Homo Bapiens
US-09-560-198A-2
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 문
 US-09-560-198A-2
 Matches
 Query Match
Best Local Similarity
 Matches
 GENERAL INFORMATION:
 Best Local
 APPLICANT: Thompson, Julia
APPLICANT: Lennard, Simon
APPLICANT: Wilton, Alison
APPLICANT: Braddock, Peta
APPLICANT: Du Fou, Sarah I
 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
 FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/5
FILING DATE: 12-OCT-1990
ATTORNSY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
 quence 2, Application US/09560198A
 REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
 MOLECULE TYPE: peptide
 NAME/KBY: Protein LOCATION: 1..119 OTHER INFORMATION: OTHER INFORMATION:
 TYPE: amino acid
 STRANDEDNESS:
TOPOLOGY: 111
 94;
 13
 1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
96; Conservative
 h 78.1%;
Similarity 78.0%;
 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFD-YWGQGTLVTVSS
 Du Fou, Sarah L
McCafferty, John G
 Braddock, Peta SH
 Conservative
 (415) 543-5043
 linear
 single
 78.2%;
78.3%;
 /note= "Human fetal immunoglobulin
56Pl'CL VH region"
 9;
 Score 485.5; DB 4;
Pred. No. 3.6e-41;
7; Mismatches 17;
 Score 486.5; DB 3;
Pred. No. 2.7e-41;
 Mismatches
 16;
 Indels
 Length 119;
 Indels
 Length 123;
 1;
 ų.
 Gaps
 Gaps
 119
```

US-09-560-198A-4

Sequence 4, Application US/09560198A Patent No. 6492497

```
RESULT 8
US-09-025-769B-24
 밁
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 ঠ
 APPLICANT: G., VIC
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
ITILE OF INVENTION: Procein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
밁
 5
 밁
 5
 US-09-025-769B-24
 Patent No.
 Sequence 24, Application US/09025769B
 Matches
 Query Match
Best Local Similarity
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
 ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TOPOLOGY: 1i
 TELECOMMUNICATION INFORMATION:
 NAME: James F. Haley, REGISTRATION NUMBER:
 APPLICATION NUMBER: PILING DATE: 18-FE
 STRANDEDNESS:
 TYPE: amino acid
 TELEPHONE:
 REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MO
 13
 61
 61
 61 ADSVKGRPAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
 1 BVQLVBSGGGLVQPGRSLRLSCVDSGLTFSSSYGMHWVRQAPGAGLEMVAVISYDGNDKYY 60
 96; Conservative
 10021
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTÄVYYCARTGEYSGYDTSGVELWGQGTTVT 120
 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIABA---LWGOGTLVT 117
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGGSG---DYWGQGTLVTVSS
 USA
 linear
 (212)596-9000
 protein
 Floppy disk
 18-FEB-1998
 77.9%;
80.0%;
 US/09/025,769B
 24:
 MORPHO/5
 4; Mismatches
 Score 484.5; DB 4
Pred. No. 4.2e-41;
 c/o Fish & Neave
 DB 4;
 Length 117;
 Indels
 ω
--
 Gape
 60
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CLASSIFICATION:

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RESULT 5
US-08-759-804A-46
 밁
 US-08-331-397B-46
 Sequence 46, Application US/08759804A Patent No. 5990296
 Matches
 Query Match
 GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
 TYPE: amino acids
STRANDEDNESS:
TOPOLOGY
 APPLICATION NUMBER: US 07/767,331
PILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: Tumor-Specific Antibody Fragments, TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein
 NAMB/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
 APPLICATION NUMBER: US/08/759,804A FILING DATE: 03-DEC-1996 CLASSIFICATION: 536
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
 Match 78.2%;
Local Similarity 78.3%;
 61 ADSVKGRFAISRDNAKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
 94; Conservative
 1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY
 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARRSARTYYFD-YWGQGTLVTVSS 119
 California
 9; Mismatches 16; Indels 1;
 Score 486.5; DB 2;
Pred. No. 2.7e-41;
 Length 119;
 Gaps
 60
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밁
 US-09-227-693-46
 US-08-759-804A-46
 Patent No. 6287562
GENERAL INFORMATION:
 Matches
 Query Match
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/227,693

PILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331,396
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
 TELEPAX: (415) 576-031 INFORMATION FOR SEQ ID NO:
 APPLICANT: P
APPLICANT: B
APPLICANT: P
APPLICANT: J
APPLICANT: J
 NATIONNAL MADER Ellen L. ARME: Weber Ellen L. REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 015280-126140US
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (415) 576-0200
 SEQUENCE CHARACTERISTICS:
 PILING DATE:
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
 APPLICANT: LEE, Byungkook TITLE OF INVENTION: HUMANI
 NAME/KEY: Protein LOCATION: 1..119 OTHER INFORMATION: OTHER INFORMATION:
 MOLECULE TYPE: protein
 Local Similarity
 CITY: San Francisco
STATE: California
 STREET:
 ADDRESSEE:
 TOPOLOGY:
 STRANDEDNESS
 TYPE: amino acid
APPLICATION NUMBER:
 LENGTH:
 61 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCARRSARTYYFD-YWGQGTLVTVSS
 1 EVQLVESGGGLVQPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAVISYDGNDKYY 60
 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDTAVYYCAKDLIESNIAEALWGQGTLVTVSS 120
 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY
 Application US/09227693
 RE: Townsend and Townsend Khourie and Crew
Steuart Street Tower, One Market Plaza
 119 amino acids
 BENHAR, Itai
PADLAN, Eduardo A.
 Conservative
 PASTAN,
 linear
 Sun-Hee
 78.2%; Score 486.5; DB 2; 78.3%; Pred. No. 2.7e-41;
 /note= "Human fetal immunoglobulin
56P1'CL Variable Heavy chain (V-H)"
 Release #1.0, Version
 US 07/767,331
 46:
 9
 Mismatches
 16; Indels
 Length 119;
 1:
 60
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RESULT 5
US-08-652-816A-6
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 US-08-652-816A-1
 Sequence 6, Application US/08652816A Patent No. 5872215
 Matches
 Query Match
Best Local Similarity
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 23-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9525004.9

FILING DATE: 07-DEC-1995
 GENERAL INFORMATION:
APPLICANT: Osbouri
 TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 1
 APPLICATION NUMBER: GI
FILING DATE: 02-DEC-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE
FILING DATE: 02-DEC-15
 APPLICANT:
 SEQUENCE CHARACTERISTICS
LENGTH: 123 amino acid
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 23-MAY-19:
PRIOR APPLICATION DATA:
 TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 02-DEC-1
PRIOR APPLICATION DATA:
 FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 23-MAY-
 COMPUTER READABLE FORM:
TUMBER OF SEQUENCES:
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 REFERENCE/DOCKET NUMBER: 28
 NAME: David W. Clough
 APPLICATION NUMBER: US 08/244,597 FILING DATE: 01-JUN-1994
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
 TOPOLOGY:
 121
 112 VSS 114
 13
 19
 98;
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFY--IWGQGTMVT 111
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 amino acid
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 VSS 123
 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGRSHNYELYYYYMDVWGQGTMVT 120
 123 amino acida
 McCafferty, JG
 Allen, DJ
 Conservative
 linear
 TUMBER: GB 9610824.6
23-MAY-1996
 02-DEC-1992
 02-DEC-1991
 MBER: GB 9125579.4
02-DEC-1991
 23-MAY-1996
 82.5%;
79.7%;
 덪
 PCT/GB92/02240
 GB 9125579.8
 US/08/652,816A
 8
 28111/33308
 Score 492.5; DB 2; Length 123;
Pred. No. 1.2e-43;
8; Mismatches 8; Indels 9
 9;
 Gaps
 60
 60
 2
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RESULT 6
US-08-652-816A-8
 문
 S
 문
 S
 밁
 Matches
 Best Local
 Query Match
 TELEPHONE: 312-474-63
INFORMATION FOR SEQ ID NO:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9200

PRIOR APPLICATION NUMBER: GB 9200

PRIOR APPLICATION NUMBER: GB 9200

PRIOR APPLICATION NUMBER: DATE: 23-SEP-1000
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 23-MAY-1996
 SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
 REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 STREET: Chicago
 CORRESPONDENCE ADDRESS:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9:
PTI.TNG DATE: 07-DEC-1995
 REGISTRATION NUMBER:
 TOPOLOGY:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 OPERATING SYSTEM:
 ADDRESSEE:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 121 VSS 123
 112 VSS 114
 61
 61
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
 l Similarity 79.7
98; Conservative
 AQKPQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWPY--IWGQGTMVT 111
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 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY
 David W. Clough
 E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
 United States of America
 PatentIn Release #1.0,
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 312-474-6300
 02-DEC-1991
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 23-MAY-1996
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79.7%;
 US/08/652,816A
 US 08/244,597
 PCT/GB92/02240
 GB 9525004.9
 GB 9206372.6
 GB 9125579.8
 GB 9125579.4
 GB 9610824.6
 GB 9206318.9
 36,107
 ٠.
 Score 492.5; DB 2;
Pred. No. 1.2e-43;
8; Mismatches 8;
 Version #1.25 (EPO)
 Length 123;
 Indels
 9
 Gaps
 60
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Sequence 8, Application US/08652816A Patent No. 5872215 GENERAL INFORMATION:

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 US-08-652-816A-8
 Matches
 Query Match
 FILING DATE: 23-MAY-1S
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GENERAL CATION NUMBER: GENERAL CATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GENERAL CATION NUMBER: GENER
 INFORMATION FOR SEQ ID NO:
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: US/08/652,816A
 APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
 SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
 FILING DATE: 23-SEP-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 FILING DATE: 24-MAR-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-JUN-
 FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90
FILING DATE: 23-MAY-1996
 REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
 ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MEDIUM TYPE:
 COUNTRY:
 CITY: Chicago
STATE: Illinois
 FILING DATE:
 ADDRESSEE:
 Local
 REGISTRATION NUMBER:
 TELEPHONE:
 TOPOLOGY:
 112
121
 61 AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCARHNHNYELYYYYMDVWGQGTMVT
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFY--IWGQGTMVT 111
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTESSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 98;
 Similarity
 amino acid
VSS 123
 VSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY
 David W. Clough
 E: Marshall, O'Toole, 6300 Sears Tower, 233
 United States of America
 Osbourn,
 Conservative
 312-474-6300
 NUMBER: GB 9125579.8
02-DEC-1991
 Ploppy disk
 23-SEP-1992
 02-DEC-1991
 02-DEC-1992
 01-JUN-1994
 24-MAR-1992
 23-MAY-1996
 82.5%;
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 Specific
 GB 9125579.4
 US 08/244,597
 GB 9206372.6
 PCT/GB92/02240
 GB 9525004.9
 GB 9206318.9
 GB 9610824.6
 36,107
 8:
 8
 Score 492.5; DB 2;
Pred. No. 1.2e-43;
 28111/33308
 binding members, materials
 Mismatches
 Gerstein, Murray & Borun
South Wacker Drive
 8
 Indels
 Length 123;
 9;
 Gaps
 60
 6
```

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RESULT 7
US-08-652-816A-9
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 ફ
 US-08-652-816A-9
 Sequence 9,
Patent No. 9
 Matches
 Query Match
Best Local S
 GENERAL INFORMATION:
APPLICANT: Osbour
 TELEPHONE: 312-474-63
INFORMATION FOR SEQ ID NO:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 02-DEC-1991
 SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: US/08/652,81
 SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acid
 PRIOR APPLICATION NUMBER: GB 9610824.6
APPLICATION NUMBER
FILING --
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 COMPUTER READABLE FORM:
 TITLE OF INVENTION:
 APPLICANT:
 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 FILING DATE:
 FILING DATE:
 FILING DATE:
 Local Similarity
 TYPE: amino acid
TOPOLOGY: linear
 APPLICATION NUMBER:
 REFERENCE/DOCKET NUMBER:
 REGISTRATION NUMBER:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 ADDRESSEE:
 FILING DATE:
61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----
 98;
 Chicago
 David W. Clough
 Application US/08652816A
 123 amino acide
 United States of America
 3: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
 McCafferty, JG
 Conservative
 Allen, DJ
 Osbourn,
 312-474-6300
SEO ID NO: 9:
 UMBER: GB 9206372.6
23-SEP-1992
 23-MAY-1996
 24-MAR-1992
 01-JUN-1994
 07-DEC-1995
 02-DEC-1991
 methods.
 82.5%;
79.7%;
 낮
 Specific binding members, materials and
 US 08/244,597
 GB 9125579.8
 GB 9125579.4
 GB 9525004.9
 PCT/GB92/02240
 GB 9206318.9
 US/08/652,816A
 36,107
 Score 492.5; DB 2;
Pred. No. 1.2e-43;
8; Mismatches 8;
 28111/33308
 Version #1.25
 Length 123;
 Indels
 Borun
 ELDWFY--IWGQGTMVT
 9
 Gape
```

2; 60 60

```
APPLICANT: Ruben et al.

APPLICANT: RUben et al.

FILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PELLING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 7001-05-25
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 S
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region US-10-125-687-1
Search completed: December 30, 2003, 11:45:25 Job time : 24.4484 secs
 밁
 ঠ
 ; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
 US-09-880-748-1509
 RESULT 15
 NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1509
 Sequence 1509, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
 Query Match 85.1%;
Best Local Similarity 85.8%;
Matches 103; Conservative
 Query Match 84.9%; Score 507; DB 11; Best Local Similarity 79.7%; Pred. No. 1.9e-42; Matches 102; Conservative 4; Mismatches 8;
 LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 121
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 61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAREQGYDILTGYYPEGGWFDPWGK 120
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 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 120
 19
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
 GTMVTVSS 128
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS 114
 Score 508; DB 15; Length 120; Pred. No. 6.6e-43; 3; Mismatches 8; Indels
 œ
•-
 Length 253;
 Indels 14;
 6;
 Gaps
 Gaps
 2;
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```
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 191
LENGTH: 119
 RESULT 11
US-10-308-817-191
 밁
 S
 밁
 á
 ; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-49
 밁
 Ś
 밁
 Ś
 US-10-269-805-19
 RESULT 12
 US-10-308-817-191
 Sequence 191, Application US/10308817 Publication No. US20030219861A1 GENERAL INFORMATION:
Sequence 19, Application US/10269805
Publication No. US20030124129A1
GEMERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
 GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
 Sequence 49, Application US/10269805 Publication No. US20030124129A1
 Matches 104; Conservative
 Query Match
Best Local Similarity
 SEQ ID NO 49
 Matches 101; Conservative
 Query Match
 FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
 TYPE: PRT
ORGANISM: human
 Local Similarity
 61
 61
 61
 5
 _
 \vdash
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC---ELDW-FYI--WGQGTMVTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY 60
 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGRIIPILGIANY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYYYYYGMDVWGQGTTVTVSS
 AOKFOGRVTITADESTSTAYMELSTLISEDTAVYYCELDWFY----IWGQGTMVTVSS 114
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCATSRLEWLLYLDYWGQGTLVTVSS
 86.0%;
84.9%;
 86.1%;
 4; Mismatches
 ა
•
 Score 514; DB 15;
Pred. No. 1.7e-43;
 Score 513.5; DB 1
Pred. No. 1.9e-43;
 Mismatches
 DB 12;
 8
 Length 120
 Indels
 AGENTS
 Indels
 Length 119;
 6
 <u>ن</u>
 Gaps
 120
 60
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S
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 ; ORGANISM: Homo US-10-269-805-19
 RESULT 13
US-10-025-687-1
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 RESULT 14
US-10-125-687-1
 US-10-025-687-1
 NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 121
 Sequence 1, Application US/10025687 Publication No. US20020142255A1 GENERAL INFORMATION:
 Sequence 1, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
 Matches
 Query Match
 Matches
 Query Match
Best Local Similarity
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REPERENCE: 26590-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 1
 CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
 APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION
FILE REFERENCE: 26050-705
 PRIOR APPLICATION NUMBER: US 60/328, PRIOR FILING DATE: 2001-10-11
 FEATURE: OTHER INFORMATION: Human consensus antibody heavy chain variable region
 LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
 Local Similarity
 121 S 121
 114 S 114
 103;
 103;
 61
 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARFESGYWGDAFDIWGQGTMVTVS 120
 61
 61
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL------DWFYIWGQGTMVTVS 113
 QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGTFSSHAISWVRQAPGQGLEMMGDIIPILGTGNY 60
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARWGGDGFYAMDYWGQGTLVTVSS
 Conservative
 Conservative
 варіепя
 85.7%;
85.1%;
 85.1%;
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 u
 Score 511.5;
Pred. No. 3e-
 Score 508; DB 14;
Pred. No. 6.6e-43;
 Mismatches
 Mismatches
 .5; DB
3e-43;
 DB 14;
 8
 15;
 OF HUMAN ANTIBODY LIBRARY
 Length 120;
 Indels
 Indels
 Length
 7;
 6
 Gaps
 Gaps
 60
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```
US-10-269-805-35

Sequence 35, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.1
 US-09-976-118-2
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 US-10-269-805-35
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 LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-9
 RESULT 8
 Sequence 2, Application US/09976118
Patent No. US20020058033A1
GENERAL INFORMATION:
 PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-L0-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
 Matches
 Query Match
Best Local
 Best Local
 Query Match
APPLICANT: Raisch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Alle
 CURRENT FILING DATE:
 TYPE: PRT
ORGANISM: Homo
 ENGTH: 125
 Local Similarity
 104;
 110
 121
 121 S 121
 114 S 114
 104;
 61
 61 AQXFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFYIWGQGTMVTVS
 61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAAFSPFTETDAFDIWGQGTMVTVS
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE------LDWFYIWGQGTM 109
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 Similarity
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 VTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSPIYYDILTGIDAFDIWGQGTM
 VTVSS 125
 Conservative
 Conservative
 James Allen
 86.7%;
 2002-10-10
 86.5%;
 ω
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 ω
•
 Score 517.5; DB 1:
Pred. No. 7.7e-44;
 Score 516.5; DB 15;
Pred. No. 1e-43;
 Mismatches
 Mismatches
 DB 15;
 7;
 Indels
 Length 121;
 Length
 11;
 7;
 Gaps
 Gaps
 120
 120
 113
 60
 60
 60
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```
Sequence 3, Application US/10269805

Publication NO. US20030124129A1

GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOISTIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR APPLICATION UMBER: US 60/328,604
PRIOR APPLICATION NUMBER: US 60/328,604
 RESULT 9
US-10-269-805-3
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 US-09-976-118-2
 SEQ ID NO 2
LENGTH: 270
TYPE: PRT
 Matches
 Query Match
 Query Match
 TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor TITLE OF INVENTION: Single-Chain Antibodies FILE REFERENCE: D6355
CURRENT APPLICATION NUMBER: US/09/976,118
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR APPLICATION NUMBER: US 60/240,353
RIOR PILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
 OTHER INFORMATION: amino acid sequence of anti-EGFR scFV OTHER INFORMATION: clone pSEX81-63
 ORGANISM: artificial sequence FEATURE:
 Local Similarity
wes 103; Conserv
 Local
 112
121
 109 MVTVSS 114
 121 LVTVSS 126
 61
 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGVVGDFDWLSFFDYWGQGTLVT 120
 61
 61
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 Similarity
SSA
 VSS 114
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDW---FYIMGQGTMVT 111
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPDYYGSGSYYPNWFDPWGQGT 120
 AQKFQGRVTITADESTSTAYMBLSTLTSEDTAVYYCELD------WFYIWGQGT 108
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISMVRQAPGQGLEMMGGIIPIFGTANY
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llarity 83.7%;
Conservative
 Conservative
123
 86.4%; Score 516; DB 9; Length 270; 81.7%; Pred. No. 2.6e-43;
 Score 514.5; DB 15;
Pred. No. 1.5e-43;
4; Mismatches 7;
 Mismatches
 Indels
 Length 123;
 12;
 9
 Gaps
 Gape
 60
 60
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RESULT 10 US-10-269-805-49

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US-10-300-675-12

Sequence 12, Application US/10300675

Publication No. US20030198638A1

GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519

CURRENT APPLICATION NUMBER: US/10/300,675

CURRENT APPLICATION NUMBER: US/10/300,675

PRIOR APPLICATION NUMBER: US 09/989,901

PRIOR APPLICATION NUMBER: US 09/989,901

PRIOR FILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

SEQ ID NO 12
 В
 RESULT 4
US-10-300-675-14
; Sequence 14, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
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 ; OTHER INFORMATION: US-10-300-675-10
 APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclona
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
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 ; OTHER INFORMATION: Recombinant variant US-10-300-675-12
 Matches
 Query Match
Best Local Similarity
 Matches
 Query Match
Best Local Similarity
 SEQ ID NO 10
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
 TYPE: PRT
ORGANISM: Artificial Sequence
 FEATURE:
 ORGANISM: Artificial Sequence FEATURE:
 TYPE: PRT
 ENGTH: 118
 ENGTH: 118
 101; Conservative
 61
 61
 101;
 61
 61
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 H
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISMVRQAPGQGLEMMGDIIPILGTGNY 60
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD-----WFYIWGQGTMVTVSS 114
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD----WFYIWGQGTWVTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIIPIFGTANY 60
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
 AOKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDGSGWYHYWGOGTLVTVSS 118
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDTSGWYHYWGQGTLVTVSS 118
 Conservative
 Recombinant
 87.1%;
 87.1%;
85.6%;
 Specific Monoclonal Antibodies
 6.
 6
 Score 520; DB 12;
Pred. No. 4.2e-44;
6; Mismatches 7;
 Score 520; DB 12;
Pred. No. 4.2e-44;
6; Mismatches 7
 variant
 Length 118;
 Length 118;
 Indels
 Indels
 4.
 4
 Gaps
 Gaps
```

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FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 124
 S
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 S
 RESULT 6
US-10-269-805-9
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 US-10-269-805-25
 US-10-269-805-25
 RESULT 5
 US-10-300-675-14
Sequence 9, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT; OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC
FILE REFERENCE: A-722
 Sequence 25, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
 Query Match
 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14
 Matches 101;
 Best Local Similarity
 Matches
 Query Match
 NUMBER OF SEQ ID NOS:
 PRIOR APPLICATION NUMBER: US 09/989,901 PRIOR FILING DATE: 2001-11-19
 CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
 TYPE: PRT
ORGANISM: Homo sapiens
 TYPE: PRT
 OTHER INFORMATION: Recombinant variant
 FEATURE:
 ORGANISM: Artificial Sequence
 LENGTH:
 Local
 121 TVSS
 111 TVSS 114
 105;
 61
 13
 61
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFYIWGQGTMV 110
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
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 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYDFWSGYSLDAFDIWGQGTMV 120
 AQKFQGRVTITADESTSTAYMBLSTLTSBDTAVYYCBLD----WFYIWGQGTMVTVSS 114
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 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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 Conservative
 87.1%;
85.6%;
 87.1%;
84.7%;
 6; Mismatches
 Score 520; DB 12;
Pred. No. 4.2e-44;
 Score 520; DB 15;
Pred. No. 4.4e-44;
 Mismatches
 DB 12;
 Length 124;
 Length 118;
 Indels
 Indels
 10;
 4.
 Gaps
 60
 60
 60
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CURRENT APPLICATION NUMBER: US/10/269,805

BINDING AGENTS

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Sequence:
Result
 Total number of hits satisfying chosen parameters:
 Run on:
 Scoring table:
 Perfect score:
 OM protein -
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 protein search, using sw model
 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
 US-09-674-752-51
597
1 QVQLVQSGAEVKKPGSSVKV......YCELDWFYIWGQGTMVTVSS 114
 December 30, 2003, 11:01:15; Search time 24.4484 Seconds (without alignments) 927.994 Million cell updates/sec
 BLOSUM62
 724715 seqs, 199017464 residues
 Gapop 10.0 , Gapext 0.5
 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

| No.      | Score<br>520<br>520 | Match Length<br>87.1 118 | Length<br>118 | DB 12 | US-10-300-675-6<br>US-10-300-675-10 | Description Sequence 6, Appli Sequence 10, Appl |
|----------|---------------------|--------------------------|---------------|-------|-------------------------------------|-------------------------------------------------|
| <b>,</b> | 520                 | 87.1                     | 118           | 12    | US-10-300-675-6                     | , "                                             |
| ω ,      | 520                 | 87.1                     | 118           | 12    | US-10-300-675-1                     | N C                                             |
| 4.       | 520                 | 87.1                     | 118           | 12    | US-10-300-675-14                    |                                                 |
| տ        | 520                 | 87.1                     | 124           | 15    | US-10-269-805-25                    |                                                 |
| σ        | 517.5               | 86.7                     | 121           | 15    | US-10-269-805-9                     |                                                 |
| 7        | 516.5               | 86.5                     | 125           | 15    | US-10-269-805-35                    | ٠.                                              |
| œ        | 516                 | 86.4                     | 270           | ø     | US-09-976-118-2                     |                                                 |
| 9        | 514.5               | 86.2                     | 123           | 15    | US-10-269-805-3                     |                                                 |
| 10       | 514                 | 86.1                     | 120           | 15    | US-10-269-805-49                    |                                                 |
| 11       | 513.5               | 86.0                     | 119           | 12    | US-10-308-817-19                    | Ē                                               |
| 12       | 511.5               | 85.7                     | 121           | 15    | US-10-269-805-19                    |                                                 |
| 13       | 508                 | 85.1                     | 120           | 14    | US-10-025-687-1                     |                                                 |
| 14       | 508                 | 85.1                     | 120           | 15    | US-10-125-687-1                     |                                                 |
| 15       | 507                 | 84.9                     | 253           | ב     | 110_00_000_340_1500                 | 9                                               |

GENERAL INFORMATION:

| ٦.       | Sequence | US-10-269-805-        |     | 82.8 | 494.5 | 5  |
|----------|----------|-----------------------|-----|------|-------|----|
|          | Sequence | US-09-880-748-        |     | •    | 495   | 44 |
| 1717, Ap | Sequence | US-09-                | 248 | 83.0 | 495.5 | 43 |
|          | Sequence | US-09-880-748-        |     | •    | 495.5 | 2  |
| 9        | Sequence | US-09-880-748-        |     | 83.1 | 496   | 41 |
| 5, Appli | Sequence |                       |     | 83.1 | 496   | 6  |
| 8        | Sequence | -Sn                   |     | 83.3 | 497.5 | 39 |
| Ф,       | Sequence | US-10-184-508A        |     | 83.3 | 497.5 | 38 |
| 15, Appl | Sequence | US-10-151             |     | 83.5 | 498.5 | 37 |
| -        | Sequence | US-                   |     | 83.5 | 498.5 | 36 |
| 0        | Sequence | 15 US-10-184-508A-6   |     | 83.5 | 498.5 | 35 |
| 7,       | Seguence | 15 US-10-186-186-7    |     | 83.5 | 498.5 | 4  |
| 7        | Sequence | US-10                 |     | 83.5 | 498.5 | 33 |
| 1553, Ap | Seguence | . US-09               | 257 | 83.6 | 499   | 32 |
| 1728, Ap | Sequence | US-09-880-748-        |     | 83.7 | 499.5 | 31 |
| 1727, Ap | Seguence | US-09-880-748-        |     | 83.7 | 499.5 | 30 |
| 1880, Ap | Sequence | US-09-880-748         | 253 | 83.8 | 500.5 | 29 |
|          | Seguence | US-09-880-748-        |     |      | 501.5 | 28 |
|          | Sequence | 15 US-10-269-805-15   |     | 84.1 | 502   | 27 |
| 1737     | Sequence | 11 US-09-880-748-1737 |     | 84.2 | 502.5 | 26 |
| 1732,    | Sequence | . US-09               |     | 84.2 | 502.5 | 25 |
| 1719,    | Sequence | US-09-880-748-        |     | 84.2 | 502.5 | 24 |
| 1866     | Sequence | 11 US-09-880-748-1866 |     | 84.4 | 504   | 23 |
| 47,      | Sequence | US-10                 | 627 | 84.5 | 504.5 | 22 |
| 1879, Ap | Sequence | US-09-                |     | 84.7 | 505.5 | 21 |
| •        | Sequence | US-09                 | 248 | 84.7 | 505.5 | 20 |
| 1881, Ap | Sequence | US-09                 |     | 84.7 | 505.5 | 19 |
| 37, Appl | Sequence | 15 US-10-269-805-37   |     | 84.8 | 506   | 18 |
| 173      | Sequence | US-09-880-7           | 48  | 84.8 | 506.5 | 17 |
|          | sequence | TT US-09-880-748-1733 |     | 04.0 | 000.0 | 9  |

# ALIGNMENTS

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Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION;
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P. 1X 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILLING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR FILING DATE: 2001-11-19
; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; SEQ ID NO 6
RESULT 2
US-10-300-675-10
; Sequence 10, Application US/10300675
; Publication No. US20030198638A1
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 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-300-675-6
 용
 US-10-300-675-6
 Query Match 87.1%;
Best Local Similarity 85.6%;
Matches 101; Conservative
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD----WFYIWGQGTMVTVSS 114
 1 QVQLVQSGAEVKXPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY 60
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
 AQXFQGRVTITADESTSTAYMBLSSLRSEDTAVYYCAREDSSGWYHYWGQGTLVTVSS 118
 Score 520; DB 12;
Pred. No. 4.2e-44;
6; Mismatches 7;
 Length 118;
 Indels
 4.
 Gaps
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61

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RESULT 14
ABJ18672
 S
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 Ś
 The invention relates to a novel method for the construction of a library of frecombinant antibodies. The novel method comprises clustering variable conference of a collection of antibodies having known 3D structures into at colleast two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of conformaticials mitibodies in silico which provides a structurally diverse and conformaticially more relevant source of antibody candidates which can conformaticially more relevant source of antibody candidates which can conformaticial mucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies continum immunogenecity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody candidates to the novel antibody library construction method of the
 Query Match
Best Local S
Matches 103
 Constructing a library of recombinant antibodies useful as source antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structur into structural ensembles
 ond
 17-APR-2002; 2002WO-US12202
 Antibody library related heavy variable chain protein region SEQ ID No
 06-MAR-2003
 ABJ18672 standard; Protein;
 Disclosure; Page 98-99; 119pp; English
 WPI; 2003-093043/08
 17-APR-2001; 2001US-284407P
 24-OCT-2002
 WO200284277-A1
 Unidentified
 Library; recombinant antibody; clustering variable
 Sequence
 (ABMA-)
 immunogenecity;
 103;
61
 13
 ABMAXIS INC
 Similarity
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS 114
 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 120
 (first entry)
 ξ
 antibody therapeutic
 85.1%;
85.8%;
 120
 Score 508; DB 24;
Pred. No. 3.9e-37;
3; Mismatches 8
 ζ
 8
 Length
 region;
 in silico
 6,
 60
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RESULT 15.
ABJ18718
AC ABJ18
XX ABJ188
XX ABJ188
XX ABJ188
XX ABJ18
XX ABJ18
XX ABJ18
XX Libr
XX Libr
XX Unid

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 Matches 103;
 Query Match
Best Local :
 artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenecity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the
 The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of
 Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
 06-MAR-2003
 ABJ18718;
 ABJ18718 standard;
 Sequence
 Disclosure; Fig 13B; 119pp; English.
 into structural ensembles
 17-APR-2001; 2001US-284407P
 17-APR-2002; 2002WO-US12202
 24-OCT-2002
 WO200284277-A1
 Unidentified.
 Library; recombinant antibody; clustering variable region; in silico;
 Antibody library related VH protein region 1DHA
 immunogenecity; antibody therapeutic
 2003-093043/08
 61
 61
 ABMAXIS INC
 Similarity
 QVQLVQSGAEVKXPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 120
 Conservative
 (first
 $
 Protein;
 entry)
 85.1%;
85.8%;
 ω
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 Score 508; DB 24;
Pred. No. 3.9e-37;
 Mismatches
 DB 24;
 Length 120;
 Indels
 <u>.</u>
 Gaps
 114
 120
 60
 60
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rch completed: December time : 37.756 secs

30,

2003,

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RESULT 12
AAB67618
ID AAB67
XX AAB67
XX AAB67
XX AAB67
XX AAB67
XX Human
XX Human
XX Homo
XX H
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 8888888888888888888
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 Matches
 Query Match
Best Local (
 TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is elevated. The sequences shown in ABR01502-ABR01545 represent the heavy chain regions of a human anti-TIMP-1 antibody of the invention.
AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-CW6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific
 Claim
 of humans
 Nove1
 26-AUG-1999;
 28-AUG-2000;
 01-MAR-2001.
 WO200114558-A1
 miscarriage;
 29-MAY-2001
 Sequence
 Kretzschmar T,
 AAB67618
 AAB67618 standard;
 (MORP-)
 2001-218451/22.
 sapiens
 isolated human immunoglobulin or functional immunoglobulin ent specific for human leukocyte antigen Cw6, useful for tromans and for human leukocyte antigen phenotyping -
 121
 114 S 114
 leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing; rriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
 103;
 3; Fig 1; 23pp; English.
 leukocyte antigen-Cw6
 13
 61
 MORPHOSYS
 Similarity
 S
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE--LDW-----FYIWGQGTMVTVS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGLYWAVYPYFDFWGQGTLVTVS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 121
 225
 Conservative
 2000WO-EP08388
 (first
 À,
 99EP-0116691
 Tesar
 Protein;
 entry)
 85.2%;
85.1%;
 Σ,
 Marget
 245
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 specific
 Score 508.5; DB 2
Pred. No. 6.5e-37;
 Mismatches
 ጀ
 Σ
 scFv fragment from clone
 24;
 8
'-
 Indels
 Length
 225;
 7;
 treatment
 0w6
 Gaps
 113
 60
 60
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RESULT 13
AAW2750
ID AAW27
XX
AAW2750
XX
AAW2750
AC AAW27
XX
AC AAW27
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 Query Match
Best Local &
 Matches 102;
 Matches 103;
 Query Match
Best Local
 for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
 Sequence
 The present sequence is the human antibody heavy variable region synthetic sequence VHIA, used in a human derived antibody gene library.
 N-PSDB;
 Ge L,
 18-AUG-1995;
 heavy
 AAW27550
 consensus
 WPI; 1997-179277/16.
 19-AUG-1996;
 06-MAR-1997
 Human;
 23-JAN-1998
 AAW27550
 Sequence
 Example
 Preparation of human
 WO9708320-A1
 Human Ab
 (MORP-) MORPHOSYS GES
 sapiens
 13
 chain;
 13
 Ilag
 antibody;
 Similarity
 ۲,
 Similarity
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 heavy chain variable
 standard;
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE--LDWFY-IWGQGTMVTVSS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGFDYFMDFWGQGTLVTVSS
 gequences,
for highly
 Fig
 120 AA;
 245 AA;
 Conservative
 <
 Conservative
 consensus.
 (first entry
 5A;
 95EP-0113021.
 96WO-EP03647.
 Knappik
 preparation;
 436pp;
 Protein; 120
 85.1%;
85.8%;
 derived antibody gene library
and signal consensus antibody
diverse antibody libraries
 85.2%;
87.2%;
 PROTEINOPTIMIERUNG MBH
 7
 English
 Pred.
 Moroney
 .
 Score 508;
Pred. No. 3
 Score 508.5; DB 2
Pred. No. 7.1e-37;
 library; VHIA; variable
 Mismatches

NO. 3.9e-37;
Mismatches
 region
 ₹
 Mismatches
 S
 VH1A consensus
 Pack P,
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 114
60
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S

AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS

114

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 human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antiarchritic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; ithyromimetic; hepatotropic; immune response suppressor; narcolepsy; rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroidditis; panoreatitis; primary biliary cirrhosis; irritable bowel disease; Siograen's avmiroma
The present invention describes a composition (1), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the IC50 for the suppression of immune response is 1 microM or less (1) has antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antidabetic, antisporiatic, immunosuppressive, dermatological, antithyroid, nephrotropic, thyromimetic and hepatotropic activities, and can be used as a suppressor of immune suppressing 11-2 secretion by a cell, the interaction of a cell of the immune system with another cell, immunosuppressing a patient and for killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 Composition for suppressing immune response, treating diseases immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antige expressed on a cell surface
 (GPCB-)
 Example;
 12-MAY-2000;
06-OCT-2000;
 14-MAY-2001; 2001WO-US15626
 22-NOV-2001
 WO200187338-A1
 Synthetic
 HLA-DR-specific protein MS-GPC5 VH
 18-MAR-2002
 ABB57559;
 ABB57559
 sapiens
 61
 19
 ب
 GPC BIOTECH AG.
 MORPHOSYS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIFILGTGNY 60
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 standard;
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-ELDWFYI--WGQGTMVTVSS
 Fig 15;
 Tesar M,
 2000EP-0110063
2000US-238762P
 (first
 139pp; English.
 Thomassen-Wolf
 Peptide;
 entry)
 115
 $
 H
 sequence.
 117
 114
 60
```

New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

Pan

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Knorr AM,

Schauer

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Hirth-dietrich

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Kraft

Krebs

(FARB ) (MORP-)

BAYER CORP. MORPHOSYS A

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N-PSDB;

2003-129114/12.

ABZ74781.

24-APR-2001; 2001US-285683P

The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-l and neutralises a matrix metalloprotease (MMP)-inhibiting activity

(TIMP-1)

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Claim

Page

153;

228pp;

English

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cancer

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 S
 ABR01510
 RESULT 11
 Matches
 Query Match
 on the surface of the cell, where neither cytotoxic entities nor immunological mechanisms are needed to cause or lead to the killing.

(I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myssthenia gravis, pemphigus vulgaris, glomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans. BBA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 Human anti-TIMP-1 antibody heavy chain #8.
 ABR01510;
 Sequence
 24-APR-2002; 2002WO-US12801.
 31-OCT-2002
 WO200286085-A2
 Homo
 16-APR-2003
 ABR01510
 idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer
 Local
 exemplification of the present invention.
 sapiens.
 101;
 61
 61
 -
 H
 Similarity 87.0
01; Conservative
 standard;
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARHSFFDYWGQGTLVTVSS 115
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFY-IWGQGTWVTVSS 114
 115
 (firet
 Š
 Protein;
 entry)
 85.2%;
87.8%;
 4;
 Score 508.5;
Pred. No. 3.
 Mismatches
 ;
3.4e-37;
9;
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 23;
 Indels
 Length
 115;
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 Gape
 60
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 Query Match
Best Local S
Matches 101
antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for amellorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerofic
 Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 cancer. The antibody is also useful for detecting a TIMP-1 in a preparation, or in diagnosing a disorder in which a TIMP-1 leve elevated. The sequences shown in ABRO1502-ABRO1545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 N-PSDB;
 (FARB)
(MORP-)
 Claim
 hypertrophy or lung
 Pan
 24-APR-2001;
 24-APR-2002;
 31-OCT-2002
 WO200286085-A2
 Homo
 Human
 ABR01538;
 ABR01538
 6
 'n
 sapiens.
 2003-129114/12.
 20; Page 173; 228pp;
 61
 19
 101;
 -
 Similarity
 BAYER
 ABZ74809.
 Knorr AM,
 MORPHOSYS
 standard; Protein;
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFYI--WGQGTMVTVSS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARTYYYFDSWGQGTLVTVSS
 220
 Conservative
 2001US-285683P
 2002WO-US12801
 CORP
 (first entry)
 8
 antibody heavy chain
 Schauer
 cancer
 86.3%;
 Z,
 English.
 220
 5
 Score 515; DB 24;
Pred. No. 1.7e-37;
5; Mismatches 8
 Hirth-dietrich
 ₿
 #36
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 Length
 Kraft
 Indels
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 220
 level
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 Krebs
 Gaps
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heavy
 B.
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RESULT 9
AAB67617
ID AAB6
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 នន្តន្តន្តន្ត្
 Matches
 Query Match
 are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
 pulmonary fibrosis, benign prostate hypertrophy, lung cancer or cancer. The antibody is also useful for detecting a TIMP-1 in a t preparation, or in diagnosing a disorder in which a TIMP-1 level elevated. The sequences shown in ABR01502-ABR01545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
 Claim 3;
 Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for tr
 Sequence
 AAB67617-23 represent single chain antibody (scrv) fragments which
 Kretzschmar T,
 26-AUG-1999;
 28-AUG-2000; 2000WO-EP08388
 01-MAR-2001
 WO200114558-A1
 miscarriage;
 Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 Human
 29-MAY-2001
 AAB67617;
 AAB67617
 (MORP-) MORPHOSYS
 2001-218451/22.
 sapiens.
 101;
 leukocyte
 61
 61
 _
 H
 Similarity
 Fig 1; 23pp;
 specific for husan
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFYI--WGQGTWVTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 etandard;
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARQEWYMDYWGQGTLVTVSS
 220 AA;
 Conservative
 abortion;
 (first
 99EP-0116691
 Tesar
 antigen-Cw6
 Protein;
 entry
 85.4%;
87.1%;
 English.
 Σ,
 psoriasis;
 leukocyte
 Marget
 245
 <u>ب</u>
 specific scrv fragment
 Score 510; DB
Pred. No. 4.7e
5; Mismatches
 Z,
 antibody;
 antigen
 Kroenke
 DB 24;
.7e-37;
 phenotyping
 HE.
 8
 phenotyping;
 Length
 Indels
 from clone Cw6_1.
 2;
 treatment
 Gaps
 heavy
 60
 60
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Query Match Best Local S Matches 102

al Similarity 102; Conser

85 87

2 4

Score 509.5; Pred. No. 5.8e 5; Mismatches

8e-37

22;

Length

245; ω ••

Gaps

2

Sequence

245

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The IgG1, in its nascent form, bears no sialyl-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialyl-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for
 25-MAR-2003
02-JAN-1992
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Homo
 Antibody; immunoglobulin G1
 Sequence of
 AAR24442;
 AAR24442 standard;

 used in treating
psoriasis, etc.

 N-PSDB;
 18-NOV-1991;
 Misc-difference
 Misc-difference
 Misc-
 WPI;
 11-JUN-1992.
 WO9209293-A1
 Disclosure; Fig 1; 46pp; English.
 Inhibition of cell
 (GEHO)
 23-NOV-1990;
 B
 difference
 sapiens
 1992-216789/26
 GEN HOSPITAL
 AAQ25443
 Walz G;
 in minimising inflammation on 25-MAR-2003 to correct P
 antibody molecule
 (updated)
(first en
 /note= "see ...
321
 90US-0618314
 91WO-US08605
 Location/Qualifiers 308
 369
 356
 310
 note= "Substn.
 note=
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 note=
 note=
 note=
 label= N
 label=
 label=
 label=
 label=
 label≖
 abel= N
 Protein;
 adhesion mediated through ELAM-1 chronic inflammation, rheumatoid
 entry)
 CORP
 "gee
 "see above"
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 IgG1.
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 glycan addition site"
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RESULT 7
ABROITS 7
ABROITS 7
ABROITS 11
ABROX
XX
ABROX
XX
ABROX
XX
Huma
XX
Huma
XX
Huma
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 Matches 103;
 Query Match
Best Local
The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprocease-1 (TIMP-1) and neutralises a matrix metalloprocease (MMP) inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC))RR region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, iddopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 Sequence
 variable light chain; cytostatic; nephrotropic; cardiant; liver fib alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 24-APR-2002; 2002WO-US12801
 31-OCT-2002
 Homo sapiens
 matrix
 Human;
 Human anti-TIMP-1
 16-APR-2003
 ABR01512
 ABR01512
 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disoning which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung cancer
 Pan
 24-APR-2001; 2001US-285683P
 WO200286085-A2
 Claim 20; Page 154; 228pp; English.
 N-PSDB; ABZ74783.
 idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer
 (MORP-)
 (FARB)
 ņ
 2003-129114/12.
 145
 108
 85
 61
 25
 antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
le light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;
 ,..
 Similarity
 MORPHOSYS
 BAYER CORP
 Knorr AM,
 standard;
 TLVTVSS
 SSALAMI
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDNGAYCSGGSCYSGWFDPWGQG
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 QVQLVQSGAEVKXPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 481
 Conservative
 (first
 $
 114
 151
 å
 antibody heavy chain #10.
 Schauer
 Protein;
 entry)
 86.3%;
81.1%;
 3
 Score 515.5; 1
Pred. No. 3.4e
3; Mismatches
 220
 Hirth-dietrich
 ₿
 4e-37
 В
 13;
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 8
 Indels
 Kraft
 Length
 ŝ
 481;
 13;
 Krebs
 disorder
 Gape
 8
 107
 144
 84
 60
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 The present sequence is the heavy chain variable region of a human CC tumour-specific monoclonal antibody. Neoplastic cells selectively express CC antigens which are not present on normal cells. Thus monoclonal CC antibodies can be produced that are specifically directed against CC antibodies can be produced that are specifically directed against CC cor cytostatic agents and used to selectively target cancer cells for the CC cimination of tumours. They can also be linked to diagnostic moieties CC that allow the imaging of meoplastic cells. Nucleic acids encoding human CC tumour-specific monoclonal antibodies can be used to express the CC antibodies and can be recombinantly engineered to produced modified CC antibodies with higher affinity or higher selectivity for tumour cells. The comparated by in vitro immunisation of human spleen cell cultures with CC generated by in vitro immunisation of human spleen cell cultures with CC was then isolated from the hybridoma by RT-PCR. The present sequence CC was produced by LH13 hybridoma cell line.
 Query Match
Best Local
 Matches
Query Match
 WPI;
 Human; LH13 monoclonal cytostatic; cytotoxic;
 Sequence
 Claim 10;
 determining
 and
 N-PSDB;
 Watkins
 (-YSXI)
 02-DEC-1998;
 01-DEC-1999;
 08-JUN-2000
 WO200032635-A2
 Homo sapiens.
 Human LH13 monoclonal antibody heavy chain variable region.
 20-SEP-2000
 AAY99558;
 AAY99558 standard; Protein; 118
 Sequence
 fragment
 tumor-specific human monoclonal antibody, useful for the treatment diagnosis of cancer, comprises at least one complementarity
 2000-412293/35.
DB; AAA48411.
 65
 61
 s
 μ
 ďĎ,
 IXSYS INC
 Similarity
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE---LDWFYIWGQGTMVTVSS 114
 OVOLVOSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSYYDWFDYWGQGTLVTVSS
 Page 82-83;
 271
 118
 region
 Conservative
 Huse WD;
 98US-0203768
 (first entry)
 ₹
 99WO-US28485
 87.2%;
 84pp; English
 antibody; hybridoma;
heavy chain variable
 heavy
 . 1% ;
 4.
 Score 520.5; DB Pred. No. 7e-38;
 Score
 Mismatches
 ⋛
 520;
 BB
 tumour-specific; cancer;
 21;
 region.
 8
 23;
Length 118
 Indels
 Length
 271;
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 Gaps
 64
 6
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121

LVTVSS MVTVSS 114

126

109

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RESULT 5
AAU97159
AID AAU9
XX AAU9
XX AAU9
XX AAU9
XX Huma
XX
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 Query Match
Best Local (
 Matches
 Matches 101;
 Best Local Similarity
 The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-eGFVs) solated from a human IgM phage display library using EGFR as antisen. Two isolates with different amino acid sequences were identified. The anti-EGFR-eGFVs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-eGFV is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
 treating
 Human; anti-epidermal growth
anti-EGPR-scFv; IgM; cancer;
 Sequence
 Claim 3; Fig 2; 51pp;
 Novel human anti-epidermal
 WPI; 2002-463261/49
 Raisch
 13-OCT-2000; 2000US-240353P
 18-APR-2002
 WO200230984-A1
 Homo sapiens
 Human anti-EGFR
 27-AUG-2002
 AAU97198;
 AAU97198
 (UABR-) UAB
 12-OCT-2001; 2001WO-US31857
 103; Conservative
 61
 61
 61
 61
 ξĐ,
 μ
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 -
 for diagnostic location
ng cancer -
 Similarity
AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPDYYGSGSYYPNWFDPWGQGT
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 standard;
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD----WFYIWGQGTMVTVSS 114
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD-
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISMVRQAPGQGLEMMGGIIPIPGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAREDSSGWYHYWGQGTLVTVSS
 270
 Curiel DT,
 RES
 Conservative
 (first entry
 A,
 FOUND
 single-chain
 protein;
 85.6%;
 English
 Bonner
 growth f
 u
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 270
 6
 Pred. No. 3.4e-38;
 factor receptor single-chain antibody;
tumour growth; clone pSEX81-63; cytostatic.
 Score 516; DB 23;
Pred. No. 1.7e-37;
 antibody isolated from
 JA;
 Mismatches
 ₹
 Mismatches
 factor receptor single-chain antibody assessment of tumour growth, and in
 23,
 Length 270;
 Indels
 Indels
 clone
 pSEX81-63.
 12;
 -WFYIWGOGT 108
 4
 Gaps
 Gaps
 120
 60
 60
 60
```

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RRESULT 2
AAY5097
ID AAY5
XX AAY5
AC AAY5
XX AAY5
AC AAY5
XX AAY5
XX Huma
XX Huma
XX Homc
XX H
 유
 S
 문
 र्
 Matches
 Query Match
Best Local
 This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a fragment of the human factor VIII antibody heavy chain variable region protein DP-10 which is used in the method of the invention.
 Homo
 Example
 treatment
hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a human
 WPI;
 Example 9; Fig 11A; 61pp; English.
 New polynucleotide, polypeptide and presence of neutralizing antibodies
 Voorberg
 08-MAY-1998;
 07-MAY-1999;
 18-NOV-1999
 WO9958680-A2
 Human; heavy
 Human FVIII antibody A2 scFv
 23-MAR-2000
 AAY50971;
 AAY50971 standard; Protein;
 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
 invention
 2000-053102/04.
 sapiens
 61
 61
 μ
 μ
 Similarity
 JJ,
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFYIWGQGTMVTVSS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDWFYIWGQGTMVTVSS
 of hemophilia A
 of hemophilia A patients
 114
 P.
 Conservative
 chain;
 (first
 Van Den
 8
 describes
 98EP-0201543.
 99WO-NL00285
 61pp;
 antibody; factor VIII;
A2.
 entry)
 100.0%;
 Brink EN,
 B
 English
 patients
 novel polynucleotide (I) (and complements and
 116
 0
 heavy chain protein DP-10
 Score
Pred.
 red. No. 6.1e-45;
Mismatches 0;
 ξ
 Turenhout EAM
 with these antibodies
 d antibody useful for diagnosing
s against factor VIII and for
with these antibodies -
 hemostatic,
 Length
 Indels
 0
 114
 114
 Gaps
 6
 60
 0
```

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 밁
 ঠ
 믕
 á
 Matches
 Query Match
Best Local
 Sequence
 factor VIII antibody in the method of the
 Ryk protein; antidiabetic;
 AAG66039 standard;
 WO200185789-A2
 Synthetic
 gene therapy;
 27-FEB-2002
 AAG66039;
 1b4 antibody fragment
 114;
 61
 61
 ۲
 Similarity
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCARELDWFYIWGQGTMVTVSS
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC--ELDWFYIWGQGTMVTVSS
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 116
 Conservative
 angiogenesis; variant; receptor tyrosine kinase; cytostatic;
; ophthalmological; cardiant; vulnerary; antiangiogenic;
 (first
 ophthalmological; fusion protein.
 $
 Protein; 271
 entry)
 98.2%;
 invention.
 A2 specific
 <u>,,</u>
 Score
Pred.
 Mismatches
 8CFV
 586; DB 21;
No. 5.7e-44;
 protein DP-10 which
 Length
 Indels
 is used
 2
 Gaps
 116
 114
 60
```

Modulating angiogenesis at a site, for treating or preventing metastasis, diabetic retinopathy, cardiovascular disease, wour supplying composition comprising variant Ryk protein to the si Examples; Page 79-80; 09-MAY-2001; 2001WO-US15043 N-PSDB; Roczniak S, 10-MAY-2000; 2000US-0568783 15-NOV-2001 2002-049443/06 BAYER Dubois-Stringfellow 81pp; Š Zolotorev the site ş

English

CC a composition comprising a variant Ryk protein (I) (a member of the CC receptor tyrosine kinase family), or modulating formation of cells into capillary-like structures by contacting the cells with a composition CC capillary-like structures by contacting the cells with a composition CC (preferably, within a human) or modulating the formation of cells (C (endothelial cells of human origin) into capillary-like structure. The CC (I) is useful for preventing, treating or ameliorating a medical CC condition e.g., cancer, metastasis, diabetic retinopathy, macular CC degeneration, cardiovascular disease, wound, pregnancy, or a clinical CC condition involving anglogenesis in the reproductive system, including CC regulation of placental vascularization in an individual. The variant CC protein is supplied to the individual as a source of polynucleotide concoding the protein and expressing the protein in vivo. (I) is used as an immunogen to produce an antibody against it. The antibodies are useful for modulating angiogenesis at a site. Polynucleotides encoding (I) is useful in gene therapy technique for treating above mentioned The invention relates to modulating angiogenesis at The sequence. (a member ý by supplying into

```
Title:
Perfect score:
Sequence:
 Regult
No.
 Minimum
Maximum
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Scoring table:
 OM protein -
 Database
 Searched:
 Run on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 DB B
 520.5
520
516
515.5
515
515
509.5
 Score
 seq
 protein search, using sw model
 length: 0
length: 2000000000
100.0
98.2
87.2
87.1
86.4
86.3
86.3
85.4
 Query
Match
 December 30, 2003, 10:42:39 ; Search time 36.6726 Seconds (without alignments) 493.415 Million cell updates/sec
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-674-752-51
597
 1107863 seqs, 158726573 residues
 A_Geneseq_19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
 SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997 DAT:

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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001 DAT:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001 DAT:
 QVQLVQSGAEVKKPGSSVKV.....YCELDWFYIWGQGTMVTVSS 114
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
 Length
114
116
271
118
270
270
220
220
245
 DB
21
23
23
24
24
22
 ID
 AAY50971
AAY50971
AAG66039
AAY99558
AAU97198
AAR24442
ABR01512
ABR01538
 SUMMARIES
 1107863
 Human FVIII heavy
Human FVIII antibody
scFv 1b4 antibody
Human LH13 monoclo
Human anti-EGFR si
Sequence of antibo
Human anti-TIMP-1
Human anti-TIMP-1
 Description
Human
Human
leukocyte
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| 99999999999999999999999999999999999999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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508.5<br>508.5<br>508.5<br>508.5<br>508.8<br>508.8<br>508.8<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>506.5<br>50 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| 400000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 23 ABB57<br>24 ABR01<br>22 AAB67<br>118 AAW27<br>118 ABJ18<br>24 ABJ18<br>23 ABP45<br>23 ABP45<br>23 ABP45<br>23 ABP45<br>23 ABP45<br>24 ABR01<br>24 ABR01<br>24 ABR01<br>24 ABR01<br>25 ABP45<br>26 ABP45<br>27 ABP45<br>28 ABP45<br>29 ABP45<br>20 ABP45<br>21 ABP45<br>22 ABP45<br>23 ABP45<br>23 ABP45<br>24 ABR01<br>24 ABR01<br>25 ABP45<br>26 ABP45<br>27 ABP45<br>28 ABP45<br>29 ABP45<br>20 ABP45<br>21 AAB945<br>22 ABP45<br>23 ABP45<br>23 ABP45<br>24 ABR01                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 5654977                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 7559 7618 7618 8718 87118 84718 5498 5498 55722 5723 5725 5727 5726 5727 5728 5728                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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| BLYS BLYS BLYS BLYS BLYS BLYS BLYS BLYS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

### ALIGNMENTS

RESULT 1 AAY50974

AAY50974;

AAY50974 standard; Protein; 114 AA

```
New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for
 \operatorname{Human}_i heavy chain; antibody; factor VIII; hemostatic; variable region; hemophilla A.
 Human FVIII heavy chain variable region protein fragment
 WPI; 2000-053102/04.
N-PSDB; AAZ43867.
 Voorberg JJ,
 08-MAY-1998;
 07-MAY-1999;
 WO9958680-A2
 Homo sapiens.
 23-MAR-2000
 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
 18-NOV-1999
 (first entry)
 Van Den Brink EN,
 98EP-0201543.
 99WO-NL00285
 Turenhout EAM
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No.
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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 Total number of hits satisfying chosen parameters:
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Perfect score:
 Scoring table:
 OM protein - protein search, using sw model
 on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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503.5

492.5

492.5

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492.5

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477.5

477.5
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 December 30, 2003, 10:47:45; Search time 11.576 Seconds (without alignments)
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US-09-652-816A-1
US-08-652-816A-9
US-08-652-816A-9
US-08-652-816A-9
US-08-652-816A-9
US-08-428-197-13
PCT-US93-10555-13
PCT-US93-10555-13
PCT-US93-10555-13
US-08-378-939-10
US-08-378-939-10
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US-08-652-816A-63
US-08-652-63-63
US-08-08-653-63
US-08-08-353-55
US-08-308-655-63
 summaries
 Compugen
 Million cell updates/sec
 Ltd
Sequence 35, Appl Sequence 21, Appli Sequence 21, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 63, Appli Sequence 65, Appli Sequence 672, Appli Sequence 690, Appli Sequence 6
 Description
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|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
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| 117               | 117               | 117               | 117               | 118              | 118               | 449              | 235              | 222              | 119               | 122               | 129               | 129               | 129               | 125               | 128               | 128               | 128               |
| <b>ب</b>          | -                 | _                 | -                 | w                | N                 | ۳                | _                | _                | -                 | 5                 | v                 | 4                 | N                 | ω                 | 4                 | w                 | _                 |
| US-08-487-200-105 | US-08-474-040-105 | US-08-477-728-105 | US-07-634-278-105 | US-07-987-264-60 | US-08-428-257A-78 | US-08-458-516-13 | US-08-458-516-23 | US-08-458-516-22 | US-08-458-516-10  | PCT-US95-00067-2  | PCT-US95-01219-45 | US-08-525-539A-77 | US-08-561-521-45  | US-09-199-149-3   | US-08-635-109-3   | US-08-964-690-22  | US-08-202-047-22  |
|                   |                   | Sequence 105, App | ٠.                | •                | •                 | •                | •                | •                | Sequence 10, Appl | Sequence 2, Appli |                   | Sequence 77, Appl | Sequence 45, Appl | Sequence 3, Appli | Sequence 3, Appli | Sequence 22, Appl | Sequence 22, Appl |

# RESULT 1 US-09-025-769B-35 Sequence 35, Applicat Patent No. 6300064 GENERAL INFORMATION: Application US/09025769B

ALIGNMENTS

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF ESQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York APPLICANT: APPLICANT: APPLICANT: Knappik, Achim Pack, Peter Ilag, Vic

STATE: NC. STATE: NC. USA COUNTRY: USA 10021 New York USA

COMPUTER READABLE PORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

PILING DATE: 18-FEB-1998

PRIOR APPLICATION NUMBER: EP 95 11 3021.0

PILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

TELERHONE: (212)596-900
TELERAX: (212)596-9000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acide STRANDEDNESS: TOPOLOGY: lin MOLECULE TYPE: TELECOMMUNICATION INFORMATION: TYPE: amino acid 120 amino acids linear (212)596-9000

Query Match
Best Local Similarity 85.
Matches 103; Conservative 85.1**%**; Score 508; DB 4; Length 120, Pred. No. 2.8e-45; 3; Mismatches 8; Indels

6,

Gaps

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protein

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US-09-025-769B-57
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 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-57
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 5
 US-09-025-769B-21
 Patent No.
Sequence 21, Application US/09025769B Patent No. 6300064
 Matches 103; Conservative
 Query Match
Best Local (
 APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Bsq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
 TELEPHONE: (212)596-900
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
 APPLICANT:
 APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/{Poly}peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
 SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acid
 APPLICANT: Knappik, Achim APPLICANT: Pack, Peter
 Local Similarity
 CITY: New York
STATE: New York
 TYPE: amino acid
TOPOLOGY: linear
 COUNTRY:
 INFORMATION:
 13
 61
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS
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 Application US/09025769B
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 Pack, Peter
Ilag, Vic
 USA
 Ge, Liming
 85.1%;
 57:

 Mismatches

 Score 508; DB 4;
Pred. No. 2.8e-45;
 Length 120;
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 120
 114
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 RESULT 4
US-08-652-816A-1
 US-09-025-769B-21
 APPLICATION NUMBER: US/09/025,769B
PRIOR APPLICATION DATE: 18-FEB-1998
PRIOR APPLICATION DATE: 18-FEB-1995
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
PILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAMB: James P. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
 sequence 1, Application US/08652816A Patent No. 5872215
 Query Match
 Matches 101;
 TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acide
 APPLICANT: Knappi
APPLICANT: Pack,
 GENERAL INFORMATION:
APPLICANT: OBDOURN, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
 COMPUTER REALABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
 APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
 CORRESPONDENCE ADDRESS:
 NUMBER OF BROUBNCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEB: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
 TOPOLOGY: linear MOLECULE TYPE: protein
 NUMBER OF SEQUENCES:
 CITY: New York
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 New York
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 B: James P. Haley, Jr., Esq. c/o Pish & Neave
1251 Avenue of the Americas
 119 amino acids
 USA
 Conservative
United States of America
 21:
 3;
 Score 503.5; DB 4;
Pred. No. 8.1e-45;
 Mismatches
 Gerstein, Murray & South Wacker Drive
 Version #1.30
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 Length 119;
 Indels
 (BPO)
 5;
 Gaps
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Sequence:
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No.
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Maximum DB
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87.2
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23:
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 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen
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271
118
270
270
481
220
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 ä
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AAY50971
AAG66039
AAY99558
AAU97198
AAR24442
ABR01512
ABR01538
AAB67617
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Human FVIII antibo
scFv 1b4 antibody
Human LH13 monoclo
Human anti-EGFR si
Sequence of antibo
Human anti-TIMP-1
Human anti-TIMP-1
Human leukocyte an
 Description
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N-PSDB; AAZ43867.
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 Human; heavy chain; antibody; factor VIII; hemostatic; variable region; hemophilia {\tt A.}
 Human FVIII heavy chain variable region protein fragment
 23-MAR-2000
 AAY50974 standard; Protein; 114
 Voorberg JJ, Van Den Brink EN,
 08-MAY-1998;
 18-NOV-1999.
 WO9958680-A2
 Homo
 AAY50974;
 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
 sapiens.
 (first entry)
 98EP-0201543.
 99WO-NL00285
 ⋧
 Turenhout EAM
```

New polynucleotide, polypeptide and antibody useful for diagnosing presence of neutralizing antibodies against factor VIII and for

the

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RESULT 4
AAY99558
ID AAY9
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 SXS
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 Query Match
Best Local :
 Matches
 tumour-specific monoclonal antibodies can be used to express the antibodies and can be recombinantly engineered to produced modified antibodies with higher affinity or higher selectivity for tumour cells. Tumour-specific antibodies were produced by hybridomas that were generated by in vitro immunisation of human spleen cell cultures with breast carcinoma cells. The nucleic acid encoding the monoclonal antibody was then isolated from the hybridoma by RT-PCR. The present sequence
 tumour-specific antigens. The antibodies can be conjugated to cytotoxic or cytostatic agents and used to selectively target cancer cells for the elimination of tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human
 Watkins JD,
 Human; LH13 cytostatic;
 AAY99558 standard; Protein; 118
 Sequence
 Claim 10;
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 01-DEC-1999;
 08-JUN-2000
 WO200032635-A2
 Homo sapiens.
 Human
 20-SEP-2000
 AAY99558;
 fragment
 tumour-specific monoclonal antibody. Neoplastic cells selectively antigens which are not present on normal cells. Thus monoclonal antibodies can be produced that are specifically directed against
 The present sequence is the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively (
 and diagnosis of cancer,
 (IXSY-) IXSYS INC
 was produced by LH13 hybridoma
 Local Similarity
 tumor-specific human
 2000-412293/35
 LH13 monoclonal
 61
 65
 S
 -
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 EVQLVQSGAEVKKPGSSVKVSCKASGGTESSYAISWVRQAPGQGLEWMGGIIPIFGTANY 64
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSYYDWFDYWGQGTLVTVSS 121
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE---LDWFYIWGQGTMVTVSS 114
 Page 82-83; 84pp;
 cytotoxic;
 271
 87.2%;
ilarity 87.2%;
Conservative
 Huse WD
 (first entry)
 $
ξ
 98US-0203768
 99WO-US28485
 antibody heavy chain variable region.
 antibody; hybridoma;
heavy chain variable
 monoclonal antibody, useful for the treatment comprises at least one complementarity
 English.
 4
 Score 520.5; DB
Pred. No. 7e-38;
4; Mismatches
 cell line
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 tumour-specific;
 23;
 8
 Indela
 Length
 271;
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 cancer;
 Gaps
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Query Match

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Score 520;

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 Query Match
Best Local Sim
Matches 103;
 Best Local Similarity
 The present invention relates to human anti-epidermal growth factor receptor single-chain antibodies (anti-EGFR-eCFVs) isolated from a human IgM phage display library using EGFR as antigen. Two isolates with different amino acid sequences were identified. The anti-EGFR-eCFVs are useful for treating cancer, and for the diagnostic location and assessment of tumour growth, where the anti-EGFR-eCFV is radiolabelled. The present sequence represents human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
 Human; anti-epidermal
anti-EGFR-scFv; IgM;
 Human anti-EGFR single-chain antibody isolated from clone
 Sequence
 Novel human anti-epidermal growth factor receptor single-chain antibody useful for diagnostic location and assessment of tumour growth, and in
 Raisch
 12-OCT-2001;
 18-APR-2002
 27-AUG-2002
 AAU97198;
 AAU97198 standard; protein;
 Claim 3; Fig 2; 51pp;
 WPI; 2002-463261/49
 13-OCT-2000; 2000US-240353P
 WO200230984-A1
 Homo sapiens.
 (UABR-)
 13
61
 19
 51
 -
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 -
 ξŸ,
 UAB
 Similarity
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 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELD----WFYIWGQGTMVTVSS
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 270 AA;
 Conservative
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 Conservative
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 2001WO-US31857
 (first entry)
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 86.4%;
81.7%;
 85.6%;
 cancer;
 growth
 English
 Bonner
 270
 Score 516; DB 23;
Pred. No. 1.7e-37;
 Pred. No.
 tumour
 factor receptor
 JA;
 ₿
 Mismatches
 Mismatches
 growth;
 . 3.4e-38;
7;
 clone pSEX81-63;
 Length 270;
 Indels
 Indels
 pSEX81-63.
 antibody;
 12;
 4.
 WFYIWGOGT
 cytostatic.
 Gaps
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 60
 108
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 120
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RRESULT 8
ABRO1538
IID ABRO
XX ABRO
XX HUMB
DE HUMB
XXX HUMB
XXX HUMB
XXX HUMB
XXX HUMB
XXX HOMO
XX HO
 Query Match
Best Local S
Matches 101
 The invention relates to a novel purified preparation of a human antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting activity of a TIMP-1. It is especially useful for ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3; matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic; variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis; alcoholic liver disease; cardiac fibrosis; acute coronary syndrome; lupus nephritis; glomerulosclerotic renal disease; lung cancer; lupus nephritis; lupus nephr
 New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies, for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 cancer. The antibody is also useful for detecting a TIMP-1 in a preparation, or in diagnosing a disorder in which a TIMP-1 level preparation. The sequences shown in ABR01502-ABR01545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
 31-OCT-2002
 Human anti-TIMP-1 antibody heavy chain #36
 ABR01538
 Sequence
 Claim 20;
 N-PSDB;
 24-APR-2001; 2001US-285683P
 24-APR-2002;
 WO200286085-A2
 Homo
 (MORP-)
 (FARB)
 ú
 2003-129114/12
DB; ABZ74809.
 eapiens
 101;
 61
 13
 Similarity
 Knorr AM,
 MORPHOSYS
 BAYER CORP
 standard;
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 or lung
 Conservative
 2002WO-US12801
 (first
 173;
 8
 န
 Protein;
 Schauer
 228pp;
 entry)
 86.3%;
87.1%;
 glomerulosclerotic
 Į,
 English.
 220
 5
 Score 515;
Pred. No. 1
 Hirth-dietrich
 Mismatches
 .7e-37
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 24;
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 Length
 Indels
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RESULT 9
AAB67617
ID AAB6
XX AAB6
XX Huma
XX Homc
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 맑
 Query Match
Best Local S
 AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HAA)-Cv6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HIA-Cv6. The HIA-Cv6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HIA-Cv6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HIA-Cv6. The anti-HIA-Cv6 immunoglobuli fragments are useful for the preparation of a pharmaccutical for the treatment of humans. They are also useful for HIA phenotyping.
 pulmonary fibrosis, benign prostate hypertrophy, lung cancer or cancer. The antibody is also useful for detecting a TIMP-1 in a t preparation, or in diagnosing a disorder in which a TIMP-1 level elevated. The sequences shown in ABR01502-ABR01545 represent the chain regions of a human anti-TIMP-1 antibody of the invention.
 Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for troof humans and for human leukocyte antigen phenotyping -
 Sequence
 WPI; 2001-218451/22.
 26-AUG-1999;
 28-AUG-2000; 2000WO-EP08388
 01-MAR-2001
 WO200114558-A1
 Homo sapiens.
 miscarriage;
 Human leukocyte
 Human
 29-MAY-2001
 AAB67617
 (MORP-) MORPHOSYS AG
 leukocyte
 101;
 61
 61
 \vdash
 -
 Similarity
 Fig 1;
 standard;
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEMMGGIIPIFGTANY
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 220
 Conservative
 abortion;
 (first entry)
 99EP-0116691
 antigen;
 antigen-Cw6 specific
 Tesar
 Protein;
 85.4%;
87.1%;
 English.
 Σ,
 psoriasis;
 HLA;
 Marget
 245
 5
 Score
Pred.
 HLA-Cw6; natural killer cell silencing, sis; antibody; HLA phenotyping; ss.
 Mismatches
 ξ
 Σ,
 510; DB 24;
No. 4.7e-37;
 scfv fragment from
 Kroenke
 8
 Length
 clone
 2
 CW6
 treatment
 Gaps
 test
 colon
 114
 60
 60
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Query Match Best Local Similarity Matches 102; Conserv

85.3%;

Score 509.5; DB 2 Pred. No. 5.8e-37; 5; Mismatches

22;

Length

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Gaps

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Sequence

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888888888888888

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RESULT 12
AAB67618
ID AAB67
XX AAB67
XX AAB67
XX AAB67
XX Human
XX Human
XX Human
XX Homo
XX Clain
 Query Match
Best Local :
 Matches
 TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and a variable light chain (VLC)DR3 region. An antibody preparation of the invention has hepatotropic, cytostatic, nephrotropic and cardiant activity. The human antibody is useful for decreasing an MMP-inhibiting symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The antibody is also useful for detecting a TIMP-1 in a test preparation, or in diagnosing a disorder in which a TIMP-1 level is elevated. The sequences shown in ABRO1502-ABRO1545 represent the heavy chain regions of a human anti-TIMP-1 antibody of the invention.
AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cv6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific
 Novel isolated human immunoglobulin or functional immunoglobulin fragment specific for human leukocyte antigen Cw6, useful for troof humans and for human leukocyte antigen phenotyping -
 01-MAR-2001
 miscarriage;
 29-MAY-2001
 AAB67618 standard; Protein;
 Sequence
 26-AUG-1999;
 Human leukocyte
 Human leukocyte
 28-AUG-2000;
 WO200114558-A1
 (MORP-) MORPHOSYS
 114
 103;
 121
 61
 61
 _
 Similarity
 S 114
 OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 დ-
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE--LDW-----FYIWGQGTMVTVS 113
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGLYWAVYPYFDFWGQGTLVTVS 120
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 Fig 1; 23pp;
 225 AA;
 'n
 Conservative
 2000WO-EP08388
 abortion;
 (first entry)
 99EP-0116691
 Tegar
 antigen; HLA; HLA-Cw6; natural killer cell silencing;
 antigen-Cw6 specific scFv fragment from clone Cw6
 85.2%;
85.1%;
 English.
 Σ,
 psoriasis; antibody; HLA phenotyping;
 Marget
 245
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T
 Score 508.5; DB 2
Pred. No. 6.5e-37;
 Mismatches
 Z,
 Kroenke
 DB 24;
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 Indels
 Length 225;
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 Query Match
Best Local S
Matches 103
 Matches
 Query Match
Best Local &
 for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
 Homo
 N-PSDB;
 AAW27550 standard; Protein;
 Sequence
 Sequence
 The present sequence is the human antibody heavy chain variable region synthetic sequence VHIA, used in the p
 Preparation of human consensus sequences, framework for highly
 Ge L,
 18-AUG-1995;
 06-MAR-1997.
 Human; antibody; preparation;
 AAW27550
 Example 1;
 WPI; 1997-179277/16.
 19-AUG-1996;
 WO9708320-A1
 heavy chain;
 23-JAN-1998
 human
 sapiens
 103;
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 102;
 5
 13
 Ilag V,
 e region
derived
 MORPHOSYS
 AAT87948.
 Similarity
 Similarity
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISMVRQAPGQGLEMMGDIIFILGTGNY
 heavy
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE--LDWFY-IWGQGTMVTVSS 114
 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
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 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGFDYFMDFWGQGTLVTVSS
 Fig 5A; 436pp; English
 120
 245 AA;
 Conservative
 Conservative
 (first entry)
 consensus.
 ζ
 synthetic
antibody g
 95EP-0113021
 96WO-EP03647
 chain
 Knappik A,
 GES PROTEINOPTIMIERUNG
 85.1%;
85.8%;
 85.2%;
87.2%;
 derived antibody gene library
and signal consensus antibody
diverse antibody libraries
 variable
 gene
 sequence VHIA,
gene library.
 120
 Moroney
 Score 508; DB 18; Pred. No. 3.9e-37;
 Score 508.5; DB 22; Pred. No. 7.1e-37;
 library; VHIA; variable region;
 region VH1A consensus.
 Mismatches
 Mismatches
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 Length
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 Indels
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' gene as
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 120;
 245;
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61

AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCBL---DWFY---IWGQGTMVTVSS

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Database
 Title:
Perfect score:
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 Result
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Total number of hits satisfying chosen parameters:
 Scoring table:
 Sequence:
 protein -
 Pred. No. is the score greater the and is derived by
 seq length: 0 seq length: 2000000000
 Published Applications AA:*

1: /cgn2_6/prodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/prodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

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13: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/prodata/2/pubpaa/US108_PUBCOMB.pep:*

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17: /cgn2_6/prodata/2/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/prodata/2/pubpaa/US108_PUBCOMB.pep:*

19: /cgn2_6/prodata/2/pubpaa/US108_PUBCOMB.pep:*

10: /cgn2_6/prodata/2/pubpaa/US108_PUB.pep:*

10: /cgn2_6/prodata/2/pubpaa/US108_PUB.pep:*
 protein search, using sw model
 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
Query
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-674-752-51
597
 December 30, 2003, 11:01:15 ; Search time 24.4484 Seconds (without alignments) 927.994 Million cell updates/sec
 724715 seqs, 199017464 residues
 QVQLVQSGAEVKKPGSSVKV.....YCELDWFYIWGQGTMVTVSS 114
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
```

| 15                 | 14                | 13                | 12                | 11                | 10                | 9                 | 8                 | 7                 | 6                 | v                | 4                 | w                | N                 | _                 | ő            |
|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|--------------|
| 507                | 508               | 508               | 511.5             | 513.5             | 514               | 514.5             | 516               | 516.5             | 517.5             | 520              | 520               | 520              | 520               | 520               | Score        |
| 84.9               | 85.1              | 85.1              | 85.7              | 86.0              | 86.1              | 86.2              | 86.4              | 86.5              | 86.7              | 87.1             | 87.1              | 87.1             | 87.1              | 87.1              | Match        |
| 253                | 120               | 120               | 121               | 119               | 120               | 123               | 270               | 125               | 121               | 124              | 118               | 118              | 118               | 118               | Match Length |
| 11                 | 15                | 14                | 15                | 12                | 15                | 15                | ø                 | 15                | 15                | 15               | 12                | 12               | 12                | 12                | 80           |
| US-09-880-748-1509 | US-10-125-687-1   | US-10-025-687-1   | US-10-269-805-19  | US-10-308-817-191 | US-10-269-805-49  | US-10-269-805-3   | US-09-976-118-2   | US-10-269-805-35  | US-10-269-805-9   | US-10-269-805-25 | US-10-300-675-14  | US-10-300-675-12 | US-10-300-675-10  | US-10-300-675-6   | ID           |
| 15                 | Sequence 1, Appli | Sequence 1, Appli | Sequence 19, Appl | Sequence 191, App | Sequence 49, Appl | Sequence 3, Appli | Sequence 2, Appli | Sequence 35, Appl | Sequence 9, Appli | N                | Sequence 14, Appl | -                | Sequence 10, Appl | Sequence 6, Appli | Description  |

; Sequence 10, Application US/10300675; Publication No. US20030198638A1; GENERAL INFORMATION:

RESULT 2 US-10-300-675-10

| 5                | 44                 | 43                 | 42                 | 41                 | 40              | 39              | 38               | 37               | 36              | 35               | ω<br><b>4</b>   | w                | 32                 | <u>3</u> 2 | 30      | 29                 | 28                 | 27               | 26                 | 25                 | 24                 | 23                 | 22               | 21                 | 20                 | 19                 | 18               | 17                 | 16            |
|------------------|--------------------|--------------------|--------------------|--------------------|-----------------|-----------------|------------------|------------------|-----------------|------------------|-----------------|------------------|--------------------|------------|---------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|------------------|--------------------|---------------|
| 494.5            | 495                | 95                 | 495.5              | 496                | 496             | 497.5           | 497.5            | 498.5            | 498.5           | 498.5            | 498.5           | 498.5            | 499                | 499.5      | 499.5   | 500.5              | 501.5              | 502              | 502.5              | 502.5              | 502.5              | 504                | 504.5            | 505.5              | 505.5              | 505.5              | 506              | 506.5              | 506.5         |
| •                |                    | 83.0               | •                  | •                  | •               | •               | •                | •                |                 |                  | 83.5            | •                | 83.6               |            |         |                    |                    |                  | 84.2               |                    |                    |                    | 84.5             | •                  | •                  | 84.7               | ٠                | 84.8               | •             |
| 123              | 252                | 248                | 246                | 256                | 120             | 218             | 218              | 245              | 222             | 222              | 219             | 219              | 257                | 248        | 248     | 253                | 248                | 120              | 248                | 248                | 248                | 254                | 627              | 248                | 248                | 244                | 120              | 248                | 248           |
| 15               | 11                 | 11                 | 11                 | 11                 | 15              | 15              | 15               | 15               | 15              | 15               | 15              | 15               | 11                 | 11         | 11      | 11                 | 11                 | 15               | 11                 | 11                 | 11                 | 11                 | 14               | 11                 | 11                 | 11                 | 15               | 11                 | 11            |
| US-10-269-805-17 | US-09-880-748-1666 | US-09-880-748-1717 | US-09-880-748-2062 | US-09-880-748-1600 | US-10-269-805-5 | US-10-186-186-8 | US-10-184-508A-8 | US-10-151-882-15 | US-10-186-186-6 | US-10-184-508A-6 | US-10-186-186-7 | US-10-184-508A-7 | US-09-880-748-1553 | -748-172   | -09     | US-09-880-748-1880 | US-09-880-748-1741 | US-10-269-805-15 | US-09-880-748-1737 | US-09-880-748-1732 | US-09-880-748-1719 | US-09-880-748-1866 | US-10-047-542-47 | US-09-880-748-1879 | US-09-880-748-1718 | US-09-880-748-1881 | US-10-269-805-37 | US-09-880-748-1734 | -09           |
| 17.              | 166                | 171                | 206                | 160                | <b>5</b>        | Φ,              | о<br>Ф           | 15               | φ,              | σ,               | ٦,              | ,7               | 15                 | 17         | 17      | 18                 | 17                 | 15               | 17                 | 17                 | 17                 | 18                 | 47,              | 1879               | 1718               | 1881               | 37,              | 1734               | Sequence 1733 |
| Appl             | ٠<br>م             | 7.<br>Ap           | Α<br>P             | ∂                  | Appli           | Appli           | ppli             | App1             | Appli           | ppli             | ppli            | ppli             | A<br>Ap            | 28, Ap     | ν<br>Ap | ,<br>Ap            | ٠<br>8             | App1             | A<br>P             | ≱                  | ,<br>A             | ٠<br>م             | App1             | ≱                  | ≱                  | ₽                  | App1             | ≱p                 | Ap            |

## ALIGNMENTS

```
RESULT 1

US-10-300-675-6

; Sequence 6, Application US/10300675

; Publication No. US20030198638A1

; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/10/300.675
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR APPLI
```

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US-10-269-805-35

/ Sequence 35, Application US/10269805

/ Publication No. US20030124129A1

/ GENERAL INFORMATION:

/ APPLICANT: OLINER, JONATHAN D.

/ TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

/ FILE REFERENCE: A-722

/ CURRENT APPLICATION NUMBER: US/10/269,805

/ CURRENT APPLICATION NUMBER: US/10/269,805

/ CURRENT FILING DATE: 2002-10-10

/ PRIOR APPLICATION NUMBER: US 60/328,604

/ PRIOR FILING DATE: 2001-10-11

/ NUMBER OF SEQ ID NOS: 76

/ SOUTWARE: Patentin version 3.1

/ SEQ ID NO 35

LENGTH: 125

/ Type: Date: 125
 CURRENT FILING DATE: 2002-10-10;
PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2001-10-11;
NUMBER OF SEQ ID NOS: 76;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 9;
LENGTH: 121
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 RESULT 8
US-09-976-118-2
 ; ORGANISM: Homo sapiens US-10-269-805-35
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 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-269-805-9
Sequence 2, Application US/0976118
Patent NO. US/20020058033A1
GENERAL INFORMATION:
APPLICANT: Raisch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Allen
 Matches
 Query Match
Best Local
 Query Match 86.7%;
Best Local Similarity 86.0%;
 TYPE: PRT
 Match 86.5%;
Local Similarity 83.2%;
 114
 121
 110
 121
 104;
 61
 104;
 61
 61
 61
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 so.
 S 114
 VTVSS 125
 VTVSS 114
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC------ELDWFYIWGQGTMVTVS 113
 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARSPIYYDILTGIDAFDIWGQGTM
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE---
 AOKFOGRVTITADKSTSTAYMELSSLRSEDTAVYYCAAFSPFTETDAFDIWGQGTMVTVS
 121
 Conservative
 Conservative
 2002-10-10
 60/328,604
 س
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 Score 516.5; DB 15;
Pred. No. le-43;
 Score 517.5; DB 1
Pred. No. 7.7e-44;
 Mismatches
 Mismatches
 DB 15;
 7;
 Indels
 Indels
 Length
 Length
 ----LDWFYIWGQGTM 109
 11;
 7;
 Gaps
 Gaps
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 RESULT 9
US-10-269-805-3
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RESULT 10
US-10-269-805-49
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 US-10-269-805-3
 US-09-976-118-2
 PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 270
Type: """
 Query Match
Best Local Sim
Matches 103;
 Sequence 3, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
 SEQ ID NO 3
 Matches 103;
 Query Match 86.4%;
Best Local Similarity 81.7%;
 APPLICANT: OLINBR, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
 LENGTH: 123
TYPE: PRT
ORGANISM: Homo &
 CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTMARE: Patentin version 3.1
 TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor TITLE OF INVENTION: Single-Chain Antibodies FILB REFERENCE: D6355
 CURRENT APPLICATION NUMBER: US/09/976,118
CURRENT FILING DATE: 2001-10-12
 OTHER INFORMATION:
OTHER INFORMATION:
 TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
 112 VSS 114
 121
 121 LVTVSS 126
 109 MYTYSS 114
 13
 61
 61
 \vdash
 ب
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEMMGDIIPILGTGNY
 Similarity
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDW---FYIWGQGTMVT 111
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 Conservative
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 123
 amino acid sequence of anti-EGFR scFV clone pSEX81-63
 86.2%;
83.7%;
 Score 514.5; DB 15;
Pred. No. 1.5e-43;
4; Mismatches 7;
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 Score 516; DB 9;
Pred. No. 2.6e-43;
 DB 15;
 в.
 Length 270;
 Indels
 Length 123;
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 9.
 Gaps
 60
 120
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Sequence 1509, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/216,216

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/273,499

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATE 2001-05-25

SUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATE 2001-05-25

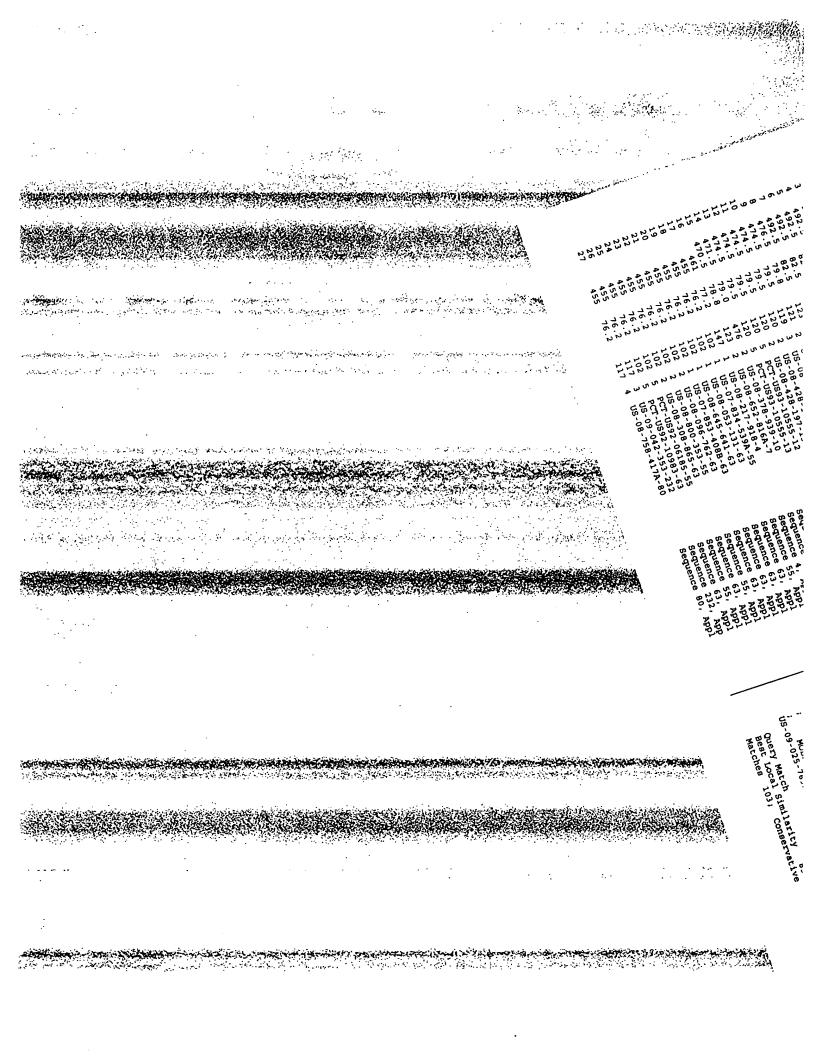
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CREMING SEG ID NOS: 3239

SOFTWARE: PATE 2001-05-25

TYPE: PRT

CREMING SEG ID NOS: 3239
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Search completed: December 30, 2003, 11:45:25
Job time : 24.4484 secs
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 RESULT 15
US-09-880-748-1509
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 ; ORGANISM: Homo Bapiens
US-09-880-748-1509
 Query Match
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 / Match 84.9%; Score 507; DB 11; Length 253;
Local Similarity 79.7%; Pred. No. 1.9e-42;
heB 102; Conservative 4; Mismatches 8; Indels 1
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 61
 7 GTMVTVSS 114
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1 GTMVTVSS 128
 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYC------ELDWFYIWGQ 106
 85.1%; Score 508; DB 15; Length 120;
85.8%; Pred. No. 6.6e-43;
Live 3; Mismatches 8; Indels
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Minimum DB
Maximum DB
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No.
 Title:
Perfect score:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Total number of hits satisfying chosen parameters:
 Scoring table:
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 95:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 length: 0
length: 2000000000
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// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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| atch<br>cal s                           | ANA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 488.5<br>488.5<br>487.5<br>487.5<br>484.5<br>484.5<br>484.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>481.5<br>5<br>481.5<br>5<br>481.5<br>6<br>6<br>7<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8<br>8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| $\alpha \vdash$                         | Applicat<br>3300064<br>3300064<br>3500064<br>3500064<br>3600000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75<br>75                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| larity<br>Conservat                     | Application US 300064 Spondation F: Application US South Ach F: Pluck, Peter F: Ilag, Vic F: Ede, Liming F: Plueckthun, FIVENTION: Pro SEQUENCES: 37 UDENCE ADDRESS: SEE: James F. H 1251 Avenue o New York F: USA 10021 READABLE FORM: TYPE: Ploppy d READABLE FORM: TYPE: PRE-1 DATE: 18 PETE-1 PLICATION NUMBER: U DATE: 18 PETE-1 PLICATION NUMBER: E STION NUMBER: I S-OG STI |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 81.8<br>82.0<br>tive                    | ication US/09025769B iCN:  applik, Achim ck, Peter 29, Vic 20, Liming rorney, Simon roney, Simon RMCES: 373 ADDRESS: James F. Haley, Jr., I Avenue of the Amer rork A BLE FORM: Ploppy disk Ploppy disk Ploppy disk Ploppy disk Ploppy Action Refease #1.0 MINBER: US/09/025,7 18-FEB-198 INFORMATION: 18-FEB-198 INFORMATION: 18-MG-1995 INFORMATION: 18-MG-1995 INFORMATION: 27,794 MUMBER: 389 MUMBER: 27,794 MUMBER: 3900 MUMBER: 27,794 MUMBER: 3900 MUMBER: 27,794 MUMBER: 3900 MUMBER: 3900 MUMBER: 389 MUMBER: 3900 MUMBER: | 123<br>116<br>1176<br>1176<br>1177<br>1177<br>1179<br>1179<br>1179                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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| Score<br>Pred.<br>0; Mi                 | स्वा अम्च इस्ट्रें ह                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | US-01 PCT-1 PCT-1 US-02 US-03 US-03 US-04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| re 525<br>d. No.<br>Mismat              | /5 21 69 1c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 09-315-57 08-428-19 -US93-004 08-983-60 08-983-60 08-983-60 07-988-92 08-362-78 08-362-78 08-958-20 08-958-20 08-958-20 08-958-20 08-958-20 08-958-20 08-958-20 08-958-20 08-958-20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ore 525; I<br>ed. No. 1.9<br>Mismatcher | o e e e e e e e e e e e e e e e e e e e                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | US-09-315-574-3 US-08-428-197-2 PCT-US93-08-35- US-08-983-607-3 US-09-157-370-1 US-08-983-607-4 US-07-988-925-1 US-08-362-780-1 PCT-US93-08-35- US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-2 US-08-958-201-3 US-08-958-201- |
| DB 4<br>. 9e-4                          | c/o 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 0 040 044400 0040                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 3,                                      | libraries<br>Fish & N                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ΄ω΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄ ΄                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| ٠.<br>۵                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Сарв                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ννν· · οοφημα· φω· · ο                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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 SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
 Patent No. 6300064
GENERAL INFORMATI
 Query Match
Best Local
 Matches
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amin acid
 APPLICANT:
APPLICANT:
APPLICANT:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
 TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
 TOPOLOGY:
 TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
 STATE: New York
 COUNTRY: USA
 ADDRESSEE:
 119
 121
 121 SS 122
 tch 81.8%; Score 525; DB 4; Length 120, al Similarity 82.0%; Pred. No. 1.9e-43; 100; Conservative 10; Mismatches 10; Indels
 INFORMATION:
 63, Application US/09025769B
 61
 61
 61
 61
 1:0021
 New York
 : 120 amino acids amino acid
 SS
 SS 122
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGYKYYGMDVWGQGTTVTV 120
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGKKYYGMDVWGQGTTVTV 120
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 ADSVKGRFTÍSRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV 118
 EVOLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
 Pack, Peter
Ilag, Vic
 120
 Knappik, Achim
 linear
 protein
 Floppy disk
 63:
 -FYAMDYWGQGTLVTV 118
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 Gaps
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 RESULT 4
US-10-039-785-53
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 US-09-025-769B-178
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 US-09-025-769B-178
Sequence 53, Applicate Patent No. 6538938 GENERAL INFORMATION:
APPLICANT: Salcedo
 Sequence 178, Patent No. 63(
 Query Match
81.8%; Score 520; Dest Local Similarity 82.0%; Pred. No. 4.9e-
 APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794 REFERENCE/DOCKET NUMBER: MORPHO/5 TELECOMMUNICATION INFORMATION:
 GENERAL INFORMATION:
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
APPLICANT:
 APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-POS/MS-DOS
OPERATING SYSTEM: PC-POS/MS-DOS
 FILING DATE: 18-FEB-1998 PRIOR APPLICATION DATA:
 SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 MOLECULE TYPE: protein
 APPLICANT:
 TYPE: amino acid TOPOLOGY: linear
 COUNTRY: U
 CITY: New York
STATE: New York
 APPLICATION NUMBER: US/09/025,769B
 ADDRESSEE:
 TELEPHONE:
 LENGTH:
 119
 144 SS 145
 121 SS 122
 61
 98
 26
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGKKYYGMDVWGQGTTVTV 120
 SS
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 Application US/10039785
 B: James F. Haley, Jr., Esq.
1251 Avenue of the Americas
 Knappik, Achim
Pack, Peter
Ilag, Vic
 Application US/09025769B
 281 amino acids
 120
 USA
 (212)596-9090
 (212)596-9000
et al
 EP 95 11 3021.0
 Score 525; DB 4;
Pred. No. 4.9e-43;
 c/o Fish & Neave
 10;
 Length 281;
 (EPO)
 Indels
 2
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RESULT 5
US-07-934-373C-21
 ; OTHER INFORMATION: T1006F07 SCFV US-10-039-785-53
 Sequence 21, Application US/07934373C Patent No. 5821337
 SOFTWARE: P
 Patent No. 5821337
GENERAL INFORMATION:
 Matches
 Query Match
 PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
 PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
 CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
 NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver.
 PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/341,237
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors
 TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
 APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
UNMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ENGTH: 249
 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 SOFTWARE: WinPatin (Genentech)
 COUNTRY:
 Local
APPLICATION NUMBER:
 ADDRESSEE:
 APPLICATION NUMBER: 60/294,981 FILING DATE: 2001-06-04
 APPLICATION NUMBER: 60/293,473
 121
 118 VTVSS 122
 al Similarity
100; Conser
 61
 61
 94080
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREPSFQQWGHYSYGMDVWGQGTM 120
 EVQLVESGGDLVQPGGSLRLSCAASGPTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 VIVSS 125
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR---GRGGYKYYGMDVWGQGTT 117
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 USA
 Conservative
 Genentech, Inc.
 2001-05-25
 Receptors
 81.7%; Score 524.5;
80.0%; Pred. No. 4.80
tive 12; Mismatches
US/07/934,373C
 4.8e-43;
 DB 4;
 10;
 Length 249;
 Indels
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 Sequence
 Matches
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RESULT 6
US-08-437-642B-21
 7OPOLOGY:
US-07-934-373C-21
 Patent No.
 Query Match
Best Local S
APPLICATION NUMBER: US/08/437,642B FILING DATE: 09-May-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/934373 FILING DATE: 21-AUG-1992 PRIOR APPLICATION NUMBER: 08/146206 FILING DATE: 17-MOV-1993 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992
 GENERAL INFORMATION:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
 PILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION UNMBER: 40,378
REFERENCE/DOCKET NUMBER: 9070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT: Paul J. Ca:
APPLICANT: Leonard G.
TITLE OF INVENTION: II
 PILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7:
 CLASSIFICATION: 530 PRIOR APPLICATION NUMBER: 1
 STREET:
 STATE:
 CITY: South San Francisco
 FILING DATE:
 ADDRESSEE:
 y 21, ...
6054297
 120 VSS 122
 120 VSS 122
 101; Conservative
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRVGYSLSGLYDYWGQGTLVT
 61
 -
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 94080
 Similarity
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY 60
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGM-DVWGQGTTVT 119
 California
 Application US/08437642B
 1 DNA Way
 USA
 Linear
 Genentech, Inc.
 21-Aug-1992
 Carter
 Immunoglobulin Variants: 47
 80.7%;
82.1%;
 PCT/US92/05126
 Presta
 07/715272
 Score 518; DB 2;
Pred. No. 9.1e-43;
9; Mismatches 11
 P0709P2
 DB 2; Length 122;
 Indels
 <u>ب</u>
 Gaps
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FILING DATE: 14-JUN-1991 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

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 US-08-146-206C-21
 US-08-437-642B-21
 SOPTMARE: WinPatin (Genentech)
SOPTMARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UNW-1991
AITORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
 Patent No. 6407213
GENERAL INFORMATION:
 Sequence 21,
 Matches 101;
 Best Local Similarity
 Query Match
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ITS NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
 REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
 REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS
 LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
 NAME: Lee, Wendy M.
 COUNTRY:
 ADDRESSEE:
 ENGTH:
 120 VSS 122
 61
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 94080
 South San Francisco California
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRVGYSLSGLYDYWGQGTLVT 119
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGM-DVWGQGTTVT
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY
 Application US/08146206C
 E: Genentech, Inc.
1 DNA Way
122 amino acids
 USA
 Conservative
 80.7%;
82.1%;
 26
 P0709P1
 9; Mismatches
 P0709P2C1
 Score 518; DB 3; Pred. No. 9.1e-43;
 DB 3; Length 122;
 11; Indels
 119
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 US-08-146-206C-21
 PCT-US93-07832-21
 RESULT 8
 PCT-US93-07832-21
 Sequence 21, Application PC/TUS9307832 GENERAL INFORMATION:
 Best Local Similarity
 Query Match
 Query Match
Best Local Similarity
Matches 101; Conserv
 Matches 101;
 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
 REGISTRATION NUMBER: 70
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: 07/7
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 TITLE OF INVENTION: Immunoglobulin Variants
 APPLICANT: Genentech, Inc.
 TOPOLOGY:
 TELEFAX:
 APPLICATION NUMBER: FILING DATE: 21-AUC
 APPLICATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992
 CLASSIFICATION:
 APPLICATION NUMBER: FILING DATE: 19930
 COUNTRY: U
 STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
 TOPOLOGY:
 120 VSS 122
 120 VSS 122
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRVGYSLSGLYDYWGQGTLVT 119
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGM-DVWGQGTTVT 119
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 California
 BVQLVESGGGLVQPGGSLRLSCAASGFTPSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY
 USA
 415/952-9881
 Conservative
 Conservative
 linear
 Linear
 UMBER: 07/934373
21-AUG-1992
 19930820
 80.7%;
 80.7%;
 07/715272
 PCT/US93/07832
 21:
 Score 518; DB 4;
Pred. No. 9.1e-43;
 709P2PCT
 9
 9,
 Score 518; DB 5;
Pred. No. 9.1e-43;
9; Mismatches 11
 Mismatches
 DB 4; Length 122;
 Length 122
 2;
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 Gaps
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NAME/KEY:
US-08-983-607-32
 RESULT 9
US-08-983-607-32
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 TELEPAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 140 residues
TYPE: amino acid
Query Match 79.9%; Score 513; DB 3; Length 140; Best Local Similarity 80.2%; Pred. No. 3.2e-42; Matches 101; Conservative 11; Mismatches 8; Indels
 Sequence 32, Appli
Patent No. 6140470
 COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: WOR'D PROCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/
FILING DATE: June 28, 1996
 GENERAL INFORMATION:
 IMMEDIATE SOURCE:
LIBRARY: DM414 BCFV antibodies obtained from
LIBRARY: fUSE5 fusion phage construct
CLONE: V86
FEATURE:
 DESCRIPTION: ORIGINAL SOURCE:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
 TITLE OF INVENTION: Human A TITLE OF INVENTION: bodies NUMBER OF SEQUENCES: 51 CORRESPONDENCE ADDRESS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 203-773-9544
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
 MOLECULE TYPE:
 ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
 REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 0
 STRANDEDNESS:
 STREET:
 TOPOLOGY:
 COUNTRY: United States of America
 ADDRESSEE:
 ADDRESSEE: Department of Molecular Biophysics
 120
 120
 61
 5
 06520-8114
 Mary M. Krinsky
 VSS 122
 VSS 122
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGM-DVWGQGTTVT 119
 ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCA-RGRVGYSLSGLYDYWGQGTLVT 119
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY 60
 Connecticut
 Application US/08983607
 266 Whitney Avenue
 heavy chain and linker
 ss: single
linear
 polypeptide
 PCT/IB96/01032
 US/08/983,607
 OCR-679
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 Gaps
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 ; MOLECULE TYPE: US-09-069-821-3
 RESULT 10
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 US-09-069-821-3
 Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILPUL
 Query Match
Best Local Similarity
Matches 101; Conserv
 Sequence 3,
 FILING DATE: 30-APR-1998
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION NUMBER: US 60/063,074
PILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
 TELEPHONE: (202)371-2600
TELEPAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 30-APR-1998
 MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTBINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
 SEQUENCE CHARACTERISTICS:
 FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 NUMBER OF SEQUENCES:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
 TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: not re
 LENGTH:
 NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40
REFERENCE/DOCKET NUMBER:
 COUNTRY: U
 APPLICATION NUMBER: US 6: FILING DATE: 23-JUN-1997
 ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE.,
 119
 117
 61
 61
 _
 WASHINGTON
 MVTVSS 124
 TVTVSS 122
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 ADSVKGRPTISRDNSKNTLYLOMNSLRAEDTAVYYCARGWGLRGEEG-DYY-MDVWGKGT 118
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK----RGRGGYKYYGMDVWGQGT 116
 QVQLVQSGGGLVQPGGSLRLSCAASGPTFSSYAMSWVRQAPGKGLEWVAAISGSGGSTYY
 8
 Application US/09069821
 263 amino acide
 RSS: single
not relevant
PB: peptide
 WHITLOW, MARC
LEE, LIHSYNG S.
 USA
 WANG, MAOLIANG
SHORR, ROBERT
 Conservative
 PatentIn Release #1.0, Version #1.30
 FILPULA, DAVID
 Floppy disk
79.4%; Score 510; DB 4; Length 263; 77.1%; Pred. No. 1.3e-41; Live 11; Mismatches 9; Indels
 US 60/044,449
 US/09/069,821
 US 60/050,472
 40,679
 0977.2280003
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 RESULT 11
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 RESULT 12
US-08-428-197-1
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 Query Match
Best Local S
Matches 101
 Sequence 6, Application US/09420592A Patent No. 6333396 GENERAL INFORMATION:
 Sequence 1, Application US/08428197 Patent No. 5891438 GENERAL INFORMATION:
 SEQ ID NO 6
 APPLICANT:
APPLICANT:
 CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 199-10-19
FRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.1
 NAME/KEY: UNSURE
LOCATION: (234)
OTHER INFORMATION: NAME/KEY: UNSURE
LOCATION: (239)
 APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
 NAME/KEY: UNSURE
LOCATION: (232)
OTHER INFORMATION: May
 LENGTH: 283
TYPE: PRT
ORGANIAM: Artificial Sequence
FEATURE:
 OTHER INFORMATION:
 OTHER INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
 249
 112
 130
 130
 249
 112
 190
 101;
 _
 59
 \vdash
 Similarity
 WGQGTLVTVSS
 WGQGTTVTVSS
 YYADSVKGRFTISRDNSKVTLYLOMNSLRAEDTAVYYCA-RGRXGXSLSGXYYYYHYFDY 248
 FYADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGG-----YKYYGMDV 111
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGKTDGGST
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRS--GTT
 FYADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGG------YKYYGMDV 111
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRS--GTT 58
 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRXGXSLSGXYYYYHYFDY 248
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGKTDGGST
 WGQGTLVTVSS
 WGQGTTVTVSS 122
 Filpula, David R.
 Conservative
 May
 May be any amino acid
 Consensus
 Description
 122
 79.4%;
 259
 þe
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 any
 any
 Score 510; DB 4;
Pred. No. 1.4e-41;
1; Mismatches 9
 amino
 amino
 of Artificial Sequence:
 acid
 9
 Length 283;
 Indels
 10;
 Gaps
 189
 58
 189
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; NAME/KEY:
; LOCATION:
US-08-428-197-1
 Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIM.
TITLE OF INVENTION: VARIABLE REGION
TITLE OF INVENTION: VACCINATION WITH
TITLE OF INVENTION: THERBOY
NUMBER OF SEQUENCES: 51
 RESULT 13
PCT-US93-10555-1
 Matches
 Query Match
Best Local
 TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/
PILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
 TITLE OF INVENTION: VA
TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: pept
 REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite
 FEATURE:
 IMMEDIATE SOURCE:
 COMPUTER READABLE FORM:
 CITY: Los Angeles
STATE: California
 CLONB:
 STRANDEDNESS:
 CLASSIFICATION:
 FILING DATE:
 APPLICATION NUMBER:
 COUNTRY: USA
 ADDRESSES:
 TELEPHONE:
 ENGTH:
 118 GTLVTVSS 125
 115
 13
 61 ADSVKGRFTISRDNSKVTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYG-----MDVWGQ 114
 99;
 _
 -
 amino acid
 Similarity
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTK---GQVLYYGSGSYHWFDPWGQ 117
 18/2
 GTTVTVSS 122
 8: Spensley Horn Jubas
1880 Century Park East
 125 amino acids
 SILVERMAN, GREGG J.
VENTION: METHOD FOR STIMULATING PRODUCTION OP
VENTION: METHOD FOR STIMULATING PRODUCTION OP
VENTION: VARIABLE REGION GENE PAWILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
 Conservative
 (619) 455-5100
 peptide
 single
 78.9%;
77.3%;
 THEREOF
 VACCINATION WITH A B-CELL SUPERANTIGEN
 51
 PCT/US93/10555
 US/08/428,197
 FD-2630
 9.
 Score 506.5; DB 2
Pred. No. 1.2e-41;
9; Mismatches 11
 1 80
 Lubitz
Suite
 500
 500
 DB 2;
 #1.25
 11;
 Indels
 Length 125;
 AND CONJUGATES
 9;
 Gaps
 2
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 밁
 US-08-974-899-6
 PCT-US93-10555-1
 Best Loc
Matches
 Sequence 6, Application US/08974899 Patent No. 6037454
 Query Match
 GENERAL INFORMATION:
 TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
 MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
 REFERENCE/DOCKET NUMBER: FD TELECOMMUNICATION INFORMATION:
 FEATURE:
 IMMEDIATE SOURCE:
 MOLECULE TYPE:
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 NAME: Howells, Stacy REGISTRATION NUMBER:
 APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1993
 Local
 NAME/KEY:
 CLASSIFICATION:
 COUNTRY:
 COUNTRY:
 ADDRESSEE:
 LOCATION:
 TOPOLOGY:
 STRANDEDNESS:
 TELEPHONE:
 ENGTH:
 118
 115
 19
 61
 99;
 94080
 Similarity
APPLICATION DATA:
 amino acid
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 Los Angeles
California
 GTLVTVSS 125
 GTTVTVSS 122
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTÁVÝÝCTK---GQVLYÝGSGSYHWFDPWGQ 117
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYG-----MDVWGQ 114
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 78.9%; ilarity 77.3%; Conservative
 USA
 USA
 linear
 Peptide
 Genentech, Inc.
 (619) 455-5100
 peptide
 single
 34,842
 PCT/US93/10555
 <u>..</u>
 1.44 Mb floppy disk
 9;
 FD-2630
 Score 506.5; DB 5
Pred. No. 1.2e-41;
9; Mismatches 11
 DB 5;
 11;
 Indels
 Length 125;
 9
 Gaps
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; Patent No. 5681722

; GENERAL INFORMATION:

; APPLICANT: Newman, Roland A

; APPLICANT: Hanna, Nabil

; APPLICANT: Raab, Ronald W.

; TITLE OF INVENTION: Recombi
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 밁
 RESULT 15
US-08-478-039-99
 밁
 S
 밁
 US-08-974-899-6
 Sequence 99, Application US/08478039 Patent No. 5681722
 Matches
 Query Match
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/478,039
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
 ZIP: 22313-1404
COMPUTER READABLE FORM:
 SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acid
 TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
 APPLICATION NUMBER: 60/0 FILING DATE: 11/27/96 ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS
 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES:
 COUNTRY: USA
ZIP: 22313-1404
 TYPE: Amino Acid
 REGISTRATION NUMBER: 40 REFERENCE/DOCKET NUMBER:
 FILING DATE:
CLASSIFICATION:
 APPLICATION NUMBER: US 0:
FILING DATE: 23-MAR-1992
 APPLICATION NUMBER: US/08/974,899
 Local Similarity
 ADDRESSEE:
 TOPOLOGY:
 112
 121 SS 122
 61
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 96; Conservative
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 Alexandria
 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-----
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGDGGSTYY
 ٧×
 699 Prince St.
 Newman, Roland A.
 Linear
 BURNS, DOANE, SWECKER & MATHIS
 Wendy M.
 78.1%;
78.7%;
 Recombinant Antibodies for Human Therapy
 US 07/856,281
 60/031971
 40,378
 9; Mismatches
 P1014R1
 Score 501.5; DB 3
Pred. No. 3.2e-41;
 DB 3;
 œ
 Length 113;
 Indels
 -GFDYWGQGTLVTV
 9
 Gaps
 60
```

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APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: anno acide
TYPE: anno acide
TYPE: anno acide
TYPE: poptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99
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 5
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 Query Match 77.8%; Score 499.5; DB 1; Length 125; Best Local Similarity 77.3%; Pred. No. 5.6e-41; Matches 99; Conservative 8; Mismatches 12; Indels 9;
118 GTLVTVSS 125
 115 GTTVTVSS 122
 Gaps
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Search completed: December 30, 2003, 11:05:37 Job time : 13.4716 secs

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Appl
Appli
 Sequence 35, Appl
Sequence 57, Appl
 December 30, 2003, 10:47:45; Search time 11.576 Seconds (without alignments) 416.677 Million.cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 597
1 QVQLVQSGAEVKKPGSSVKV......YCELDWFYIWGQGTMVTVSS 114
 Sequence 21
 Description
 Sequence
 Sequence
 Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
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 328717
 Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 US-09-025-769B-57
US-09-025-769B-21
US-08-652-816A-6
US-08-652-816A-9
US-08-652-816A-9
US-08-652-816A-9
US-08-212-081B-41
US-08-212-081B-41
US-08-212-081B-41
US-08-212-197-13
PCT-US93-10555-13
US-08-217-918-4
US-08-217-918-4
US-08-217-918-4
US-08-645-641-63
 Total number of hits satisfying chosen parameters:
 US-08-758-417A-80
 328717 segs, 42310858 residues
 SUMMARIBS
 - protein search, using sw model
 Listing first 45 summaries
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Post-processing: Minimum Match 0% Maximum Match 100%
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-674-752-51
 Query
Match Length DB
 Title:
Perfect score:
 Scoring table:
 Score
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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| , App.           | Appl             | Appli           | Appli           | , Appl           | , Appl            | , Appl            | Appli            | Appl.            | , Appl           | , Appl           |                  |                   | , Appl           |                   |                   | 5, App            | _                 |
|------------------|------------------|-----------------|-----------------|------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|
| 22,              | 22               | ě               | m               | 45               | 77                | 45                | ć                | 2                | 22               | 23               | 13               | 78                | 60,              | 2                 | 2                 | 105,              | 105               |
| Sequence         | Sequence         | Sequence        | Sequence        | Sequence         | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence          | Sequence         | Sequence          | Sequence          | Sequence          | Sequence          |
| US-08-202-047-22 | US-08-964-690-22 | US-08-635-109-3 | US-09-199-149-3 | US-08-561-521-45 | US-08-525-539A-77 | PCT-US95-01219-45 | PCT-US95-00067-2 | US-08-458-516-10 | US-08-458-516-22 | US-08-458-516-23 | US-08-458-516-13 | US-08-428-257A-78 | US-07-987-264-60 | US-07-634-278-105 | US-08-477-728-105 | US-08-474-040-105 | US-08-487-200-105 |
| -                | ო                | 4               | m               | ~                | 4                 | 'n                | 'n               | ч                | -                | -                | н                | ~                 | ~                | н                 | -                 | Н                 | -                 |
| 128              | 128              | 128             | 125             | 129              | 129               | 129               | 122              | 119              | 222              | 235              | 449              | 118               | 118              | 117               | 117               | 117               | 117               |
| 75.7             | 75.7             | 75.7            | 75.3            | 74.0             | 74.0              | 74.0              | 72.9             | 72.4             | 72.4             | 72.4             | 72.4             | 72.4              | 72.4             | 72.3              | 72.3              | 72.3              | 72.3              |
| 452              | 452              | 452             | 449.5           | 441.5            | 441.5             | 441.5             | 435.5            | 432.5            | 432.5            | 432.5            | 432.5            | 432               | 432              | 431.5             | 431.5             | 431.5             | 431.5             |
| 28               | 59               | 30              | 31              | 32               | 33                | 34                | 35               | 36               | 37               | 38               | 39               | 40                | 41               | 42                | 43                | 44                | 45                |

## ALIGNMENTS

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COUNTRY: CLEAR COUNTRY: CLEAR CONTRY: CLEAR COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PER FOLDOS/MS-DOS
SOFTWARE: PARENTE NG-005/MS-DOS
SOFTWARE: PARENTIN NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INPORMATION:
MARE: James F. Haley, Dr., ESQ.
REFERENCE/DOCKET NUMBER: AND NUMBER
 85.1%; Score 508; DB 4; Length 120;
85.8%; Pred. No. 2.8e-45;
tive 3; Mismatches 8; Indels
 IB: James P. Haley, Jr., Esq. c/o Fish & Neave
1251 Avenue of the Americas
 APPLICANT: Knappik, Achim
APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
US-09-025-769B-35; Sequence 35, Application US/09025769B; Patent No. 6300064
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acida TYPE: amino acid
 MOLECULE TYPE: protein
 linear
 CITY: New York
STATE: New York
COUNTRY: USA
 STRANDEDNESS
TOPOLOGY: 1
 ADDRESSEB:
STREET: 12
 US-09-025-769B-35
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9

Best Local Similarity 85.8 Matches 103; Conservative

Query Match

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GENERAL INFORMATION:
 RESULT 4
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 AQKFQGRVTITADBSTSTAYMELSSLRSEDTAVYYCARWGGDGFYAMDYWGQGTLVTVSS 120
 61 AQKFQGRVT1TADESTSTAYMELSTLTSEDTAVYYCEL---DWFY---IWGQGTMVTVSS 114
 9
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
 1 OVOLVOSGAEVKKPGSSVKVSCKASGGTPSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 1 OVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 6; Gaps
 Sequence 57, Application US/09025769B
Sequence 57, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Hag, Vic
APPLICANT: Ge, Liming
APPLICANT: Beck, Peter
APPLICANT: Boroney, Simon
APPLICANT: PluceKthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
 COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 27,794
NEGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acide
TTYPE: amino acid
 Length 120;
 8; Indels
 Score 508; DB 4;
Pred. No. 2.8e-45;
 3; Mismatches
 US-09-025-769B-21
; Sequence 21, Application US/09025769B
; Patent No. 6300064
 85.14;
 Matches 103; Conservative
 MOLECULE TYPE: protein
 Query Match
Best Local Similarity
 US-09-025-769B-57
 RESULT 3
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1 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARAPGYCSGFDYWGQGTLVTVSS 119
 61 AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCE----LDWFYIWGQGTMVTVSS 114
 1 OVOLVOSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
 Gaps
 5
 Sequence 1, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OBSOURT, JG
APPLICANT: MCCAfferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mateball, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
 Length 119;
 CURRENT APPLICATION DATA:

SOFTWARE: Petentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

PILING DATE: 18-FBB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

APPLICATION NUMBER: EP 95 11 3021.0

ATTORNEY AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRANCE/COKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

 Indels
 c/o Fish & Neave
 APPLICANT: ilag, Vic
APPLICANT: Ge, Limin
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
WUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
 Query Match
84.3%; Score 503.5; DB 4;
Best Local Similarity 84.9%; Pred. No. 8.1e-45;
Matches 101; Conservative 3; Mismatches 10;
 ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
 Illinois
: United States of America
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Knappik, Achim
Pack, Peter
Ilag, Vic
 LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
 , MOLECULE TYPE: protein US-09-025-769B-21
 linear
 STREET: 6300 Se
CITY: Chicago
STATE: Illinoie
COUNTRY: United
 TOPOLOGY:
 US-08-652-816A-1
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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 61 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 120
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 4; Gaps
 US-10-001-934-39
US-10-001-934-39
Sequence 39, Application US/10001934
Sequence 39, Application US/10001934
Sequence 39, Application US/10001934
Sequence 39, Application US/10001934
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE TITLE OF INVENTION: HULLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
TITLE OF INVENTION: HULLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
TITLE OF INVENTION: HULLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
CURRENT APPLICATION UNDHERR: US/10/001,934
CURRENT FILING DATE: 2001-11-15
SOFTWARE: PATENT OF SEQ ID NOS: 63
SOFTWARE: PATENT OF SEQ ID NOS: 63
LENGTH: 118
 7;
 DB 12; Length 313;
 Query Match 80.8%; Score 519; DB 15; Length 118; Best Local Similarity 81.1%; Pred. No. 1.2e-40; Matches 99; Conservative 10; Mismatches 9; Indels 4
 Score 519.5; DB 12; Length
Pred. No. 2.9e-40;
9; Mismatches 11; Indels
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR PLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FBAELSEQ for Windows Version 3.0
SEQ ID NO 427
LENGTH: 313
 Search completed: December 30, 2003, 11:45:25 Job time : 26.1641 secs
 Query Match
Best Local Similarity 78.9%;
Matches 101; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-001-934-39
 ORGANISM: Homo sapiens
US-10-291-265-427
 115 GTTVTVSS 122
 180 GTLVTVSS 187
 121 $$ 122
 117 SS 118
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61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRVGYSLY--DYWGQGTLVTV 117
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSGRQAYYYYGMDVWGQGTLVTV 120
 APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al TITLE OF INVENTION NO. US20030232054Alel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAVISGDGGSTYY
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV
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 Gapa
 3; Gaps
 Sequence 1974, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR
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 Length 248;
 10; Indels
 14; Indels
 Query Match 81.0%; Score 520; DB 11;
Best Local Similarity 78.7%; Pred. No. 2.1e-40;
Matches 96; Conservative 12; Mismatches 14;
 7; Mismatches
 Sequence 427, Application US/10291265 Publication No. US20030232054A1 GENERAL INFORMATION:
 CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
 Matches 102; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-880-748-1974
 121 SS 122
 118 SS 119
 121 SS 122
 121 $$ 122
 US-09-880-748-1974
 RESULT 14
US-10-291-265-427
 SEQ ID NO 1974
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 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-RGRVGYSLY--DYWGQGTLVTV 117
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAVISGDGGSTYY 60
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 3; Gaps
 81.2%; Score 521.5; DB 15; Length 119; 83.6%; Pred. No. 7e-41;
 Length 119;
 APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
APPLICANT: Ralph Schwall
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: MATHODS OF TREATMENT USING ANTI-ErbB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENERY. 0.3A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
FRIOR APPLICATION NUMBER: 09/602,530
FRIOR APPLICATION NUMBER: 09/602,530
FRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PARCEGO for Windows Version 4.0
 Sequence 6, Application US/10268501

Sublication No. US20030086924A1

GENERAL INFORMATION:

APPLICANT: Sliwkowski, Mark X.

TITLE OF INVENTION:

CURRENT APPLICATION Treatment with Anti-ErbB2 Antibodies

FILE REFERENCE: P1467R2P1

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 09/602,812

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 6
 81.2%; Score 521.5; DB 9; Length 83.6%; Pred. No. 7e-41; tive 7; Mismatches 10; Indels
 ; OTHER INFORMATION: heavy chain consensus sequence US-10-268-501-6
 OTHER INFORMATION: Humanized Antibody Sequence
 Sequence 3, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial sequence
 Matches 102; Conservative
121 GTMVTVSS 128
 Best Local Similarity
 Best Local Similarity
 121 SS 122
 118 85 119
 US-09-811-123-3
 US-10-268-501-6
 US-09-811-123-3
 LENGTH: 119
 Query Match
 Query Match
 FEATURE:
 FEATURE:
```

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TYPE: PRT
ORGANISM: Homo sapiens
 , ORGANISM: Homo sapiens
US-09-880-748-1605
 115 GTTVTVSS 122
 118 VTVSS 122
 121 VTVSS 125
 US-09-880-748-1701
 US-09-880-748-1701
 SEQ 1D NO 1701
 SEQ ID NO 1605
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 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREPSFQQWGHYSYGMDVWGQGTM 120
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR---GRGGYKYYGMDVWGQGTT 117
 1 EVOLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 PAPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Acceptors

FILE REFERENCE: PFS50

CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT FILING DATE: 2002-06-05

PRIOR PILING DATE: 2002-04-05

PRIOR PLICATION NUMBER: 60/341,237

PRIOR PLICATION NUMBER: 60/331,310

PRIOR PLICATION NUMBER: 60/331,044

PRIOR PLICNG DATE: 2001-11-07

PRIOR PLICATION NUMBER: 60/327,364

PRIOR PLICATION NUMBER: 60/327,364

PRIOR PLICATION NUMBER: 60/327,364

PRIOR PLICATION NUMBER: 60/327,364

PRIOR PLICATION NUMBER: 60/329,176

PRIOR PLICATION NUMBER: 60/309,176

PRIOR PLICATION NUMBER: 60/309,176

PRIOR PLICATION NUMBER: 60/233,473

 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 MCS-09-880-748-1605

Sequence 1605, Application US/09880748

Sequence 1605, Application US/09880748

PUBLICANT SUBER ET STATE OF INVENTION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/216,316
 <u>ښ</u>
 Query Match
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3;
 Sequence 53, Application US/10039785
Publication No. US20020067646A1
 , OTHER INFORMATION: T1006F07 BCFV
US-10-039-785-53
 ORGANISM: Artificial sequence FEATURE:
 118 VTVSS 122
 121 VTVSS 125
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121 VTVSS 125
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| PRIOR FILING DATE: 2000-10.75
| PRIOR PILING DATE: 2000-10.7
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Gaps

2

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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV 118
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR---GRGGYKYYGMDVWGQGTT 117
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
TITLE SERENCE: FPS50
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
FRIOR FILING DATE: 2002-04-05
FRIOR FILING DATE: 2001-12-20
FRIOR FILING DATE: 2001-11-37
FRIOR FILING DATE: 2001-11-37
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-10-09
FRIOR FILING DATE: 2001-09-21
FRIOR FILING DATE: 2001-09-21
FRIOR FILING DATE: 2001-09-21
FRIOR FILING DATE: 2001-09-21
FRIOR FILING DATE: 2001-06-04
FRIOR FILING DATE: 2001-06-05
 ; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 Query Match
81.7%; Score 524.5; DB 12; Length 249;
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3;
 81.8%; Score 525; DB 15; Length 120; 82.0%; Pred. No. 3.4e-41; tive 10; Mismatches 10; Indels ;
 Sequence 53, Application US/10139785
Publication No. US20030190685A1
GENERAL INFORMATION:
 FEATURE: OTHER INFORMATION: T1006F07 SCFV
 ORGANISM: Artificial sequence
 Query Match
Best Local Similarity 82.0%:
Matches 100; Conservative
 APPLICANT: Salcedo et al.
 118 VTVSS 122
 121 SS 122
 SS 120
 US-10-139-785-53
 US-10-139-785-53
 SEQ ID NO 53
LENGTH: 249
 119
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 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK----RGRGGYKYYGMDVWGQGT 116
 61 ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 1 BVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 Sequence 4, Application US/10025687
Publication No. US20020142255A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
 1 BVQLVESGGGLVQPGGSLRLSCAASGPTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 Sequence 4, Application US/10125687
Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26050-705
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY 60
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-4
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Gaps
 2; Gaps
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 DB 10; Length 125;
 81.8%; Score 525; DB 14; Length 120;
82.0%; Pred. No. 3.4e-41;
Live 10; Mismatches 10; Indels
 9; Indels
 Ouery Match
82.8%; Score 531.5; DB 1.
Best Local Similarity 82.5%; Pred. No. 8.8e-42;
Matches 104; Conservative 8; Mismatches 9
 TYPE: PRT ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 82.0*
Matches 100; Conservative
; ORGANISM: Homo sapiens
US-09-840-459-76
 TVTVSS 122
 120 TVTVSS 125
 121 SS 122
 SS 120
 US-10-025-687-4
 US-10-125-687-4
 117
 119
 SEQ ID NO 4
 SEQ ID NO 4
 FEATURE:
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3; Gaps

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 61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRNYDFWSGXYYYYGMDVWGQ 120
 61 ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGR-----GGYKYYGMDVWGQ 114
 61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRNYDFWSGXYYYYGMDVWGQ 120
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGR-----GGYKYYGMDVWGQ 114
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 1 EVQLVESGGDLVQPGGSLRLSCAASGPTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 6; Gaps
 8; Indels
 8; Indels
 APPLICANT: LAGOGA, Gregory J.
APPLICANT: Horvath, Chistopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Ownes, S. Tarran
APPLICANT: O'Brien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ENGLOSE
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
FRIOR PELING DATE: 2000-02-03
PRIOR PELING DATE: 2000-02-03
PRIOR PELING DATE: 1999-07-22
PRIOR PELING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOSTWARE FESTERE FESTERE OF WINDOW VERSION 3.0
 Query Match

85.5%; Score 549; DB 10;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8;
 9; Mismatches
 FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(128)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79
 US-09-840-459-79
Sequence 79, Application US/09840459
Patent No. US20020150576Al
GENERAL INFORMATION:
Matches 105; Conservative
 115 GTTVTVSS 122
 TYPE: PRT
ORGANISM: Homo sapiens
 115 GTTVTVSS 122
 121 GTTVTVSS 128
 121 GTTVTVSS 128
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Sequence 84, Application US/09840459 Patent No. US20020150576A1 GENERAL INFORMATION:

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1 EVOLVESGGDLVOPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Length 125;
 Score 547.5; DB 10; Length: Pred. No. 3e-43; B; Mismatches 9; Indels
 APPLICANT: Ornes, S. Tarran
APPLICANT: O'Brien, Siohan H.
APPLICANT: O'Refe, Theresa
APPLICANT: O'Refe, Theresa
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PAPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR PILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
 US-09-840-459-76; Sequence 76, Application US/09840459; Sequence 76, Application US/09840459; Datent No. US20020150576Al; GENERAL INFORMATION:
 Query Match 85.3%;
Best Local Similarity 84.0%;
Matches 105; Conservative
 118 VTVSS 122
 121 VTVSS 125
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(without alignments)
927.994 Million cell updates/sec
 December 30, 2003, 11:01:15 ; Search time 26.1641 Seconds
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1 EVQLVESGGDLVQPGGSLRL.....GYKYYGMDVWGQGTTVTVSS 122
 Published Applications AA:*

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3. /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

4. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

7. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

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9. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

10. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13. /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14. /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

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16. /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

17. /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

18. /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

19. /cgn2_6/ptodata/2/pubpaa/USO06_PUBCOMB.pep:*

10. /cgn2_6/ptodata/2/pubpaa/USO06_NEW_PUB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/USO06_NEW_PUB.pep:*

12. /cgn2_6/ptodata/2/pubpaa/USO06_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 724715 segs, 199017464 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-674-752-53
 Title:
Perfect score:
 Scoring table:
 Database:
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              | Sequence 77, Appl | Sequence 73, Appl | Sequence 76, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 53, Appl | Sequence 53, Appl | Sequence 1605, Ap  | Sequence 1701, Ap  | Sequence 3, Appli | Sequence 6, Appli | Sequence 1974, Ap  | Sequence 427, App | Sequence 39, Appl |
|-----------|--------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|
| SUMMARIES | QI                       | US-09-840-459-77  | US-09-840-459-79  | US-09-840-459-76  | US-10-025-687-4   | US-10-125-687-4   | US-10-139-785-53  | US-10-039-785-53  | US-09-880-748-1605 | US-09-880-748-1701 | US-09-811-123-3   | US-10-268-501-6   | US-09-880-748-1974 | US-10-291-265-427 | US-10-001-934-39  |
|           | 08                       | 010               | 22                | 10                | 14                | 15                | 12                | 13                | 11                 | 11                 | 9                 | 15                | 11                 | 12                | 15                |
|           | Query<br>Match Length DB | 128               | 125               | 125               | 120               | 120               | 249               | 249               | 251                | 254                | 119               | 119               | 248                | 313               | 118               |
| •         | Query<br>Match           | 85.5              | 85.3              | 82.8              | 81.8              | 81.8              | 81.7              | 81.7              | 81.7               | 81.3               | 81.2              | 81.2              | 81.0               | 80.9              | 80.8              |
|           | Score                    | 549               | 547.5             | 531.5             | 525               | 525               | 524.5             | 524.5             | 524.5              | 522                | 521.5             | 521.5             | 520                | 519.5             | 519               |
|           | Result<br>No.            | 40                | <b>*</b> M        | 4                 | ហ                 | 9                 | 7                 | 8                 | 6                  | 10                 | 11                | 12                | 13                 | 14                | 15                |

| Sequence 76, Appl |                  | 16,          | 68,              | 989               | 196                | 908               | Sequence 487, App |                   |                 |                  | 1431               | 913,              | Sequence 921, App | 14                 | Sequence 1740, Ap  | 16                 | 17.                | 'n              | 'n              | 9               | Sequence 6, Appli | 45               | 7                  | 92               | 82    | 8                | 19                | 43               | ď                  |
|-------------------|------------------|--------------|------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-----------------|------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-----------------|-----------------|-----------------|-------------------|------------------|--------------------|------------------|-------|------------------|-------------------|------------------|--------------------|
| US-10-120-414-76  | US-09-840-459-81 | 10-040-244-1 | US-09-972-656-68 | US-09-880-748-989 | US-09-880-748-1965 | US-09-880-748-908 | US-10-045-674-487 | US-10-045-674-453 | US-10-044-896-6 | US-09-840-459-78 | US-09-880-748-1431 | US-09-880-748-913 | US-09-880-748-921 | US-09-880-748-1456 | US-09-880-748-1740 | US-09-880-748-1637 | US-09-880-748-1739 | US-09-956-086-3 | US-09-956-087-3 | US-09-983-580-6 | US-09-985-442-6   | US-10-322-673-45 | US-09-880-748-1171 | US-09-840-459-92 | 8     | US-09-840-459-89 | US-10-308-817-190 | US-10-322-673-43 | 118-10-045-674-588 |
| 12                | 10               | 15           |                  |                   |                    |                   |                   |                   |                 |                  | 11                 | 11                | 11                | 11                 | 11                 | 11                 | 11                 | 10              | 10              | 10              | 10                | 12               | 11                 | 10               | 10    | 10               | 12                | 12               | 12                 |
| 253               | 124              | 124          | 224              | 253               | 248                | 251               | 136               | 367               | 119             | 128              | 252                | 248               | 248               | 248                | 251                | 252                | 254                | 263             | 263             | 283             | 283               | 244              | 251                | 121              | 123   | 124              | 124               | 245              | 431                |
| 80.7              | 80.5             | 80.4         | 80.3             | 80.3              | 80.2               | 80.2              | 80.1              | 80.1              | 80.0            | 9.64             | 9.64               | 79.5              | 79.4              | 79.4               | 79.4               | 79.4               | 79.4               | 79.4            | 79.4            | 79.4            | 79.4              | 79.4             | 79.4               | 79.2             | 79.2  | 79.1             | 79.1              | 79.1             | 79.0               |
| 518               | 517              | 516          | 515.5            | 515.5             | 515                | 515               | 514               | 514               | 513.5           | 511              | 511                | 510.5             | 510               | 510                | 510                | 510                | 510                | 510             | 510             | 510             | 510               | 509.5            | 509.5              | 508.5            | 508.5 | 508              | 508               | 208              | 2 707              |
| 16                | 17               | 18           | 19               | 20                | 21                 | 22                | 23                | 24                | 25              | 26               | 27                 | 28                | 29                | 30                 | 31                 | 32                 | 33                 | 34              | 35              | 36              | 37                | 38               | 39                 | 40               | 41    | 42               | 43                | 44               | 45                 |

## ALIGNMENTS

```
US-09-840-459-77

US-09-840-459-77

Sequence 77, Application US/09840459

Batent No. US2020150556A1

GENERAL INFORMATION:

APPLICANT: LAFORSA, Christopher

APPLICANT: Horvath, Christopher

APPLICANT: Jones, S. Tarran

APPLICANT: Jones, S. Tarran

APPLICANT: Jones, S. Tarran

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

TITLE OF INVENTION: HUMBER: US/09/840,459

CURRENT APPLICATION NUMBER: DCT/US01/03537

FILE REFERENCE: 1855.1052-012

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR PILING DATE: 2000-02-03

PRIOR PILING DATE: 1999-07-23

PRIOR PILING DATE: 1999-07-23

PRIOR PILING DATE: 1999-07-23

PRIOR PILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PRESCO FOR Windows Version 3.0

SOFTWARE: PRESCO FOR Windows Version 3.0

SOFTWARE: PRESCO FOR WINDOWS PRIOR TYPE: PRESCO FOR TYPE: PRESCO FOR TYPE: PRE
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us-09-674-752-53.rag

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binded to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for reating cancer in a human. The method for this further involves an antimeopatatic, anti-tumour, anti-tumoidenic or chemotherapeutic agent. The antibodies may also be useful for intreasing IGF-IR activity and thus restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the concerned of the second of the second of the concerned of the second of the increasents an anti-insulin-like growth factor I receptor antibody of the 

124 AA; Sequence

2 VQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFYA 61 3; Gaps 81.5%; Score 523.5; DB 23; Length 124; 80.6%; Pred. No. 1.7e-41; tive 9; Mismatches 12; Indels 3; Best Local Similarity 80.6 Matches 100; Conservative Query Match ઠે

1 VQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMWWVRQAPGKGLEWVSAISGSGTTFYA 60

8 ઠે

**TVSS 122** 119

TVSS 124 121 ઠે

ABP56504 standard; Protein; 121 AA. RESULT 19

(first entry) 20-MAR-2003 ABP56504;

Human anti-Pc-epsilon-R1 alpha autoantibody heavy chain LTM-alpha-15.

Autoantibody, Fc-epsilon-R1 receptor alpha-chain, immunosuppressive, allergic disease, urticaria, late phase allergic reaction, malignancy, intrinsic asthma; drug intolerance; food intolerance; immunoglobulin Econditional autoimmunity; IgE mediated disease.

sapiens

Synthetic

40200282085-A2

17-OCT-2002

03-APR-2002; 2002WO-EP03660.

04-APR-2001; 2001US-281024P.

(ZLBB-) ZLB BIOPLASMA

Miescher S;

WPI; 2003-103348/09. 

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The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor alpha-chain and a autoantibody against its alpha-chain. Also described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and city a compound identified by the method, which binds but does not activate the receptor; and (4) a polypeptide capable of specific binding to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. altergic descase (urticaria, late phase allergic reactions, intrinsic asthma, drug intolerance and food intolerance), IgE mediated disease or malignancy. The compound is useful autoimmunity. The present sequence represents a human recombinant autoimmunity respections.
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 9
 Identifying and obtaining inhibitor of a pathological process for treating e.g. autoimmunity comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor and an
 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 1; Gaps
 DB 24; Length 121;
 10; Indels
 Query Match 81.4%; Score 522.5; DB 2. Best Local Similarity 82.8%; Pred. No. 2.1e-41; Matches 101; Conservative 10; Mismatches 10
 autoantibody against its alpha-chain
 Claim 20; Page 22; 29pp; English
 the present invention
 121 AA;
 SS 122
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completed: December 30, 2003, 10:54:38 Job time : 40.3295 secs Search

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This invention describes novel antibodies that immunospecifically bind to bymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
 BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 2; Gaps
 The present sequence is the consensus single chain fragment VH3.V-kappa-2. VH3-V-kappa-2, which comprises the human antibody heavy and light chain variable region consensus sequences VH3 and V-kappa-2, was used in the preparation of a human derived antibody gene library.
 Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
 DB 18; Length 281;
 Match B1.8%; Score 525; DB 18; Length 2 Local Similarity 82.0%; Pred. No. 3e-41; les 100; Conservative 10; Mismatches 10; Indels
 ä
 Choi GH, Vaughan T, Hilbert
 Claim 1; Page 2318-2319; 3148pp; English.
 CAMBRIDGE ANTIBODY TECHNOLOGY
 Human BLyS binding acFv SEQ ID 1605.
 Ź
 ABP45594 standard; Protein; 251
 2000US-240816P.
2001US-276248P.
2001US-277379P.
 (HUMA-) HUMAN GENOME SCI INC
 15-JUN-2001; 2001WO-US19110.
 2000US-212210P
 25-MAY-2001; 2001US-293499P
 (first entry)
 Ruben SM, Barash SC,
 WPI; 2002-114799/15.
 281 AA;
 SS 122
 SS 145
 WO200202641-A1.
 21-MAR-2001;
 16-JUN-2000;
 17-OCT-2000;
 16-MAR-2001;
 Bapiens
 19-AUG-2002
 10-JAN-2002
 ABP45594;
 56
 121
 Sequence
 Query Match
 (CAMB-)
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 RESULT 13
 ABP45594
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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSYDILTGYYTYGMDVWGKGTM 120
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRG---GYKYYGMDVWGQGTT 117
cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABPA 3990-ABPA 1728 represent the antibodies and fragments of the antibodies described in the method
 9
 9
 to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
 Novel humanized, chimeric monoclonal antibody that specifically binds
 1 BYQLVQSGGGLVQPGGSLRLSCAASGFTFSSYAMSWYRQAPGKGQEWYSAISGSGGSTYY
 EVOLVESGGDLVOPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Gaps
 Ξ
 Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.
 Gallo
 3,
 Score 524.5; DB 23; Length 251; Pred. No. 3e-41;
 Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 Corvalan JR,
 11, Indels
 11, Mismatches
 Miller PE, Moyer JD,
 ABG77138 standard; Protein; 124 AA.
 81.7%;
 20-DEC-2001; 2001WO-US51113
 05-JAN-2001; 2001US-259927P
 (first entry)
 Query Match
Best Local Similarity 80.0%
Matches 100; Conservative
 Beebe J,
 (PFIZ) PFIZER INC. (ABGE-) ABGENIX INC
 WPI; 2002-575410/61
N-PSDB; ABS62700.
 118 VTVSS 122
 121 VTVSS 125
 251 AA;
 of the invention.
 atherosclerosis
 WO200253596-A2.
 Homo sapiens.
 24-OCT-2002
 11-JUL-2002.
 Cohen BD,
 ABG77138;
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Claim 13; Page 127; 172pp; English

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61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV 118
artificial antibodies in silico which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenecity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWYRQAPGKGLEWVSAISGSGGSTYY
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
 Human, antibody; preparation; library; VH3; variable region; light chain; heavy chain; V-kappa-2; single chain; consensus
 Length 120;
 Plueckthun
 10; Indels
 81.8%; Score 525; DB 24;
82.0%; Pred. No. 1.2e-41;
ive 10; Mismatches 10;
 Pack P,
 Consensus single chain fragment VH3-V-kappa-2.
 (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 Ge L, Ilag V, Knappik A, Moroney S,
 Location/Qualifiers
 /label= sig_peptide
 mat_peptide
 AAW27560 standard; Protein; 281 AA
 Example 2; Fig 8; 436pp; English
 95EP-0113021
 23-JAN-1998 (first entry)
 Matches 100; Conservative
 WPI; 1997-179277/16.
 Local Similarity
 120 AA;
 N-PSDB; AAT87958.
 119 $$ 120
 121 SS 122
 19-AUG-1996;
 18-AUG-1995;
 варіепв
 WO9708320-A1
 06-MAR-1997
 Sequence
 invention.
 Synthetic
 AAW27560;
 Query Match
 Peptide
 Peptide
 Ношо
 RESULT 12
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 118
 The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of
 120
 Antibody library related heavy variable chain protein region SEQ ID No 4.
 9
 9
 61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCARWGGDG--FYAMDYWGQGTLVTV
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Library; recombinant antibody; clustering variable region; in silico; immunogenecity; antibody therapeutic.
 Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries
 Gaps
 Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures
 The present sequence is the human antibody heavy chain variable region synthetic sequence VH3, used in the preparation of a human derived antibody gene library.
 7
 81.8%; Score 525; DB 18; Length 120;
82.0%; Pred. No. 1.2e-41;
ive 10; Mismatches 10; Indels
 Disclosure; Page 101; 119pp; English.
 ABJ18675 standard; Protein; 120 AA.
 Example 1; Pig 5D; 436pp; English
 17-APR-2002; 2002WO-US12202
 17-APR-2001; 2001US-284407P
 (first entry)
 into structural ensembles
 Matches 100; Conservative
 WPI; 2003-093043/08.
 (ABMA-) ABMAXIS INC
 Similarity
 120 AA
 N-PSDB; AAT87951
 SS 122
 SS 120
 40200284277-A1
 Unidentified.
 06-MAR-2003
 24-OCT-2002
 Sequence
 121
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119

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Query Match Local

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8X222XXXXXXXXX

120

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Gaps

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a cell expressing CCR2. They are useful for inhibiting or treating
HIV infection. The proteins of the invention are useful for inhibiting
leukocyte trafficing, for treating CCR2-mediated disorders such as
leukocyte trafficing, for treating CCR2-mediated disorders such as
inflammatory disorder, autoimmune disorders such as rheumatoid
arthitis and multiple sclerosis, atherogenesis and atherosclerosis,
and for inhibiting restenosis. They are useful in therapy or disgnosis,
and in the manufacture of a medicament for treating CR2-2 mediated
disease. They are also useful for treating allergy, anaphylaxis,
malignancy, chronic and acute inflammation, histamine and IgB-
mediated allergic reaction, shock, stenois, allograft rejection,
fibrotic disease, asthma, inflammatory glomerulopathies, acquired
intervention, including angioplasty and/or stent placement in a mammal.
Humanised antibodies are also useful for inhibiting narrowing of the
lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
a vessel in a mammal, preferably associated with vascular intervention.
The present sequence is human heavy chain variable (VH) region, 038064.
 116
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDIEDTAMFPY-YYGMDVWGQGT 119
 9
 Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWYRQAPGKGLEWYSAISGSGGSTYY
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK----RGRGGYKYYGMDVWGQGT
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Gaps
 .,
 Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; GF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 82.8%; Score 531.5; DB 22; Length 125; 82.5%; Pred. No. 3.1e-42; ive 8; Mismatches 9; Indels 5;
 Amino acid seguence of anti-IGP-1R antibody 2.13.2 Vh domain.
 Corvalan JR,
 Moyer JD,
 ABG77157 standard; Protein; 470 AA
 Cohen BD, Beebe J, Miller PE,
 20-DEC-2001; 2001WO-US51113
 05-JAN-2001; 2001US-259927P
 24-OCT-2002 (first entry)
 Best Local Similarity 82.5
Matches 104; Conservative
 (PFIZ) PFIZER INC. (ABGE-) ABGENIX INC.
 WPI; 2002-575410/61
 120 TVTVSS 125
 117 TVTVSS 122
 Query Match
Best Local Similarity
 125 AA;
 atherosclerosis
 WO200253596-A2.
 Homo gapiens
 11-JUL-2002
 Sequence
 ABG77157;
 RESULT 9
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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for treating cancer in a human. The method for this further involves an antinoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and replastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and invention is also useful for inducing apoptosis of specific cells in a invention is also useful for inducing apoptosis of specific cells in a patibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies and thus increase the represents an anti-insulin-like growth factor I receptor antibody of the
 80 ADSVKGRFTISRDNSRTTLYLQMNSLRAEDTAVYYCAKDLGWSDSYYYYYGMDVWGQGTT 139
 79
 20 BVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMWWRQAPGKGLEWVSAISGSGGTTFY
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR---GRGGYKYYGMDVWGQGTT
 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 3; Gaps
 82.3%; Score 528.5; DB 23; Length 470; 80.8%; Pred. No. 2.5e-41; ive 9; Mismatches 12; Indels 3;
 Plueckthun A;
 Human, antibody; preparation; library; VH3; variable region; heavy chain; consensus.
 Human Ab heavy chain variable region VH3 consensus.
 Pack P,
 (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 Moroney S,
 Claim 16; Figure 19B; 172pp; English.
 AAW27553 standard; Protein; 120 AA.
 96WO-EP03647.
 95EP-0113021
 Knappik A,
 23-JAN-1998 (first entry)
 Best Local Similarity 80.8
Matches 101; Conservative
 118 VTVSS 122
 140 VTVSS 144
 470 AA;
 Ge L, Ilag V,
 19-AUG-1996;
 Homo sapiens
 WO9708320-A1
 .8-AUG-1995;
 AAW27553;
 invention
 Sequence
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 AAW27553
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WPI; 1997-179277/16.

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WO200157226-A1
 Homo sapiens
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 09-AUG-2001
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 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK-RGRGG--YKYYGMDVWGQGTT 117
 61 ADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLGYGDFYYYYYGMDVMGQGTT 120
 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
 9
 9
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 EVQLLESGGGLVQPGGSLRLSCAASGPTPSSYAMSWVRQAPGKGLEWVSAISGSGGITYY
 Gaps
 [solated polypeptide for treatment of diseases, diagnostics, raising
 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; comato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
 Chen R, Asundi V;
 Э.,
 DB 22; Length 384;
 DB 23; Length 125;
 Score 539.5; DB 23; Length
Pred. No. 5.5e-43;
8; Mismatches 9; Indels
 83.7%; Score 537.5; DB 22; Length
78.2%; Pred. No. 2.9e-42;
tive 9; Mismatches 9; Indels
 ou P, Qian XB, Wang Z, Zhang J, Werhman T;
 Human EST encoded protein SEQ ID NO: 1626.
 Claim 20; Page 1102-1103; 1275pp; English.
 AAM24101 standard; Protein; 384 AA.
 antibodies and research use -
84.0%;
84.0%;
 25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
 03-AUG-2000; 2000US-0631451
15-SEP-2000; 2000US-0663870
 25-JAN-2001; 2001WO-US02687
 (first entry)
 Zhou P,
 protein of the invention.
 105; Conservative
 Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
 WPI; 2001-476164/51
Query Match
Best Local Similarity
 VTVSS 122
 VTVSS 125
 384 AA;
 HYSE-) HYSEO INC
 N-PSDB; AAH98760
 WO200154477-A2.
 Ното варіеля
 12-OCT-2001
 02-AUG-2001.
 AAM24101;
 118
 121
 Sequence
 Query Match
 Matches
 AAM2410
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11;

Conservative

Local Similarity

Best Local Sim Matches 104;

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80 ADSVKGRFTISRDNSQNTLYLQMNSLRAEDTAVYYCAKSHPAYYYGSGSYSSHYYYYYGM 139
 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKR-----GRGGYK----YYGM 109
 Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angiolasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; necintimal hyperplasia; VH; heavy chain variable region.
 Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Ë
 O' Keefe
 The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of
 "Complementarity determining region 1"
 5
 /note= "Complementarity determining region 3"
 "Complementarity determining region
 O'Brien S,
 Human heavy chain variable (VH) region, 038064.
 Jones ST,
 Disclosure, Page 168; 183pp; English.
 Location/Qualifiers
 AAE07013 standard, Protein, 125 AA.
 Newman W,
 (MILL-) MILLENNIUM PHARM INC
 50..66
/label= CDR2
 99..114
/label= CDR3
 31..35
/label= CDR1
 02-FEB-2001; 2001WO-US03537.
 03-FEB-2000; 2000US-0497625.
 DVWGQGTTVTVSS 122
 DVWGQGTTVTVSS 152
 (first entry)
 Horvath C,
 'note=
 'note=
 WPI; 2001-488888/53.
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61 ADSVKGRPTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGG---YKYYGMDVWGQGTT 117

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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-IR and can Inhibit in vivo tummour growth and IGF-IR tyrosine with IGF-IR and can inhibit in vivo tummour growth and IGF-IR tyrosine in prosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tummour in a subject. The antibody or its antigen-binding portion is also useful for neoplastic, anti-tummour, anti-anglogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and thus restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a
 patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psorlasis and atherosclerosis. Pully human anti-IGF-IR antibodies minimise the immunogenic and allergic responses intrinsic to mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies. The present sequence represents an anti-insulin-like growth factor I receptor antibody of the
 Germline protein sequence of anti-IGF-1R antibody DP-47(3-23)/D6-19/JH6.
 Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
 cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; lGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.
 Corvalan JR,
 Insulin-like growth factor I receptor; antibody; human;
 Moyer JD,
 Disclosure; Figure 19B; 172pp; English
 ABG77158 standard; Protein; 470 AA
 Cohen BD, Beebe J, Miller PE,
 20-DEC-2001; 2001WO-US51113
 05-JAN-2001; 2001US-259927P
 (first entry)
 (PFIZ) PFIZER INC. (ABGE-) ABGENIX INC
 WPI; 2002-575410/61
 WO200253596-A2.
 Homo sapiens
 24-OCT-2002
 11-JUL-2002
 invention
 ABG77158;
RESULT 5
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Gallo M;

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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II phosphorylation. The antibodies of the invention are useful for application. The antibodies of the invention are useful for audience in a human. The method portion is also useful for treating cancer in a human. The method for this further involves an antineplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and the antibodies may also be useful for increasing IGF-IR activity and transfer sestoring IGF-IR activity in a condition characterised by low invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, adjantism, psoriasis and atheroselerosis. Pully human anti-IGF-IR antibodies minimise the immunogenic and allergic responses intrinsic to mouse of minimise the immunogenic and allergic responses intrinsic to mouse of minimise the immunogenic and allergic responses intrinsic to mouse of mouse desiriations.
80 ADSVKGRFTISRDNSKOVTLYLQMNSLRAEDTAVYYCAKGYSSGWYYYYYYGMDVWGQGTT 139
 efficacy and safety of the administered antibodies. The present sequence represents an anti-insulin-like growth factor I receptor antibody of the
 Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in
 Gallo M;
 Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.
 Insulin-like growth factor I receptor; antibody; human;
cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
GP-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 Corvalan JR,
 Moyer JD,
 Claim 13; Page 130; 172pp; English.
 ABG77142 standard; Protein; 125 AA.
 Miller PE,
 20-DEC-2001; 2001WO-US51113.
 05-JAN-2001; 2001US-259927P.
 (first entry)
 Beebe J,
 (PFIZ) PFIZER INC. (ABGE-) ABGENIX INC.
 growth
 WPI; 2002-575410/61.
 118 VTVSS 122
 125 AA;
 140 VTVSS 144
 N-PSDB; ABS62704
 atherosclerosis
 W0200253596-A2.
 Homo sapiens
 24-OCT-2002
 11-JUL-2002.
 Cohen BD,
 nvention.
 ABG77142;
 Sequence
 humans
 RESULT 6
ABG77142
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3;

DB 23; Length 470;

84.8%; Score 544.5; DB 23; Length 83.2%; Pred. No. 8e-43; ive 9; Mismatches 9; Indels

Best Local Similarity 83.2 Matches 104; Conservative

470 AA;

Sequence

Query Match

20

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1 EVQLVESGGDLVQPGGSLRLSCAASGPTPSNPAMSWVRQAPGKGLEWVAAIGGRSGTTPY

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us-09-674-752-53.rag

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), compirating an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CCR2-mediated disorders such as leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated alignancy, chronic and acute inflammation, histamine and IgE.

C fibrolic disease, asthma, inflammation, histamine and IgE.

C fibrolic disease, asthma, inflammation, sections associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Intervention a mammal, preferably associated with vascular intervention.

The present sequence is human heavy chain variable (VH) region, 038062.
 Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
 Disclosure; Page 168; 183pp; English
WPI; 2001-488888/53
```

128 AA; Sequence

61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGR-----GGYKYYGMDVWGQ 114 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRRNYDFWSGXYYYYGMDVWGQ 120 1 BVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY Gaps 9 85.5%; Score 549; DB 22; Length 128; 82.0%; Pred. No. 7.3e-44; ive 9; Mismatches 8; Indels Query Match
Best Local Similarity 82.0
Matches 105; Conservative 115 GTTVTVSS 122 121 GTTVTVSS 128 셤 ઠે ò

AAE07021 standard; Protein; 125 AA. AAE07021; RESULT 4 

(first entry) 16-OCT-2001

Human; humanised antibody, CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody; neointimal hyperplasia; VH; heavy chain variable region. Human heavy chain variable (VH) region, 4G12.

Ното варіеля

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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating IN infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atheroscelerosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and for inhibiting restenosis. They are useful in therapy or disgnosis, and in the manufacture of a medicament for treating cCR2- mediated disgnosis, and in the manufacture of a mediamentory glomerulopathies, acquired inmunitied allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired inmunitied allergic reaction, shock, stenosis, allograft rejection, fincluding angloplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimin byperplasi of
 117
 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVVRGVISYYYYGMDVWGQGTT 120
 9
 a vessel in a mammal, preferably associated with vascular intervention. The present sequence is human heavy chain variable (VH) region, 4G12.
 Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
 1 BVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSAISGSGGSTYY
 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAK---RGRGGYKYYGMDVWGQGTT
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Gaps
 O'Keefe T;
 'n
 85.3%; Score 547.5; DB 22; Length 125; 84.0%; Pred. No. 9.9e-44; Live 8; Mismatches 9; Indels 3;
 50..66
/label= CDR2
/note= "Complementarity determining region 2"
 /note= "Complementarity determining region 3"
 "Complementarity determining region 1"
 O'Brien S,
 Jones ST,
 Disclosure; Page 171; 183pp; English.
Location/Qualifiers
 Newman W,
 99..114
/label= CDR3
 31..35
/label= CDR1
 (MILL-) MILLENNIUM PHARM INC
 02-FEB-2001; 2001WO-US03537
 03-FEB-2000; 2000US-0497625
 Local Similarity 84.0 nes 105; Conservative
 Horvath C,
 note=
 WPI; 2001-488888/53.
 121 VTVSS 125
 Sequence 125 AA;
 118 VTVSS 122
 WO200157226-A1.
 Larosa GJ,
 Query Match
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Gaps

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61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; returning the tine ficking; allergy; inflammatocy disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a fragment of the human factor VIII antibody heavy chain variable region protein DP-47 which is used in the method of the invention.
 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 "Complementarity determining region 1"
 note= "Complementarity determining region 3"
 Length 122;
 /note= "Complementarity determining region 99..117
/label= CDR3
 O'Brien S,
 Indels
 100.0%; Score 642; DB 21;
100.0%; Pred. No. 1.4e-52;
ive 0; Mismatches 0;
 chain variable (VH) region, 038062.
 Horvath C, Newman W, Jones ST,
 Location/Qualifiers
 Š
 AAE07014 standard; Protein; 128
 /label= Unknown
 (MILL-) MILLENNIUM PHARM INC
 31..35
/label= CDR1
 50..66
/label= CDR2
 03-FEB-2000; 2000US-0497625
 02-FEB-2001; 2001WO-US03537
 16-OCT-2001 (first entry)
 Best Local Similarity 100.
Matches 122; Conservative
 /note=
 122 AA;
 Misc-difference
 SS 122
 SS 122
 WO200157226-A1
 Homo gapiens
 09-AUG-2001
 Human heavy
 Larosa GJ,
 AAE07014;
 121
 121
 Sequence
 Query Match
 Region
 Region
 Region
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 hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has presence of a human antibody with factor VIII specificity which has presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents a human factor VIII antibody A2 specific scPv protein DP-47 which is used in the method of the invention.
 ö
 This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the
 9
 9
 Human; heavy chain; antibody; factor VIII; hemostatic; variable region;
 New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -
 0; Gaps
 Human FVIII heavy chain variable region DP-47 protein fragment.
 Length 122;
 Indele
 ; Score 642; DB 21;
; Pred. No. 1.4e-52;
0; Mismatches 0;
 Turenhout EAM
 (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
 AAY50975 standard; Protein; 122 AA.
 3xample 9; Fig 11c; 61pp; English.
 Example 9; Fig 11A; 61pp; English
 Van Den Brink EN,
 Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 122; Conservative 0
 99WO-NL00285
 98EP-0201543
 (first entry
 WPI; 2000-053102/04.
 122 AA;
 N-PSDB; AAZ43868
 121 SS 122
 SS 122
 Voorberg JJ,
 hemophilia A
 Homo sapiens
 409958680-A2
 07-MAY-1999;
 08-MAY-1998;
 23-MAR-2000
 18-NOV-1999
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AAY50975;

RESULT 2

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Sequence

O'Keefe T;

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Germline protein 8
Anti-IGF-IR antibo
Human EST encoded
Human heavy chain
 Human FVIII antibo
Human FVIII heavy
Human heavy chain
 Amino acid sequenc
 heavy chain
 December 30, 2003, 10:42:39; Search time 39.2461 Seconds (without alignments) 493.415 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:•
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18: /SIDS1/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:•
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:•
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA19999.DAT:•
18: /SIDS1/g
 US-09-674-752-53
642
1 EVQLVESGGDLVQPGGSLRL......GYKYYGMDVWGQGTTVTVSS 122
 Description
 Human Human H
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1107863 segs, 158726573 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 AAYS0973
AAXS0975
AAB07014
AAB07021
ABG77158
AAG77142
AABG7013
ABG77157
 Bw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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 using
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 3223332222
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 Length
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 Query
Match
 100.0
100.0
85.3
85.3
84.8
84.0
83.7
82.8
 Title:
Perfect score:
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539.5
531.5
531.5
 Scoring table:
 Score
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 12 2 4 5 9 7 8 6
 Result
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| Ē            |          | 525                                         |           | 120                  | 18           | A8W27553                     | heavy                                    |
|--------------|----------|---------------------------------------------|-----------|----------------------|--------------|------------------------------|------------------------------------------|
| 7            |          | 525                                         |           | 120                  | 24           | ABJ18675                     | ody 11                                   |
| H            |          | 525                                         |           | 281                  | 18           | AAW27560                     | Consensus single c                       |
| -i -         |          | 0.47c                                       |           | 124                  | ני כ         | ABF43374<br>ARG77138         | 195-1                                    |
| 1 #          |          | 522.5                                       |           | 121                  | 24           | ABP56504                     | n anti                                   |
| Ā;           |          | 522.5                                       |           | 121                  | 24           | ABP56506                     |                                          |
| <b>⊣</b> ∓   |          | 522                                         |           | 117                  | 2 2          | ABF45690<br>AAE12061         | Human arti-tissue                        |
| 1 ~          |          | 521.5                                       |           | 119                  | 22           | AAB62088                     | Human Vh consensus                       |
| Ñ            |          | 521.5                                       |           | 119                  | 22           | AAB60401                     | isus huma                                |
| 21           |          | 521.5                                       | 81.2      | 911                  | 2 2          | AAB61586<br>AA1174541        | Human variable nea<br>Human subdroup V H |
| i (X         |          | 521                                         |           | 222                  | 24           | ABR01515                     | anti-TIM                                 |
| Ň            |          | 520                                         |           | 248                  | 23           | ABP45963                     | Human BLyS binding                       |
| 20.0         |          | 519.5                                       |           | 313                  | 5 5          | AAU14320                     | Human novel protei                       |
| Ñ Ĉ          |          | 519                                         |           | 118                  | 2 C          | AAU83803<br>ABB57561         | MS-GPC-6 neavy cna<br>HLA-DP-specific pr |
| 7 0          |          | 518<br>818                                  |           | 253                  | 2 4          | AB319830                     | 3F-2 r                                   |
| 10           |          | 517                                         |           | 124                  | 55           | AAE07018                     | Human heavy chain                        |
| m            |          | 516.5                                       |           | 121                  | 24           | ABP56507                     | Human anti-Fc-epsi                       |
| 3            |          | 516                                         |           | 177                  | 24           | ABJ36939                     | Anti-CD40 monoclon                       |
| en i         |          | 515.5                                       |           | 221                  | 24           | ABR01534                     | Human anti-TIMP-1                        |
| m            |          | 515.5                                       |           | 253                  | 53           | ABP44978                     | Human BLys binding                       |
| m r          |          | 515                                         |           | 84.2                 | 5 6          | ABP45954                     | Human BLys binding                       |
| m r          |          | 515<br>515                                  |           | 127                  | 2 2          | ABF4489/                     | Synthetic 3-23 VH                        |
| ň ř          |          | * T C                                       |           | 367                  | 24.          | ABP55467                     |                                          |
| m            |          | 513.5                                       |           | 119                  | 33           | AAE28151                     | Human consensus he                       |
| m            |          | 513.5                                       |           | 245                  | 22           | AAB67620                     | leukocyte                                |
| 4            |          | 513                                         |           | 128                  | 18           | AAW06242                     | ıria                                     |
| 4            |          | 513                                         |           | 140                  | 18           | AAW13524                     | Anti-melanoma anti                       |
| 4            |          | 511                                         |           | 122                  | 4.           | AAR30773                     | าธนย ทา                                  |
| ক' ব         |          | 511                                         |           | 128                  | 77           | AAEU / U.L.S<br>ABD4 5420    | Human neavy chain<br>Human Rivs binding  |
| . 4.         |          | 510.5                                       |           | 121                  | 13           | AAW47180                     | Д                                        |
|              |          |                                             |           |                      |              | ALIGNMENTS                   |                                          |
|              |          |                                             |           |                      |              |                              |                                          |
| RESULT       | 1 1      |                                             |           |                      |              |                              |                                          |
| AAY50<br>ID  | 2 3      | 50973 Bt                                    | standard; | d, Protein           | in;          | 122 AA.                      |                                          |
|              |          |                                             |           |                      |              |                              |                                          |
|              | AAY5     | 50973;                                      |           |                      |              |                              |                                          |
| ž E          | 23-MAR   | AR-2000                                     | (£ j      | rst entr             | (X           |                              |                                          |
| ×            | :<br>}   | i                                           |           |                      |              |                              |                                          |
|              | Human    | n FVIII                                     | antibody  | body A2              | 8CFv         | heavy chain protein DP-47    | #2.                                      |
| <b>₹</b> ₹\$ | Huma     | Human; heavy                                | cha       | in; antibody;        | body         | "; factor VIII; hemostatic;  |                                          |
|              |          |                                             | }         | :                    |              |                              |                                          |
|              | Ношо     | sapiens                                     | . 69      |                      |              |                              |                                          |
| žž           | W099     | WO9958680-A                                 | ζ.        |                      |              |                              |                                          |
| ×            |          |                                             | •         |                      |              |                              |                                          |
| <b>교</b> ?   | 18-N     | -NOV-1999                                   |           |                      |              |                              |                                          |
| 7 A          | 07-M     | -MAY-1999                                   |           | 99WO-NL0028          | 285.         |                              |                                          |
| ×            |          | ,                                           |           |                      | •            |                              |                                          |
| P.K          | E-<br>80 | -MAY-1998                                   |           | 98 <i>EP</i> -02015  | 545.         |                              |                                          |
| <b>8</b> 83  | (SANQ-)  |                                             | STICHTING | G SANQUIN            |              | BLOEDVOORZIENING.            |                                          |
| <b>E</b>     | Voor     | Voorberg JJ                                 | ', Van    | n Den Bri            | ink          | EN, Turenhout BAM;           |                                          |
|              | WPI;     | 2000-02                                     | 53102/    | /04.                 |              |                              |                                          |
|              | ;        | •                                           |           |                      |              |                              |                                          |
|              | pres     | new polynucieotide,<br>presence of neutrali | neut      | de, poly<br>ralizino | pept<br>Jant | <b>ಶ</b>                     | and for                                  |
|              | trea     |                                             | of hem    | ophilia              | A pa         | itients with these antibodie | . 8                                      |

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 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTVTV 120
 20 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY 79
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 1 EVOLVESGGDLVOPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 Gaps
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 7;
 69.9%; Score 448.5; DB 11; Length 479; 70.5%; Pred. No. 1.6e-36; ive 15; Mismatches 14; Indels 7;
 Submitted (SE-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC013656; AAH13656.1; -...

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003506; Ig-v.

Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS00290; IG_MC; 2.

Hypothetical protein.

SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
 Straubberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004786, AAH04786.1; -.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR033006; Ig MHC.
InterPro; IPR03306; Ig_V.
 Pfam; PF00047; 1g; 4. -5-
SMART; SM00406; IGv; 1.
PROSITE; PS50035; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 2.
Hypothetical protein.
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 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC+2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.6 kba protein.
Mus musculus (Mouse).
 487 AA
 479 AA
 PRT;
 PRT;
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 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 (1)
SEQUENCE PROM N.A.
 NCBI_TaxID=10090;
 SS 122
 SS 134
 Strausberg R.;
 133
 121
 Query Match
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 Q91WP5
 RESULT 15
RESULT 14
 97,4419
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 20 BVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWYRQTPEKRLEWVATISDGGSYTYY 79
 1 EVOLVESGEDLYOPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 4; Gaps
Length 487;
 21; Indels
Query Match 68.4%; Score 439; DB 11;
Best Local Similarity 68.8%; Pred. No. 1.4e-35;
Matches 86; Conservative 14; Mismatches 21;
 Search completed: December 30, 2003, 11:01:10 Job time : 30.7319 secs
 118 VTVSS 122
 139 ITVSS 143
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PRELIMINARY;
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 Query Match
 Query Match
 Q9UL84
 Matches
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 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKY-----YGMDVW 112
 80 ADSVKGRPTISRDNAKNSLYLQWNSLRVEDTALYYCA---RDPTKYCSGGSCLGYYMDVW 136
 9
 20 EVQLVESGGGVVRPGGSLRLSCATSGFTFDDSGASWVRQAPGKGLEWVSSINWNGGSTNY 79
 Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
"An antibody fragment2A3 specific for native lysozyme :Isolaion from a human synthetic phage display library and characterization.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049915; BAB16829.1; --
HSSP; P01772; 2PB4.
 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
 11; Gaps
 O9HCC1
O1HAR-2001 (TEMBLrel. 16, Created)
O1-MAR-2001 (TEMBLrel. 16, Last sequence update)
O1-MAR-2003 (TEMBLrel. 13, Last annotation update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
Single chain Fv (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Query Match 71.3%; Score 457.5; DB 4; Length 499; Best Local Similarity 70.0%; Pred. No. 2.1e-37; Matches 91; Conservative 12; Mismatches 16; Indels 11
 TISGUE-BLOOd;

TISGUE-BLOOd;

Strausberg R.;

Strausberg R.;

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPR003299; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003597; Ig.

R InterPro; IPR003597; Ig.

R InterPro; IPR003596; Ig.

R SMART; SM00409; IG; 4.

R SMART; SM00409; IG; 4.

R SMART; SM00409; IG; 4.

R SMART; SM00409; IG; 1.

R PROSITE; PS00390; IG.MLC; 1.

R PROSITE; PS00390; IG.MLC; 1.

R PROSITE; PS00390; IG.MC; 1.

R PROSITE; PS00290; IG.MC; 1.
 Q8NSK4;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
 499 AA
 PRELIMINARY;
 113 GQGTTVTVSS 122
 137 GKGTTVTVSS 146
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
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 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus":
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035030; AAD5266.1; -
HSSP; P0172; 2FB4.
InterPro: IPR00110; 1g-like.
InterPro: IPR003006; 1g-MtC.
InterPro: IPR003596; 1g-V.
SMART; SM00406; IGy.1.
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                       Ouery Match
71.0%; Score 456; DB 4; Length 112;
Best Local Similarity 72.0%; Pred. No. 4.5e-38;
Matches 85; Conservative 14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; Score 453; DB 4; Length 122; 74.6%; Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00147; Ig_V.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 11 112
NON_TER 112 112
SEQÜENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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Best Local S
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Q9Y509;
Q1-NOV-1999
O1-NOV-1999
O1-MAR-2003
VH3 protein
VH3.
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NON TER
SEQUENCE 147 AA
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MEDLINE=96071149; PubMed=7475288;

Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C

Lichtenstein A.K., Berenson J.R.;

"A CD10-positive subset of malignant cells is identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                   Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
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                                                                                                                                      MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                          Young D.C.;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                    (Fragment)
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Immunol. Immunopathol. 87:184-192(1998)
AF035024; AAD56260.1; -.
P01772; 2FB4.
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90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;
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71.4%;
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Last sequence update)
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Pred. No. 2e-38;
9; Mismatches
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                                                                                                                                                Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

NON_TER 113 113

NON_TER 113 113

SEQUENCE 113 AA; 12437 MW;
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
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Q9UL93;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Myosin-reactive immunoglobulin heavy chain variable
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InterPro;
InterPro;
                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AP035021; AAD56257.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
DEGE: DEGO.77. (2.1)
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                               92;
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 S 122
                           DSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVMGQGTTVTVS 121
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                                                                                     VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA
                                                                                                      VQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                                        116 AA;
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12437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
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76.0%;
                                                                                                                                                                                                          12434 MW;
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                                                                                                                                              Score 459.5; DB 4;
pred. No. 2.1e-38;
8; Mismatches 16;
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Pred. No. 2.1e-38;
9; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                           0DA0348154DD6061 CRC64;
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EMBL; BC020240; AAH20240.1; -.
InterPro; IPR0031016; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL91
Q9UL91;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WUK1;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98277139; PubMed=9614934;
MEDLINE-98277139; PubMed=9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo mapiens (Human)
Eukaryota, Metazoa, Chordata,
Mammalia; Eutheria, Primates;
   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                          EMBL; AF035023; AAD
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis fetus.";
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llarity 73.8%;
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; Pred. No. 6e-38;
11; Mismatches 19
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RC TISSUE-Mammary gland;

RI ISOGAI T., Otauki T., Suzuki Y.,

RA IISOGAI T., Otauki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Cono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Wamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

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RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

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RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Nakamura M.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Naka Y.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Nakamura M.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., N
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Best Local S
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Matches 89
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical protein FLJ14473.
Homo sapiens (Human)
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89; Conservative
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                                                                                                                                 RDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCARDSCNGAICYGFSPWGQGTLVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                          72.1%;
71.3%;
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73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 463; DB 4; 1
Pred. No. 5.8e-38;
L4; Mismatches 21;
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Pred. No. 9.7e-39;
3; Mismatches 15
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InterPro; IPR003006; Ig_-like.
InterPro; IPR003006; Ig__wC.
InterPro; IPR003596; Ig__v.
Pfam; PF00047; ig; 5.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
PROSITE; PS00290; IG_MHC; 3.
SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96BB9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                Q9UL71 PRELIMINARY; PRT; 121 AA.
Q9UL71;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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                                                                                                                        NCBI
                                                  SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Homo sapiens (Human).
                                      "Myosin-reactive autoantibodies in rheumatic carditis
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Immunol. Immunopathol. 87:184-192(1998) AF035043; AAD56279.1; -.
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                                                               P.L., Kalis N.N.,
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Best Local S
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Best Local S
Matches 88
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC024289; AAN24289.1; -.

R InterPro; IPR007110; Ig-1ike.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 4.

R Pfam; PF00046; IGV; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS0085; IG_LIKE; 4.

R PROSITE; PS00290; IG_MHC; 2.

W Hypothetical protein.

NW Hypothetical Protein.
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01-JUN-2002
01-MAR-2003
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SMART; SM00406; IGV; 1.
SROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Butheria;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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InterPro; IPR00711
InterPro; IPR00300
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Homo sapiens (Human)
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SS
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                                                                                         ADSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLRQLTSYWYFDLWGRGTLVTV
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2 (TrEMBLrel. 21,
3 (TrEMBLrel. 23,
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121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
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  141
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Primates;
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                                                                                                                                                                                                                                                                         73.2%; Score 470; DB 4; 72.1%; Pred. No. 1.1e-38; tive 18; Mismatches 16
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4: sp_human:*
5: sp_invertebrate
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Q8WCY7
Q8WCY1
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336	338	338	339	342	347.5	349.5	351.5	352.5	356	359.5	365	368	369	375.5	381	384	384.5	391	394	395	399.5	402.5	413.5	416	417.5	418.5	433	435
52.3	52.6	•	•	53.3		54.4	54.8	54.9	55.5	56.0	56.9	57.3	57.5	58.5	59.3	59.8	59.9	60.9	61.4	61.5	62.2	•	64.4	4	5	5	67.4	67.8
121	145	145	116	145	117	473	484	119	500	125	124	124	124	104	437	159	112	298	95	484	521	486	131	469	480	493	473	118
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Q99NG4	Q924R4	Q924R1	Q9UL89	Q924P7	Q9QXE9	Q9D8L4	Q99LA6	Q9UL94	Q9BRV0	Q9UL95	O9NOW6	Q9NOW4	Q9UL92	Q9UL87	Q9R1A4	Q96QS0	Q9UGP3	Q9QYF0	Q9ULB6	Q8VEA0	Q8N4Y9	Q91Z07	Q9UL88	Q8R3V9	Q91XE1	QBNCL6	Q91Z05	Q9UL72
Q99ng4 mus musculu	Q924r4 mus musculu	Bnu	O O O	Q924p7 mus musculu	Bn			OWO		Q9ul95 homo sapien	Q9n0w6 oryctolagus	Q9n0w4 oryctolagus	homo	O M O	4 mus	homo	-		-	enm 0	_	7 mus	homo	mug		-	Q91z05 mus musculu	Q9ul72 homo sapien

ALIGNMENTS

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Best Local S
Matches 99
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC021276; AAH21276.1; -.
R InterPro; IPR007110; Ig-1ike.
R InterPro; IPR00306; Ig_MHC.
R InterPro; IPR00306; Ig_V.
R Pfam; PP00047; 1g; 4.
R Pfam; PP00047; 1g; 4.
R SMART; SM00406; IGV; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS05035; IG_LIKE; 2.
R PROSITE; PS05030; IG MHC; 2.
W Hypothetical protein.
Q SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBWUJS, PRELIMINARY; PRT; 573 AA.

OBWUJS, O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
 80
                                61
                                                                 20
                                                                                                                                 99;
                                                                                                                                               Similarity
                                                                                    EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
                  ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGY--KYYGMDVWGQGTTV 118
                                                                 EVQLVESGGGLVQPGRSLRLSCAASGPTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY 79
 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKHGSGSYIGYYYGMDVWGQGTTV 139
                                                                                                                                 Conservative
                                                                                                                               80.2%; Score 515; DB 4; Length 573; 79.8%; Pred. No. 4.4e-43; tive 9; Mismatches 14; Indels
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HV21-MOUSE
ID HV21-I
AC P0175
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AC P0176
DT 21-U
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HV18 MOUST
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DT 21-JI
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P01790;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upd:
15-SEP-2003 (Rel. 42, Last annotation upd:
15 heavy chain V region M511.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01789; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                           P01787;
P01787;
P01787;
P01787;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
-- heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
                                                                                                                                                                                                                                                                                                                                                                                      WOUSE
                               SEQUENCE (TEPC 15).

MEDLINB=7622762; PubMed=819932;

Rudikoff S., Potter M.;

"Size differences among immunoglobulin heavy chains phosphorylcholine-binding proteins.";

Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                                                                                                                                                                                                     Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3. Mus musculus (Mouse). Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NON_TER
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Robinson E.A., Appella E.;
"Complete amino acid sequence of a mouse immunoglobulin alpha (MOPC 511).",
Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  SEQUENCE FROM N.A. (H107).
                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSG--TT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains 1 immunoglobulin-like domain
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Search completed: December 30, Job time: 7.54102 secs

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R InterPro; IPR003006; Ig_wHC.

R Pfam; PF00047; ig; 1.

R SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin v region; Hybridoma.
DOMAIN
NON TER 123 123
SEQUENCE 123 AA: 13777 ***
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MEDLINE=81197602; PubMed=7231520;

Gearhart P.J., Johnson N.D., Douglas

"IgG antibodies to phosphorylcholine
their IgM counterparts.";

Nature 291:29-34(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-76110488; PubMed-813561;
Rudikoff S., Barstad P., Potter M., H.
Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE
-i- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM
- HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
-i- SIMILARITY: Contains 1 immunoglobulin-like doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80199926; PubMed=6769593;
Early P., Huang H., Davis M., Calame K., Hood I
"An immunoglobulin heavy chain variable region
three segments of DNA: VH, D and JH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A93804; AVMST5.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 19:981-992(1980).
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                                                                                                                                                                                                                                                                                                                                                th 65.5%;
Similarity 68.5%;
85; Conservative 1
   SSVT
                                                                                                               EYSASVKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCA-RDYYGSSYWYFDVWGAGTTV
                                                                                                                                                                                                                                                                        EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSG--TT
                                                         TVSS 122
                                                                                                                                             FYADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTTV 118
                                                                                                                                                                                                                                 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKANDYTT
123
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13777 MW; 9D58086DE12F7000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                Score 420.5; DB 1;
Pred. No. 3.2e-36;
l3; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE.
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RESULT 12
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ID HV3J-HUMAN
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Best Local
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GO; GO:0003823; F:antigen binding activit
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
InterPro; IPKUU---
Pfam; PF00047; ig; 1.
Pfam; PF00046; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V 1 11 IG-LIKE.

1 11 PYRROLIDONE CARBOXYLIC
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NON_TER
SEQUENCE
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P01771;
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ଜ୍ୟୁ ନ୍ଦ୍ର
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
'Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:553-560(1979).
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region HIL.
Homo sapiens (Human)
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                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; P:antigen binding actions; GO; GO:0006955; P:immune response; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A.,
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HSSP; P01772; 2FB4.
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SIMILARITY: Contains 1 immunoglobulin-like domain.
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122 AA;
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13166 MW; 74E5B6959E84100A CRC64;
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                                                                IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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Best Local S
Matches 82
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin v region.
DOMALN 1 112
NON_TER 119 119
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Rao D.N., Rudikoff S., Krutzsch H., Potter M.;

Rad D.N., Rudikoff S., Potter M.;

Rad D.N., Rudikoff S., Rudikoff S., Potter M.;

Rad D.N., Rudikoff S., Rudikoff S., Potter M.;

Rad D.N., Rudikoff S., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                       EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYMMSWVRQAPGKGLEWIGEINPDSSTINY
                                                                                                                                                        EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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119
119 AA;
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13566 MW;
                                                                                                                                                                                                                                                                                                      13169 MW;
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67.2%;
                                                                                                                                                                                                                     65.7%; Score 422; DB 1; Lt 66.7%; Pred. No. 2.1e-36; 66.7%; mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 427.5; DB
; Pred. No. 6e-37;
12; Mismatches
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region.

DOMAIN 1 11

NON TER 120 120

SEQUENCE 120 AA; 13227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra J.D., Hopper J.E.;

"Comparative studies on monotypic IgM lambda and IgG kappa from an individual patient. III. The complete amino acid sequence of the V region of the IgM paraprotein.";

Immunochemistry 13:995-999(1976).

-i- MISCELLANGOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region BRO.
Homo sapiens (Human).
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GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006555; P:immune response; NAS.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                EVQLVESGGGLVQPGGSLRLSCAASGFTFSYYNMMVRQVTGKGLEWVSAI-GTAGDQYY
                                                                                                                                                                                                                                                          EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQAPGKGLEWVAAIGGRSGTTFY
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Pred. No. 1.7e-37;
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SEQUENCE
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid

DOMAIN

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TOTALIKE.

CARBOXYLIC
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PIR; A02046; MHHUWE.
HSSP; P01772; 2F84.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0005825; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003396; Ig_W.
SEQUENCE.

MEDLINE=74175307; PubMed=4208843;

Plorent G., Lehman D., Putnam P.W.;

"The switch point in mu heavy chains
Biochemistry 13:2482-2498(1974).
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-SEP-2003 (Rel.
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114 AA;
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01, Last sequence update)
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12256 MW; D88294FB418A07B7 CRC64;
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2.4e-37;
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Matches 86; Conserv
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
PFAm; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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NON_TER
SEQUENCE
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Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-i- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P01772; 2FB4.
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122 AA;
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HV3K HUMAN
P01772;
21-JUL-1986
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PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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  13718 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
SWART; SM00406; IGv; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN
1 112
IG-LIKE.
                                                          MEDLINE-78137069; PubMed=416441;
Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain gaz immunoglobulin of the A2m (2) allotype.";
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
-i- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALREGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 heavy chain V-III region BUT.
Homo sapiens (Human)
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Proc. Natl. Acad. Sci. U.S.A. 77:339-3243(1980).
-i- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PATIENT WITH MACROGLOBULINEMIA.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates;
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                 SIMILARITY: Contains; A02050; A2HUBU.
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GO:0003823; F:antigen binding activ
GO:0006955; P:immune response; NAS.
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122 AA;
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                                         immunoglobulin-like
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Pred. No.
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PYRROLIDONE CARBOXYLIC ACID.
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Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
DOMAIN
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1975) to
-!- MISCELLANEOUS: THIS
MACROGLOBULIN.
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15-SEP-2003 (Rel. 42, Last a
17 heavy chain V-III region
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                     Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding
GO; GO:0006955; P:immune response;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                           - |- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISION TO 28-33.
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21-JUL-1986
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  116 AA;
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42, Last annotation update)
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Pred. No. 3.3
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-III region VH26 precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region.",
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                   DOMAIN
NON TER
SEQUENCE
                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regin; Signal; 3D-structure.
                                                                                                                                                                    Genew; HGNC:5545; IGHV@.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003833; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003059; Ig_W.
                                                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=81101090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                    PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
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EMBL; M35415; AAA58735.1; -.
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85.7%;
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 Score 453; DB 1; 1
Pred. No. 1.4e-39;
9; Mismatches 5;
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                         Length 117;
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P01765;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003066; Ig_V.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977)
-i- MISCRLLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V-III region TIL.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang A.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=78005528; PubMed=409716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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12356 MW;
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73.0%;
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Pred. No. 8.1e-39;
9; Mismatches 17
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-HV3G HUMAN P01768; 21-JUL-1986 21-JUL-1986 15-SEP-2003

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Last sequence update)

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Gapop 10.0 , Gapext 0.5
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642
1 EVQLVESGGDLVQPGGSLRL......GYKYYGMDVWGQGTTVTVSS 122
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Copyright (c) 1993 - 2003 Compugen Ltd.
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      DB
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78 115	16 136 119 136	15290.1; 21. 21. 10:95.11ke 10:96; Ig_MHC. 96; Ig_v. 96; Ig_v. 96; I. Gv; 1. IG LIKE; 1 regin; Sign	ry is or Institution institution institutions institutions itatemen licens	ubMed=4 in C., of spo 1977).	ubMed= skind le reg	1, Created 1, Last 86 2, Last ar 2, Last ar gion MOPC (), Chordata, Rodentia	DARD;	113 117 118 119 119 113 113 117 119 119 119 119 113 113 113 113 113 113
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Search completed: December 30, 2003, 11:03:20 Job time : 11.6946 secs
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R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23624
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31114
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A;Molecule type: DNA
A;Residues: 1-143 <OLE>
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A; Residues: 1-123 < RAA>
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fan

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Ig heavy chain V region (M43) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: D36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: D36005
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A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
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Ig heavy chain V region -
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A;Map position: 14q32.33-14q32.33
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(;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin pomology < MM>
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A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
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A;Cross-references: GDB:118731; OMIM:146910
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Pred. No. 1.1e-37;
9; Mismatches 18
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 331686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Bescription: Mechanisms that generate human immunoglobulin diversity operate from A;Reference number: S31686
A;Accession: S31686
A;Status: preliminary
A;Status: preliminary
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-140 < CUI>
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Best Local Similarity 76.8%; Pred. No. 1.4e-37;
Matches 96; Conservative 13; Mismatches 11
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 138 VSS 140
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                                                                         SDSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYYCAKCPFAGGSPSF--DYWGQGTLVT
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                              77.0%; Score 494.5; DB 2
78.9%; Pred. No. 3.1e-37;
ative 11; Mismatches 12
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Ig heavy chain - human C;Species: Homo sapiens (man) C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

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A;Accession: C36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: GB.M18513
A;Cross-references: GB.M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: (06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38499
C;Accession: S38499
R;Marke, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a A;Reference number: S38488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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S38489
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C;Accession: S31108
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Pred. No. 7.6e-38;
LO; Mismatches
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Pred. No. 1.8e-38;
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C;Accession: B36005
R;Schroeder Jr., H.W.; Wang, J.Y.
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 18
A;Title: Preferential utilization of conserved
A;Reference number: A36005; MUID:90349571; PMII
A;Accession: E36005
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R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity
                                                                                                              Ig heavy chain V region (M72) - human C;Species: Homo sapiens (man) C;Date: 21-Dec-1990 #sequence_revision
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A; Residues: 1-140 < CUI>
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A;Reference number: S31589
A;Accession: S31588
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A;Molecule type: DNA
A;Residues: 1-127 <MAR>
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78.9%;
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74.8%;
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Pred. No. 1.1e-37;
1; Mismatches 12
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Pred. No. 8.1e-38;
1; Mismatches 14
                                                                                                                    21-Dec-1990
                      rved immunoglobulin heavy PMID: 2117273
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A;Molecule type: mRNA
A;Residues: 1-147 <RES>
A;Residues: 1-147 <RES>
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31666
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585
A;Accession: S31666
A;Status: preliminary
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                                                                                       C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin P;34-117/Domain: immunoglobulin homology <IMM>
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Eur. \bar{J}. Immunol. 22, 247-251, 1992 A; Title: Restricted utilization of germ-line V(H)3 genes and A; Reference number: S31104; MUID:92111633; PMID:1730252
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A; Residues: 1-138 < CUI>
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Pred. No. 1.4e-39;
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Pred. No. 4.9e-39;
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Ig heavy chain V region (30p1) - human (55pecies: Homo sapiens (man) (75pecies: Homo sapiens (man) (75pecies: 1-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996 (7)Accession: C36005 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
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submitted to the EMBL Data Library, October 1994
A; Description: Molecular characterization of natural human
A; Reference number: S48797
A; Accession: S48798
A; Status
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: mRNA A;Residues: 1-119 <RAA>
RESULT
C36005
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A;Residues: 1-120 <MANA
A;Cross-references: EMBL: 246382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IVM>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S48798
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Pred. No. 9.7e-39;
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Pred. No. 1.3e-38;
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Maximum Match 100%
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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2: pir2:*
3: pir3:*
4: pir4:*
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          GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Ig heavy chain pre
Ig variable region
Ig heavy chain v r
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Qy 118 VTVSS 122 Db 140 VTVSS 144	OY 61 ADSVKGRFTISRDNSKNTVYLEMNSLRAEDTAIYYCAKRGRGGYKYYGMDVWGQGTT 117	OY 1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFAMSWVRQADGKGLEWVAAIGGRSGTTFY 60 :	Query Match 85.3%; Score 547.5; DB 2; Length 160; Best Local Similarity 84.0%; Pred. No. 6.5e-42; Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;	A;Molecule type: mRNA A;Residues: 1-144 <kisq> A;Residues: 1-144 <kisq> A;Cross -references: EMBL:X14584 A;Cross -references: EMBL:X14584 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <sig> F;20-160/Product: Ig heavy chain (fragment) #status predicted <mat> F;34-117/Domain: immunoglobulin homology <imm></imm></mat></sig></kisq></kisq>	A;Cross-reterences: MML:X.14584 R;Ktishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M. Nucleic Acids Res. 17, 4385, 1989 A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains A;Reference number: S04601; MUID:89296497; PMID:2500644 A:Accession: S04602	submitted to the EMBL Data Library, March 1989 A;Reference number: 805270 A;Accession: 805271 A;Molecule type: mRNA A;Residues: 1-160 <kis1></kis1>	RESULT 1 905271 Ig heavy chain precursor - human (fragment) C;Species: Homo sapiens (man) C;Species: 0-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996 C;Accession: S05271; S04602 R;Kishimoto, T.	ALIGNMENTS	3 462.5 72.0 121 2 331106 Ig heavy chain 4 462 72.0 145 2 311239 Ig heavy chain 5 461.5 71.9 119 2 P36005 Ig heavy chain	0 464.5 72.4 127 2 S19878 Ig heavy chain V 464 72.3 139 2 S31674 Ig heavy chain V 2 462 5 72.0 121 2 S31104 Ig heavy chain V	467 72.7 136 1 GIMS21 Ig heavy chain pr 466.5 72.7 12 S19666 Ig heavy chain v 465.7 72.4 139 2 S38808 Ig heavy chain -	4 469 73.1 141 2 S31669 IG heavy cha 5 467 72.7 108 2 PH1648 IG heavy cha 6 467 72 7 128 2 S36790 IG heavy cha	1 470 73.2 128 2 831595 Ig heavy chain 2 469.5 73.1 117 2 878486 Ig heavy chain 3 469 73.1 140 2 870442 Ig heavy chain	0 470.5 73.3 134 2 831679 Ig heavy chain V
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of.

Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
R;Demalson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

RESULT 2

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                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Plapy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
FRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 926318.9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9525004.9
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
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APPLICATION NUMBER: GB 9610824.6
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Query Match
Best Local Similarity
                                                                                                                                                                  INFORMATION
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amin
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APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                               TYPE: amino acid
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77.2%;
Score 470.5; DB 2; Length 123; Pred. No. 2.1e-41;
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South Wacker Drive
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Search completed: December 30, 2003, 11:05:36
Job time : 11.6593 secs
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                                                      121
                                                                                 112
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                                                                                                                                                                                                                   95;
                                                                                                                                                                                1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY
                                                      VSS 123
                                                                               VSS 114
                                                                                                          AQKFQGRLTITADESTSTAYMELSSLRSEDTAVYYCAGANSCNRSYYYYMDVRGQGTMVT 120
                                                                                                                                                               QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNSPINWLRQAPGQGLEWMGSIIPSFGTANY
                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                  60
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842

FD-2630

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PCT-US93-10555-13
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GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 90667
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 1
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FD. TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
PILING DATE: 29-OCT-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: 811
TOPOLOGY: linear
MOLECULE TYPE: pepi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KBY: Peptide LOCATION: 1..120
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILVERMAN, GREGG J.

VENTION: METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                      FD-2630
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                                                                                                                                                                                                                                                                                                            Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
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                                                                                                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10
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; LOCATION: 1..120
PCT-US93-10555-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10,
                                                           Matches
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                                                                                        Query Match
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                                                                                                                                                                         TELBEAX: (202) 783-631
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952
PILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: ROTHWELL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDYGRPFDFWGQGTLVTVSS 120
                                                           92;
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5876961
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QMQVVQSGABVKKPGSSVTVSCKASGGTESNYAISMVRQAPGQGLEMMGGIIPLFGTPTY
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555 THIRTEENTH ST. N.W.
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78.3%;
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                                                           11; Mismatches
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                                                        Score 471.5; DB 2;
Pred. No. 8.4e-41;
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RESULT 11
US-08-428-197-13
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Patent No. 5891438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: WETHOD FOR
TITLE OF INVENTION: VARIABLE R
TITLE OF INVENTION: VACCINATIO
TITLE OF INVENTION: THEREOF
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: Spensley
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TITLE OF INVENTION:
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                                                                        NUMBER OF SEQUENCES: 5
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LOCATION:
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STATE: California
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                                                          ADDRESSEE:
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Los Angeles
California
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1880 Century Park East - Suite
                                   E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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79.2%;
                                                                                                                  WETHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 474.5; DB 2; Length Pred. No. 8e-42; Indels
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; LOCATION:
US-08-428-197-13
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CURRENT APPLICATION NUMBER: PCT/US93/10cc PILING DATE: 29-007
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US9:
PILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 120 amino acid
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TITLE OF INVENTION:
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ZIP: 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                          STREET:
                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEGYGDYGRPFDFWGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANYA 60
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California
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                                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9310555
                                                                                                                                                                                                          B: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite!
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                                                                                                                                                                                                                                                                              SILVERMAN, GREGG J.

SILVERMAN, GREGG J.

VENTION: METHOD FOR STIMULATING PRODUCTION OF VENTION: VARIABLE REGION GENE FAMILY RESTRICTED VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN
                                                                                                                                                               USA
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78.3%;
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Pred. No. 8e-42;
7; Mismatches
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AND CONJUGATES
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US-08-232-0818-41
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                                                                     US-08-983-607-50
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GENERAL INFORMATION:
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Best Local Similarity
                               Sequence 50, Application US/08983607 Patent No. 6140470
                                                                                                                                                                                                                                                                                                                                                             Matches
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INFORMATION FOR SEQ ID NO: 41:
              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
MOLECULE TYPE: pepti
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acid
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NAME: SVENSSON, LECNARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKST NUMBER: 20-3484
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDBYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
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                                                                                                                                                                                                                                  AQKFQGRVTITADESTSTAYMELSTLTSEDTAVYYCELDW------FYIWGQGTMVTVS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 amino acids
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linear
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77.71;
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Pred. No. 5.1e-42;
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Sequence 12, Application US/084281 Patent No. 5891438 GENERAL INFORMATION: APPLICANT: SILVERMAN, GREGG J. TITLE OF INVENTION: METHOD FOR

METHOD FOR STIMULATING PRODUCTION OF

Application US/08428197

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RESULT 10
US-08-428-197-12
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                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MATY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 203-773-1183 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRILING DATE: June 28,
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fUSE5
LIBRARY: fusion phage construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOPTWARE: Word Processing
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Human J
TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: fur
CLONE: 2-71
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens (melanoma patient ORGANISM: immunized with autologous tumor cells) INDIVIDUAL ISOLATE: petiberal blood lympho-INDIVIDUAL ISOLATE: cytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United ZIP: 06520-8114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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                                                                                                   68 VTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFYIWGQGTMVTVSS 114
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                                                                                                                                                                             8 GABVKKPGSSVKVSCKASGGTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNYAQKFQGR 67
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                                                                             VTITADKSTSTAYMELSSLRSEDTAVYYCARGGGRYDAFDIWGQGTLVTVSS 119
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                                                                                                                                                                                                                                                                                                                                 heavy chain
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N: 435
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                                                                                                                                                                                                                                 Score 474.5; DB Pred. No. 8e-42; 4; Mismatches
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                                                                                                                                                                                                                                                                         DB 3;
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